Supplementary Online Content

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eTable 1. Description of Study Cohort (n = 426) by Year Tested

eTable 2. Frequency of Individuals With Diagnostic Variants, Categorized by Ethnicity and Causative Genes

This supplementary material has been provided by the authors to give readers additional information about their work.
### Table 1. Description of Study Cohort (n = 426) by Year Tested

| Demographics                  | 2019, n=92 | 2020, n=201 | 2021, n=128 |
|-------------------------------|------------|-------------|-------------|
| Age, median (range), years    | 7 (0-18)   | 7 (0-18)    | 10 (0-18)   |
| Gender                        |            |             |             |
| - Female                      | 45 (48.9)  | 106 (52.7)  | 48 (37.5)   |
| - Male                        | 47 (51.1)  | 95 (47.3)   | 79 (61.7)   |
| - Trans                       | 0 (0)      | 0 (0)       | 1 (0.8)     |
| Under-represented minority    |            |             |             |
| - URM                         | 63 (68.5)  | 147 (73.1)  | 91 (71.1)   |
| - Not URM                     | 27 (29.4)  | 52 (25.9)   | 35 (27.3)   |
| - Declined to state           | 2 (2.2)    | 2 (1.0)     | 2 (1.6)     |
| Race/Ethnicity^               |            |             |             |
| - Hispanic                    | 32 (34.8)  | 101 (50.3)  | 61 (47.7)   |
| - Asian                       | 13 (14.1)  | 30 (14.9)   | 22 (17.2)   |
| - Black                       | 5 (6.5)    | 18 (9.0)    | 10 (7.8)    |
| - White                       | 26 (28.3)  | 57 (28.4)   | 22 (17.2)   |
| - Other                       | 22 (23.9)  | 29 (14.4)   | 23 (18.0)   |
| Primary language              |            |             |             |
| - English                     | 56 (60.9)  | 116 (57.7)  | 79 (61.7)   |
| - Spanish                     | 22 (23.9)  | 57 (28.4)   | 34 (26.6)   |
| - Mandarin, Cantonese         | 3 (3.3)    | 6 (3.0)     | 5 (3.9)     |
| - American Sign Language      | 2 (2.2)    | 7 (3.5)     | 0 (0)       |
| - Other language              | 9 (9.8)    | 15 (7.5)    | 10 (7.8)    |
| Insurance                     |            |             |             |
| - Private                     | 31 (33.7)  | 45 (22.4)   | 35 (27.3)   |
| - Public                      | 61 (66.3)  | 155 (77.1)  | 92 (71.9)   |
| - None                        | 0 (0)      | 1 (0.5)     | 1 (0.8)     |
| Comorbidities                 |            |             |             |
| ICD-10 codes, median (range)  | 1 (0-25)   | 2 (0-40)    | 2 (0-25)    |
| ICD-10 organ systems involved, median (range) | 1 (0-5) | 1 (0-9) | 0 (1-10) |
| ASA score, mode (range)       | 2 (1-4)    | 2 (1-4)     | 2 (1-4)     |
| Audiologic Data               |            |             |             |
| Age at identification         |            |             |             |
| - Early identification (failed NHS) | 35 (38.0) | 85 (42.3)  | 54 (42.2)   |
| - Late identification (passed NHS) | 34 (37.0) | 56 (27.9)  | 38 (29.7)   |
| - Late discovery (unknown NHS) | 23 (25.0) | 60 (29.9)  | 26 (28.1)   |
| Characterization of HL        |            |             |             |
| - Progressive                 | 28 (30.4)  | 41 (20.4)   | 28 (21.9)   |
| - Stable                      | 64 (69.6)  | 160 (79.6)  | 100 (78.1)  |
| Laterality of HL              |            |             |             |
| - Unilateral                  | 20 (21.7)  | 41 (20.4)   | 28 (21.9)   |
| - Bilateral                   | 72 (78.3)  | 160 (79.6)  | 100 (78.1)  |
| Type of HL*       |       |       |       |
|------------------|-------|-------|-------|
| - Sensorineural   | 74 (80.4) | 154 (76.6) | 108 (84.4) |
| - Conductive     | 4 (4.4) | 7 (3.5) | 5 (3.9) |
| - Mixed          | 8 (8.7) | 16 (8.0) | 8 (6.3) |
| - Neural         | 6 (6.5) | 8 (4.0) | 4 (3.1) |
| - Unspecified    | 7 (7.6) | 22 (11.0) | 6 (4.7) |

| Severity of HL   |       |       |       |
|------------------|-------|-------|-------|
| - PTA better ear, median (range), dB | 30 (0-120) | 30 (1-116) | 34 (0-120) |
| - PTA worse ear, median (range), dB | 43 (5-120) | 46 (5-116) | 45 (5-120) |

| Genetic diagnosis |       |       |       |
|-------------------|-------|-------|-------|
| Received a genetic diagnosis | 18 (19.6) | 51 (25.4) | 37 (28.9) |
| Did not receive a genetic diagnosis | 74 (80.4) | 150 (74.6) | 91 (71.1) |

5 patients were tested from 2015 to 2018. As this was such a small cohort, their demographic information was not included in this table to protect patient privacy.

*Does not add up to 100% because patients can identify as more than one category.

ASA: American Society of Anesthesiologists Physical Classification System. HL: hearing loss. ICD-10: International Classification of Diseases 10th Revision. PTA: pure tone average. URM: under-represented minority.
**Table 2.** Frequency of Individuals With Diagnostic Variants, Categorized by Ethnicity and Causative Genes

|                      | Hispanic | Asian | Black | White | Other |
|----------------------|----------|-------|-------|-------|-------|
| **Frequency**        | 205      | 96    | 37    | 134   | 91    |
| **Diagnostic yield, n (%)** | 40 (29)  | 33 (33) | 6 (4)  | 31 (23) | 25 (18) |
| **Diagnostic variants, n** | 49       | 48    | 7     | 43    | 28    |
| **GJB2, 98**         |          |       |       |       |       |
| - c.-23+1 G>A        | 1        | 1     |       |       | 1     |
| - c.34 G>T           |          |       |       |       |       |
| - c.35del            | 11       | 1     | 1     | 12    | 6     |
| - c.35 G>T           |          |       |       |       |       |
| - c.101 T>C          | 3        |       |       | 1     |       |
| - c.109 G>A          | 3        |       | 32    | 1     | 6     |
| - c.139 G>T          | 1        | 1     |       |       | 2     |
| - c.235delC          |          |       |       | 3     |       |
| - c.269 T>C          | 1        |       |       | 4     | 1     |
| - c.283 G>A          |          |       |       |       |       |
| - c.313_326del14     |          |       |       |       | 1     |
| - Deletion involving Exon 2 |          |   |       |       |       |
| **STRC, CATSPER2, 13** |          |       |       |       |       |
| - 15q15.3 deletion   | 4        | 1     | 3     | 2     |       |
| - Deletion of Exon(s) 19-24 |          |       |       | 1     |       |
| - Deletion Including Exons 19-29 | 1 |       |       | 1     |       |
| **SLC26A4, 9**       |          |       |       |       |       |
| - c.2 T>C            |          |       |       |       | 1     |
| - c.716 T>A          |          |       |       |       |       |
| - c.916dupG          | 1        |       |       | 1     |       |
| - c.1541 A>G         |          |       |       |       | 1     |
| - c.2027 T>A         |          |       |       | 1     | 1     |
| - c.2228 T>G         |          |       |       | 1     |       |
| **MYO7A, 6**         |          |       |       |       |       |
| - c.321_322insA      |          |       |       |       | 1     |
| - c.494 C>T          |          |       |       |       | 2     |
| - c.721 C>T          |          |       |       |       | 1     |
| - c.5420_542dupAG    |          |       |       | 1     |       |
| - c.5660 C>T         |          |       |       |       | 1     |
| Gene     | Number | 1                      | 2                   |
|----------|--------|------------------------|---------------------|
| **CDH23, 5** |        |                        |                     |
| - c2329_2330delAC |        |                        | 1                   |
| - c.6050-15 G>A |        | 1                      | 1                   |
| - c.6682delG   |        |                        |                     |
| - c.9629_9632delTCAA |    |                        | 1                   |
| **MYO15A, 4** |        |                        |                     |
| - c.3336delG   |        |                        | 1                   |
| - c.3385 C>T   |        |                        | 1                   |
| - c.4252 G>A   |        |                        | 1                   |
| - c.6509+5 G>A |        |                        | 1                   |
| **USH2A, 6**  |        |                        |                     |
| - c.13040_13062del23ins10 |     |                        | 1                   |
| - c.15089 C>A  |        |                        | 1                   |
| - c.2304 C>A   |        |                        | 1                   |
| - c.9570+1 G>A |        |                        | 1                   |
| - Deletion of Exon(s) 4 | |                        | 1                   |
| **KCNQ4, 3**  |        |                        |                     |
| - c.18dupG    |        |                        | 1                   |
| - c140 T>C    |        |                        | 1                   |
| - c.835-1 G>T |        |                        | 1                   |
| **OTOGL, 5**  |        |                        |                     |
| - c.919-1 G>A |        |                        | 1                   |
| - c.2472delA   |        |                        | 2                   |
| - 2          |        |                        | 2                   |
| **GJB6, 2**   |        |                        |                     |
| - 13q12.11 Deletion | |                        | 2                   |
| **ALMS1, 2**  |        |                        |                     |
| - c.11768delA |        |                        | 1                   |
| - c.3609 T>G  |        |                        | 1                   |
| **OTOF, 2**   |        |                        |                     |
| - c.1966dupC  |        |                        | 1                   |
| - c.2225 T>C  |        |                        | 1                   |
| **OTOG, 2**   |        |                        |                     |
| - c.2489_2490ins12 | |                        | 1                   |
| - c.2701 G>T  |        |                        | 1                   |
| **PDZD7, 2**  |        |                        |                     |
| - c.561dupG   |        |                        | 1                   |
| - c.2089delG  |        |                        | 1                   |
| **SOX10, 2**  |        |                        |                     |
| - c.-84-1 G>C |        |                        | 1                   |
| Gene       | Mutation                  | Frequency |
|------------|---------------------------|-----------|
| USH1C, 2   | c.1137delC                | 1         |
| ADGRV1, 1  | c.1458_1459del            | 2         |
| EYA1, 1    | c.1547G>A                 | 1         |
| MIR96, 1   | c.880 C>T                 | 1         |
| MITF, 1    | r.12 G>A                  | 1         |
| OPA1, 1    | c.710+1 G>A               | 1         |
| OSBPL2, 1  | c.556+2 T>G               | 1         |
| POU3F4, 1  | c.180_181delCA            | 1         |
| PTPRQ, 1   | c.765 G>A                 | 1         |
| TMPRSS3, 1 | c.1359+2 T>C              | 1         |
| WFS1, 1    | c.124 C>T                 | 1         |
| Multigene deletion, 1 | 10p15.3p14 Deletion | 1         |

All children included. Blank cells indicate the frequency was zero.