

Dual Diagnoses of Genetic Hearing Loss Identified on Multigene Panels: Considerations for Clinical Care and Genetic Counseling

Amanda M. Schaefer¹, Carla J. Nishimura¹, Kathy L. Frees¹, Diana L. Kolbe¹, Kevin T. Booth^{1,2}, Rob J. Marini¹, Donghong Wang¹, Amanda O. Taylor¹, Amy E. Weaver¹, Jori E. Hendon¹, Hela Azaiez², Richard J.H. Smith¹

¹ Molecular Otolaryngology and Renal Research Laboratories, Department of Otolaryngology—Head and Neck Surgery, University of Iowa Hospitals & Clinics, Iowa City, Iowa, USA ² Medical and Molecular Genetics, Indiana School of Medicine, Indianapolis, Indiana, USA

Introduction

- Genetic testing is a vital component of care for deaf and hard-of-hearing persons.
- The American College of Medical Genetics and Genomics (ACMG) recommends a multigene hearing loss (HL) panel for patients with non-syndromic HL.¹
- Multigene HL panel testing may identify dual genetic diagnoses, presenting a challenge for genetic counseling and clinical care.
- There is little data about the frequency and subsequent challenges in genetic counseling for dual diagnoses of HL.

Here, we present a series of cases with dual genetic diagnoses identified on a multigene HL panel to highlight the complexities of genetic counseling and clinical care.

Methods

- Subjects:** Ethnically diverse cohort with hearing loss ascertained from 2012 through June 2022.
- Genetic testing:** Targeted genomic enrichment and massively parallel sequencing to screen all non-syndromic HL-associated genes and common syndromic genes (OtoSCOPE).
- Bioinformatic analysis:** Customized Galaxy pipeline and analysis for single nucleotide variants and analysis of normalized read-depth data by sample batch compared to average read-depth for copy number variation (CNV) identification.
- Genetic results:** Genetic findings were discussed at a multidisciplinary meeting with physicians, geneticists, bioinformaticians, and genetic counselors in the context of the patient's clinical data and history.
- Variant classification:** All variants were classified using ACMG/AMP Hearing Loss Specific classification guidelines.⁴

Cohort Identification

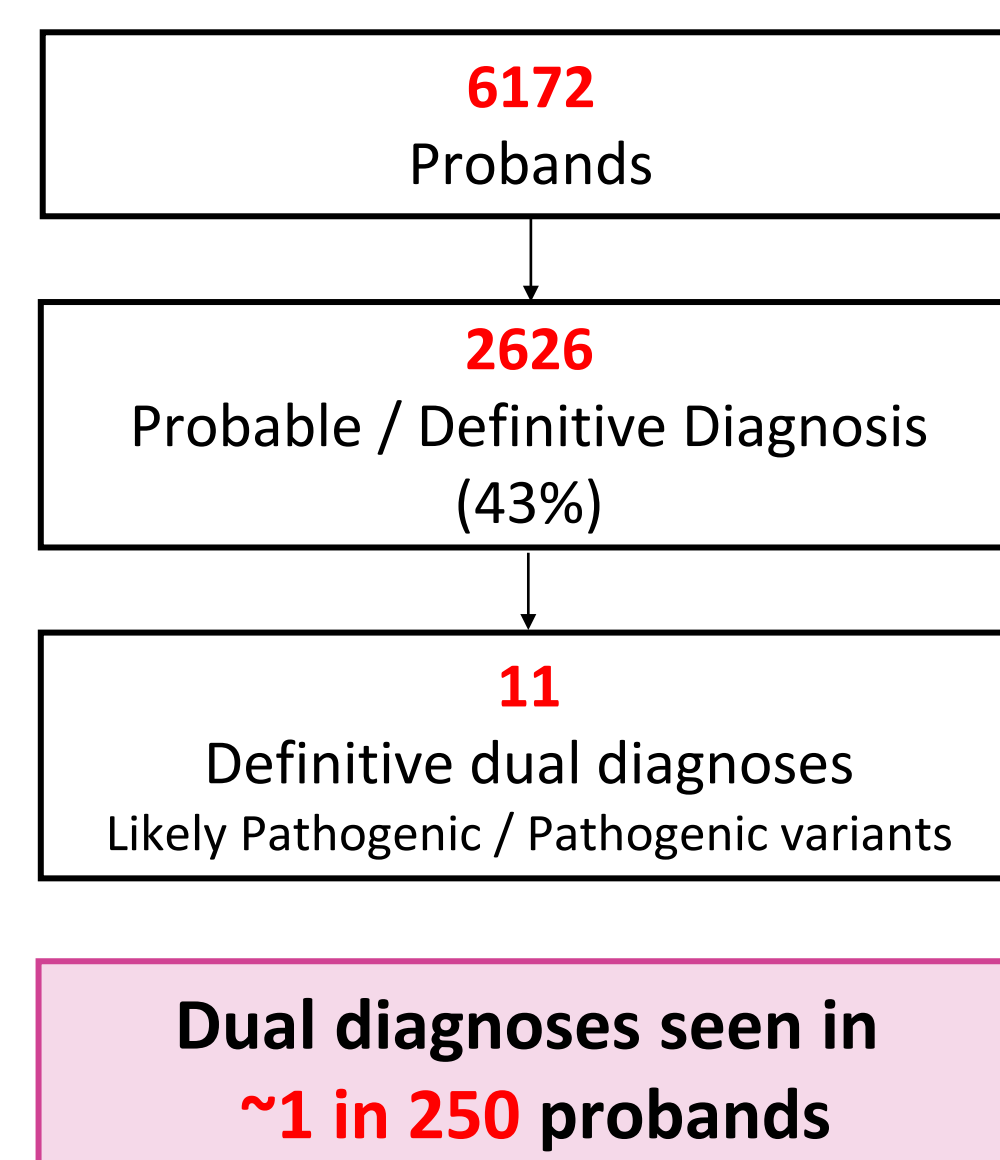


Figure 1. MORL dual diagnosis cohort identification: Of ~2600 probands with a probable genetic diagnosis, 11 probands (0.4%) were identified with dual genetic diagnoses, defined as Likely Pathogenic or Pathogenic variant(s) in 2 genes.

Dual Diagnoses Cohort

Table 1. Dual diagnoses case details.

Proband	Age at testing	HL Phenotype	Physical exam	Family history	Diagnosis 1			Diagnosis 2		
					Gene	Diagnosis	Inheritance	Gene	Diagnosis	Inheritance
1	7 m	Congenital moderate SNHL	Right ptosis	Negative; parental consanguinity	<i>GJB2</i>	DFNB1	AR	<i>OTOA</i>	DFNB22	AR
2	5 m	Congenital moderate SNHL	Normal	Negative	<i>GJB2</i>	DFNB1	AR	<i>OTOA</i>	DFNB22	AR
3	1 y	Not provided	Not provided	Not provided	<i>GJB2</i>	DFNB1	AR	<i>TECTA</i>	DFNA12	AD
4	7 y	Congenital moderate-to-severe SNHL	Normal	Negative	<i>GJB2</i>	DFNB1	AR	<i>MT-TL1</i>	MELAS / MIDD	M
5	2 m	Congenital profound SNHL	Normal	2 paternal uncles: unilateral HL	<i>GJB2</i>	DFNB1	AR	<i>USH2A</i>	Usher type 2A / non-syndromic retinitis pigmentosa	AR
6	5 y	Congenital profound SNHL	Normal	Younger brother: profound HL	<i>GJB2</i>	DFNB1	AR	<i>COL11A2</i>	non-ocular Stickler type 3	AD
7	3 y	Congenital moderate SNHL	Normal	Negative	<i>GJB2</i>	DFNA3A	AD	<i>COL4A3</i>	familial hematuria	AD
8	15 y	Early childhood onset SNHL	Normal	Mother, two maternal half siblings: bilateral HL, maternal uncle: unilateral HL	<i>TBX1</i>	22q11.2 duplication syndrome	AD	<i>MT-RNR1</i>	aminoglycoside-induced HL	M
9	1 m	Congenital mild-to-moderate SNHL	Normal	Negative	<i>TBX1</i>	22q11.2 duplication syndrome	AD	<i>GATA3</i>	Hypoparathyroidism, Deafness, Renal disease (HDR)	AD
10	6 y	Early childhood onset SNHL	Normal	Negative	<i>TBX1</i>	22q11.2 deletion syndrome	AD	<i>MYO7A</i>	DFNA11	AD
11	8 y	Early childhood onset mild-to-moderate SNHL	Normal	Negative	<i>KCNQ4</i>	DFNA2A	AD	<i>EYA1</i>	Branchiootorenal (BOR) syndrome	AD

Abbreviations: SNHL: sensorineural hearing loss, AD: autosomal dominant, AR: autosomal recessive, M: mitochondrial, MELAS: Mitochondrial Encephalopathy, Lactic Acidosis, and Stroke-like episodes, MIDD: Maternally Inherited Diabetes and Deafness

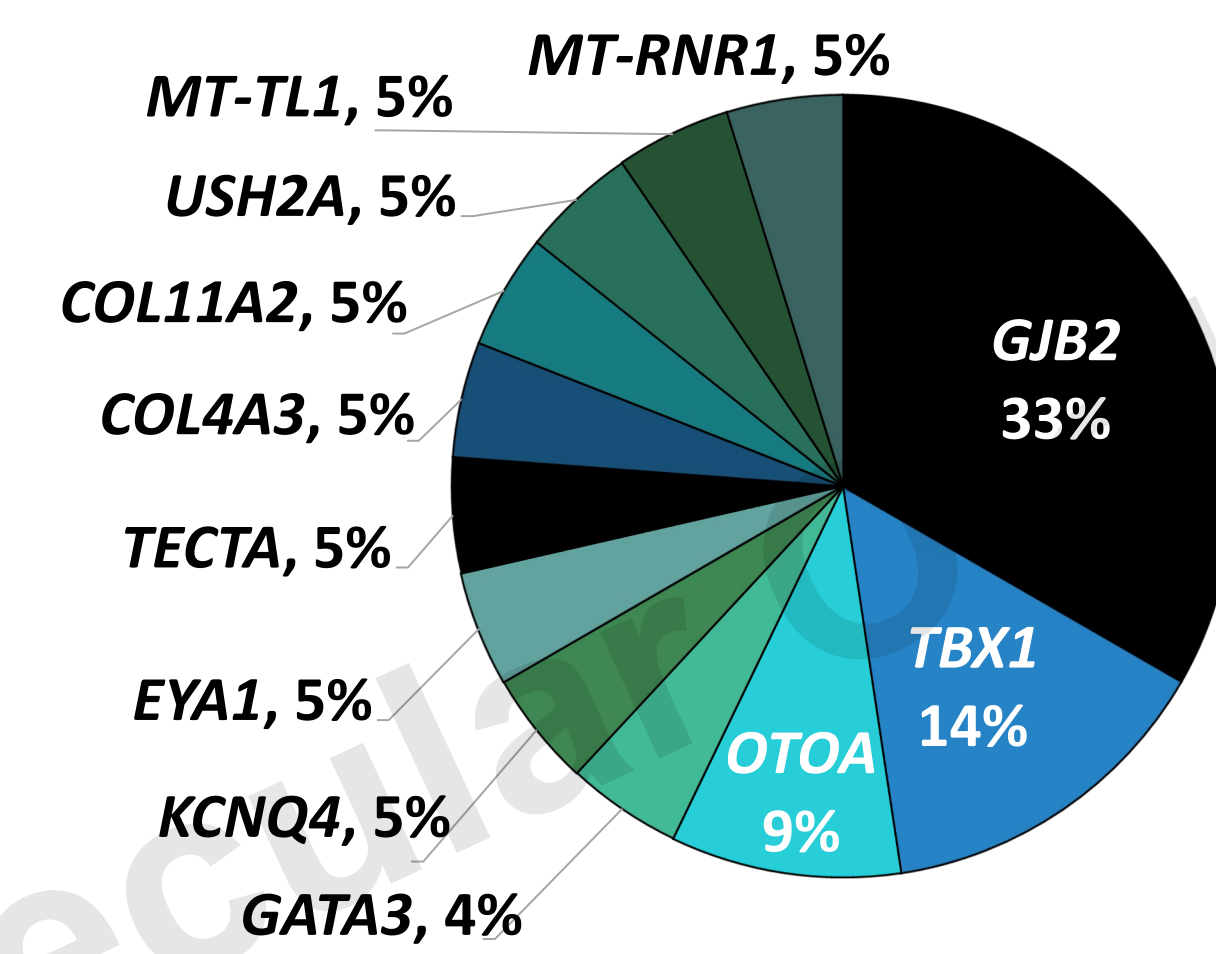


Figure 2. Causative genes in dual diagnoses cohort. A total of 12 genes were identified as causative in this cohort. *GJB2*, *TBX1*, and *OTOA* were the most frequent, comprising ~55% of diagnoses.

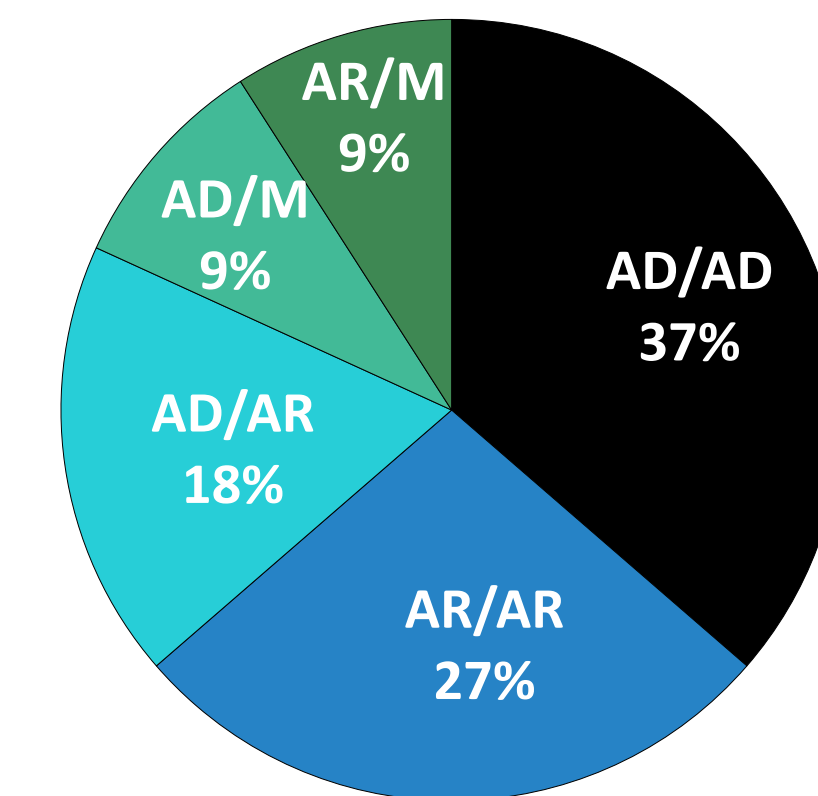


Figure 3. Inheritance pattern combinations identified. A variety of inheritance pattern combinations were seen with 2 AD or 2 AR being most common. (AD: autosomal dominant, AR: autosomal recessive, M: mitochondrial)

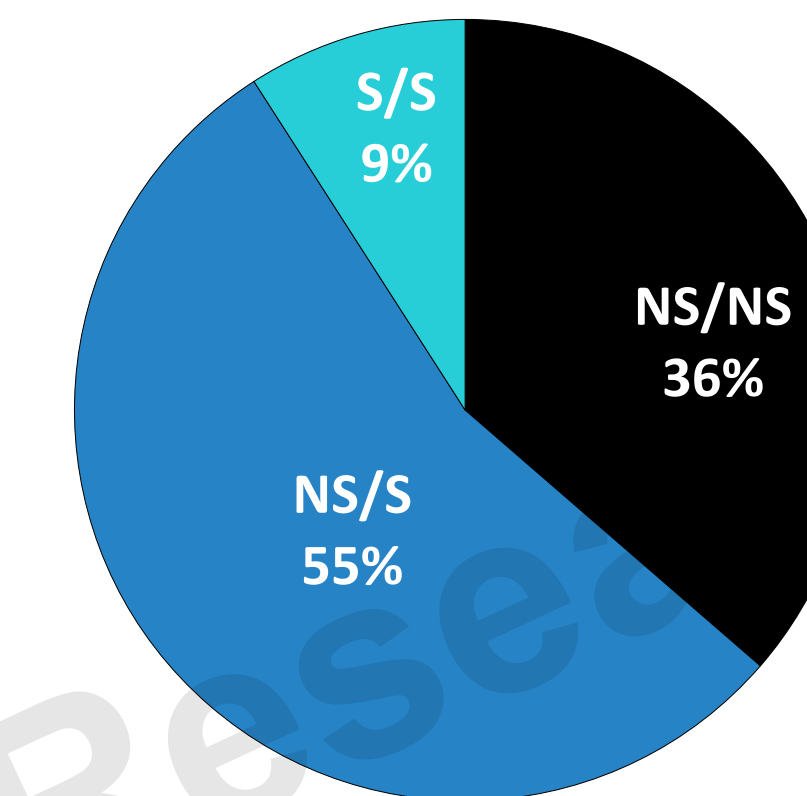


Figure 4. Syndromic versus non-syndromic diagnoses. Around 2/3 of probands had at least 1 syndromic diagnosis. (S: syndromic, NS: non-syndromic)

Illustrative Cases

Proband 5

Clinical Information:

- 2-month-old white male
- Congenital bilateral severe-to-profound SNHL
- Family history: negative

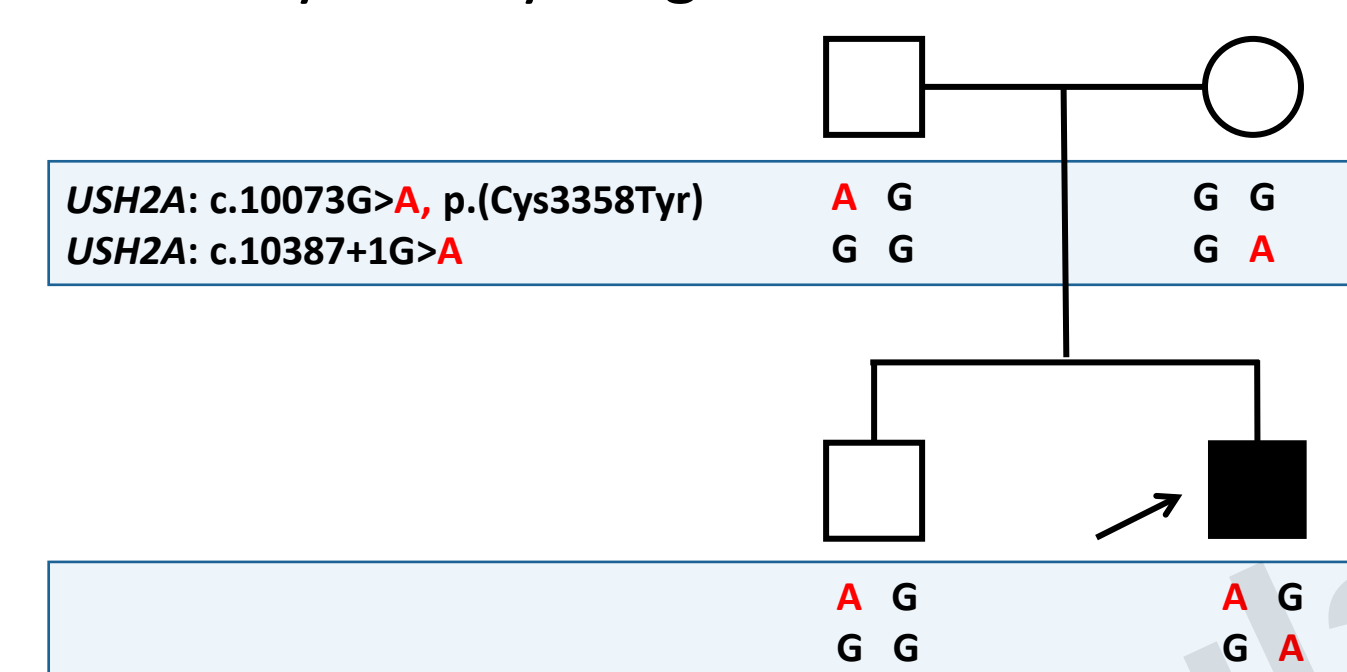


Figure 5: Pedigree showing segregation of *USH2A* variants.

Impact to genetic counseling and clinical care:

- Proband referred to ophthalmology
- DFNB1-related HL masks *USH2A*-related HL phenotype
- Prompts genetic testing for normal hearing brother
 - Biallelic loss of function variants are more often seen in Usher type 2A and biallelic missense in autosomal recessive non-syndromic retinitis pigmentosa (RP).
 - Identified missense variant enriched in non-syndromic RP.⁵
 - Brother could have inherited the second *USH2A* variant and developed non-syndromic RP despite normal hearing.

Table 2: Causative variants identified

Gene	Nuc. Change	AA Change	Max MAF gnomAD	ACMG Classification	ACMG Criteria Applied
<i>USH2A</i>	c.10073G>A	p.(Cys3358Tyr)	0.076% (NFE)	Pathogenic	BS1_Sup, PM3_VS, PP4, PP3
<i>USH2A</i>	c.10387+1G>A	NA	ND	Pathogenic	PVS1, PM2, PM3
<i>GJB2</i>	c.35delG	p.(Gly12ValfsTer2)	0.84% (NFE)	Pathogenic	PVS1, PM3_VS, PS4, BA1

Abbreviations: Nuc: nucleotide, AA: amino acid, MAF: minor allele frequency, NFE: non-Finnish European, NA: Not applicable, BS1_Sup: BS1_Supporting, PM3_VS: PM3_VeryStrong

Diagnoses:

- Autosomal recessive non-syndromic HL (DFNB1)
- Usher syndrome type 2A or autosomal recessive non-syndromic retinitis pigmentosa (ARRP)

DFNB1-related HL phenotype masks *USH2A*-related phenotype

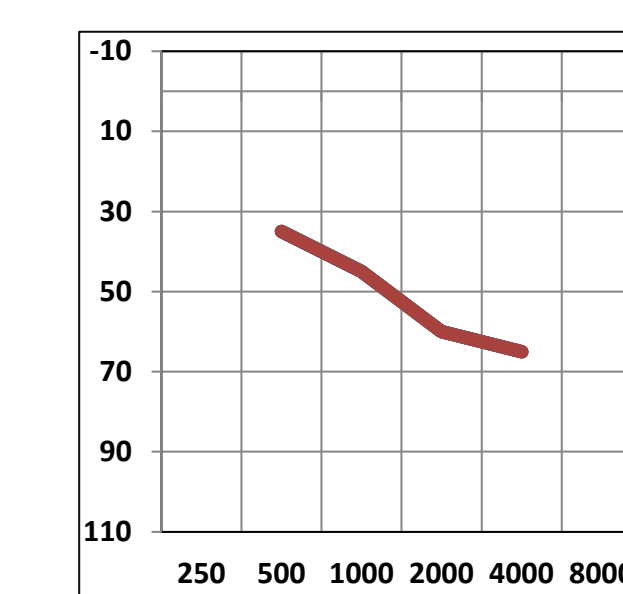


Figure 5: Audiogram of proband.

Proband 9

Clinical Information:

- 1-month-old White, Asian female
- Congenital mild-to-moderate bilateral SNHL
- Family history: adopted embryo, no HL reported in biological parents
- Physical exam: normal

Table 3: Causative variants identified

Gene	Nuc. Change	AA Change	Max MAF gnomAD	ACMG Classification	ACMG Criteria Applied
<i>TBX1</i>	whole gene duplication	NA	ND	Pathogenic	PVS1, PS4_S
<i>GATA3</i>	c.708del	p.(Ser237AlafsTer29)	ND	Pathogenic	PVS1, PM2, PS4_Mod

Abbreviations: AA: amino acid, MAF: minor allele frequency, ND: no data, PS4_S: PS4_Strong, PS4_Mod: PS4_Moderate

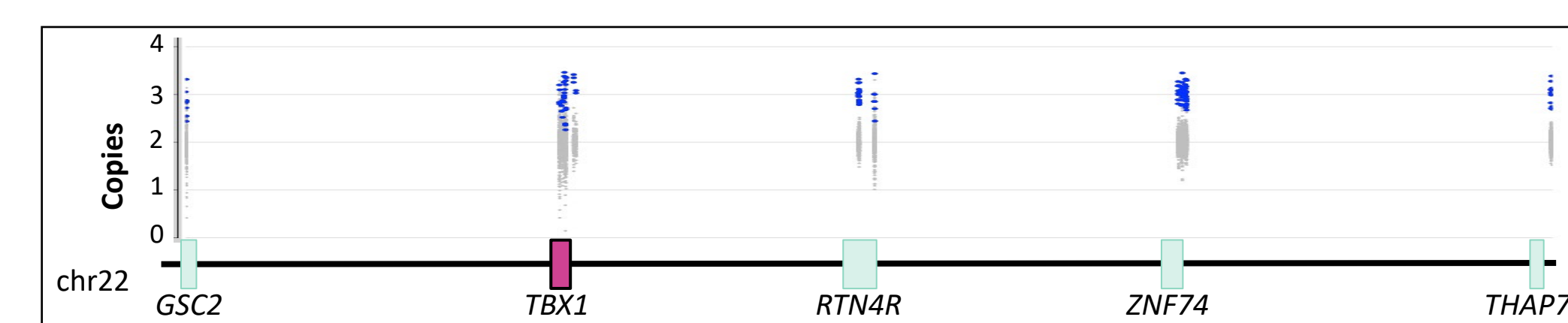


Figure 6: Heterozygous whole gene duplication of *TBX1* and surrounding critical region at 22q11.2. Dots represent normalized read-depth data by sample batch compared to average read-depth, blue: proband, grey: unrelated probands in testing batch. To determine extent of duplication, referring healthcare provider ordered a chromosome microarray from an outside lab which confirmed the diagnosis of 22q11.2 duplication syndrome due to a pathogenic 2.5 Mb duplication: arr[GRCh37]22q11.21(18915102_21466669)x3.

Impact to genetic counseling and clinical care:

- Proband referred to endocrinology, nephrology, and developmental and educational support organizations
- Education on variability of both diagnoses^{6,7}
- Blending of phenotypes and challenge of providing prognostic information on HL and other features.

22q11.2 duplication syndrome phenotype blends with HDR syndrome phenotype

Conclusions

- The possibility of dual genetic diagnoses cannot be overlooked with multigene HL panel testing.
 - Dual diagnoses were seen in ~1 in 250 probands.
- Multigene panel testing is recommended over single gene testing for *GJB2*.
 - ~1 in 100 probands diagnosed with DFNB1-related HL had a second genetic diagnosis identified.
- Pre-test counseling should include discussion of non-syndromic mimics.

~2/3 of probands with dual diagnoses were identified to have a genetic syndrome, despite normal physical exams.

Our data highlight the importance of considering dual genetic diagnoses and the complexity of genetic counseling and clinical care for these families.

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