fig. 4A

Genes	65 dB median single gene	number
COL11A1 n= 1	0	1
EDNRB n= 1	0	1
PTPRQ n= 1	20	1
TMPRSS3 n= 9	30	9
WFS1 n= 4	32.5	4
CDH23 n= 4	35	4
LOXHD1 n= 5	35	5
TMIE n= 2	50	2
TFAP2A n= 1	50	1
DIAPH1 n= 2	52.5	2
MARVELD2 n= 4	52.5	4
EYA4 n= 1	55	1
SMPX n= 3	60	3
COL2A1 n= 1	60	1
MYH14 n= 3	60	3
MYO7A n= 4	67.5	4
COL4A3 n= 4	70	4
OTOF n= 2	70	2
MT-TL1 n= 1	70	1
POU4F3 n= 1	70	1
MYO6 n= 3	75	3
USH2A n= 5	75	5
COCH n= 1	75	1
MYO3A n= 2	75	2
MYO15A n= 8	77.5	8
SLC26A4 n= 6	77.5	6
GJB2 n= 26	80	26
KCNE1 n= 2	80	2
POU3F4 n= 2	85	2
RRM2B n= 1	85	1
MITF n= 4	90	4
PAX3 n= 3	90	3
SOX10 n= 2	95	2
ACTG1 n= 2	97.5	2
LHFPL5 n= 2	97.5	2
	sum	**123**

fig. 4B

median 65 dB

	Gen	Neural	Hair Cell	Tectorial Me	Cochlear Duc
EDNRB n= 1	EDNRB	0			
TMPRSS3 n= 9	TMPRSS3	30			
WFS1 n= 4	WFS1	32.5			
TFAP2A n= 1	TFAP2A	50			
DIAPH1 n= 2	DIAPH1	52.5			
EYA4 n= 1	EYA4	55			
PAX3 n= 3	PAX3	90			
SOX10 n= 2	SOX10	95			
PTPRQ n= 1	PTPRQ		20		
CDH23 n= 4	CDH23		35		
LOXHD1 n= 5	LOXHD1		35		
TMIE n= 2	TMIE		50		
MARVELD2 n= 4	MARVELD2		52.5		
SMPX n= 3	SMPX		60		
MYH14 n= 3	MYH14		60		
MYO7A n= 4	MYO7A		67.5		
OTOF n= 2	OTOF		70		
POU4F3 n= 1	POU4F3		70		
MYO3A n= 2	MYO3A		75		
MYO6 n= 3	MYO6		75		
USH2A n= 5	USH2A		75		
MYO15A n= 8	MYO15A		77.5		
ACTG1 n= 2	ACTG1		97.5		
LHFPL5 n= 2	LHFPL5		97.5		
COL2A1 n= 1	COL2A1			60	
COL11A1 n= 1	COL11A1				0
COL4A3 n= 4	COL4A3				70
COCH n= 1	COCH				75
SLC26A4 n= 6	SLC26A4				77.5
GJB2 n= 26	GJB2				80
POU3F4 n= 2	POU3F4				85
MITF n= 4	MITF				90
KCNE1 n= 2	KCNE1				
MT-TL1 n= 1	MT-TL1				
RRM2B n= 1	RRM2B				

median all	quartile 25	quartile 75	median all	quartile 25
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60
70	45	80	85	60

70	45	80		85	60
70	45	80		85	60
70	45	80		85	60
70	45	80		85	60
70	45	80		85	60
70	45	80		85	60
70	45	80		85	60
70	45	80		85	60
70	45	80		85	60
70	45	80		85	60
70	45	80		85	60
70	45	80		85	60
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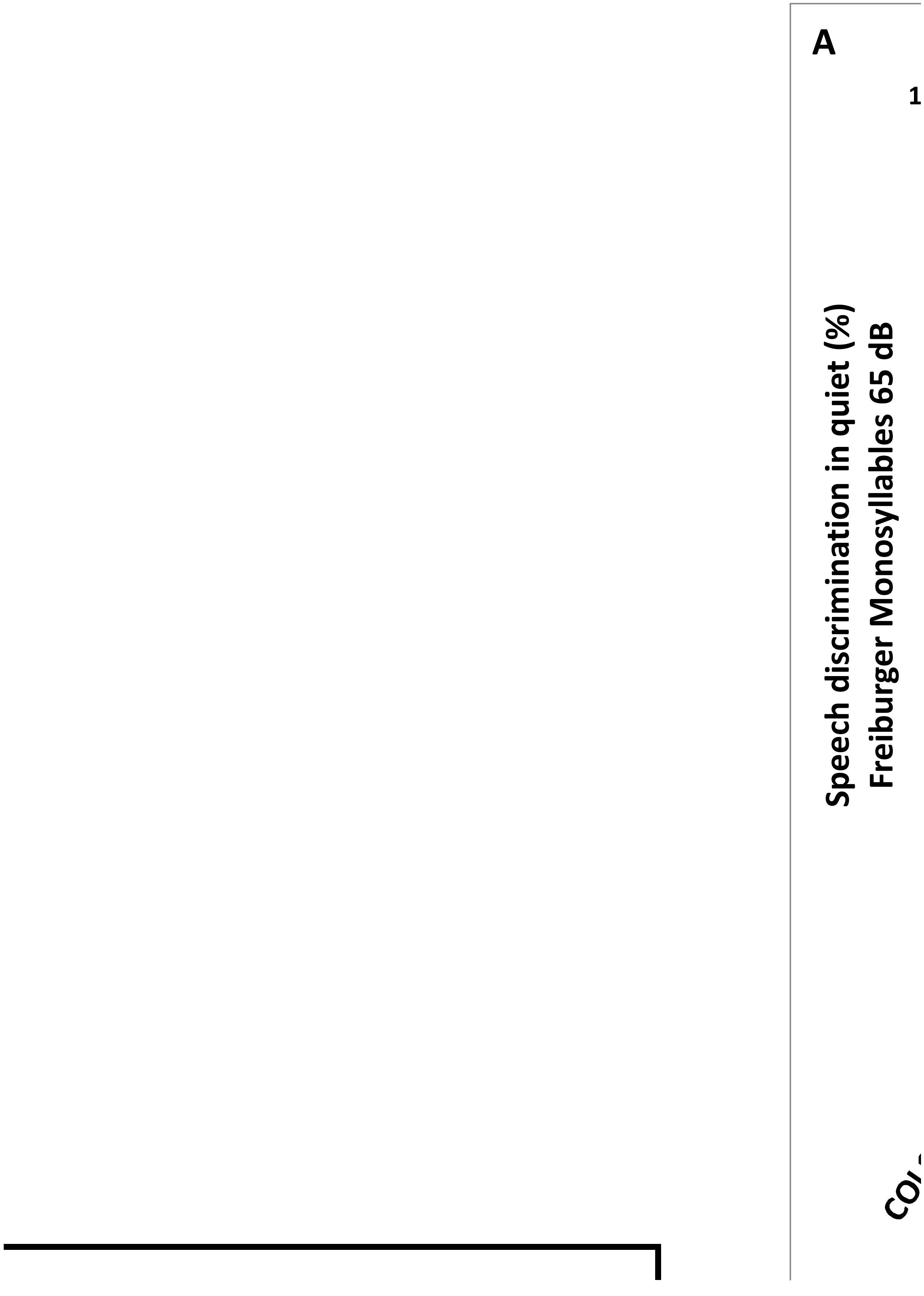
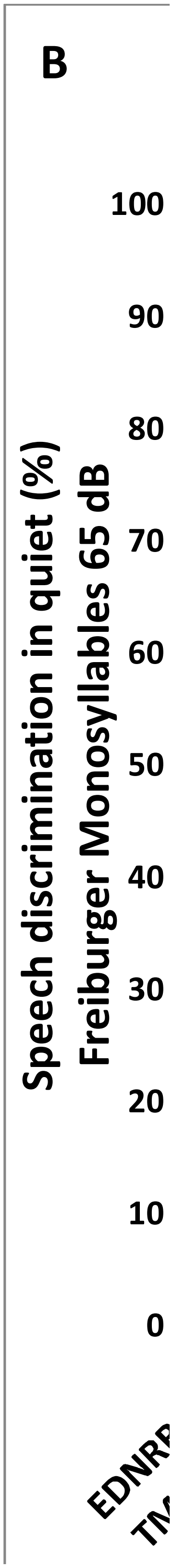
70	45	80		85	60
70	45	80		85	60


A
1
Speech discrimination in quiet (%)
Freiburger Monosyllables 65 dB
CO

Stria Vascula	Mitochondri	median all	quartile 25	quartile 75
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
		70	45	80
80		70	45	80
		70	45	80
	70	70	45	80
	85	70	45	80
		70	45	80



quartile 75

90
90
90
90
90
90
90
90
90
90
90
90
90
90
90
90
90
90
90
90
90
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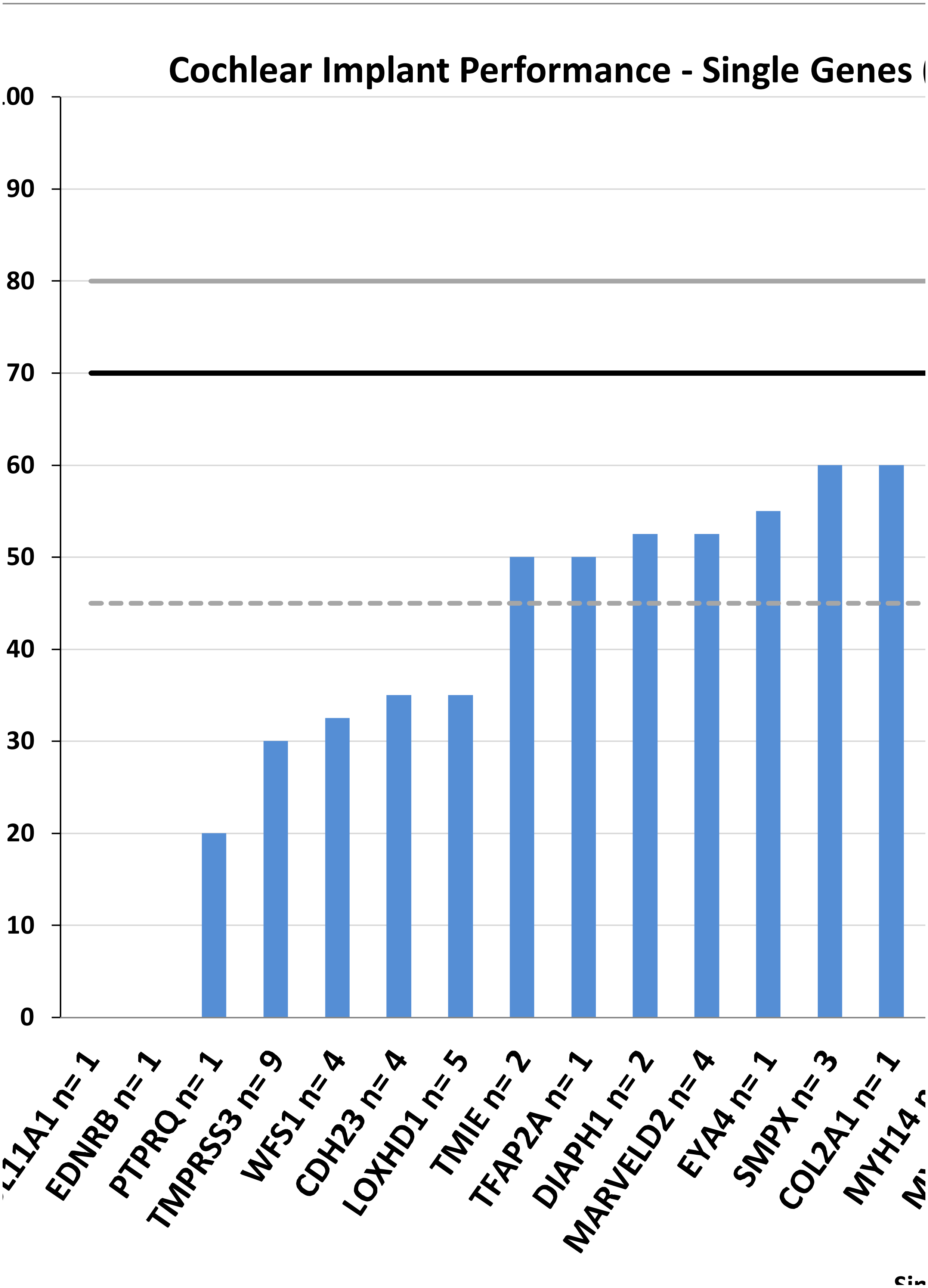
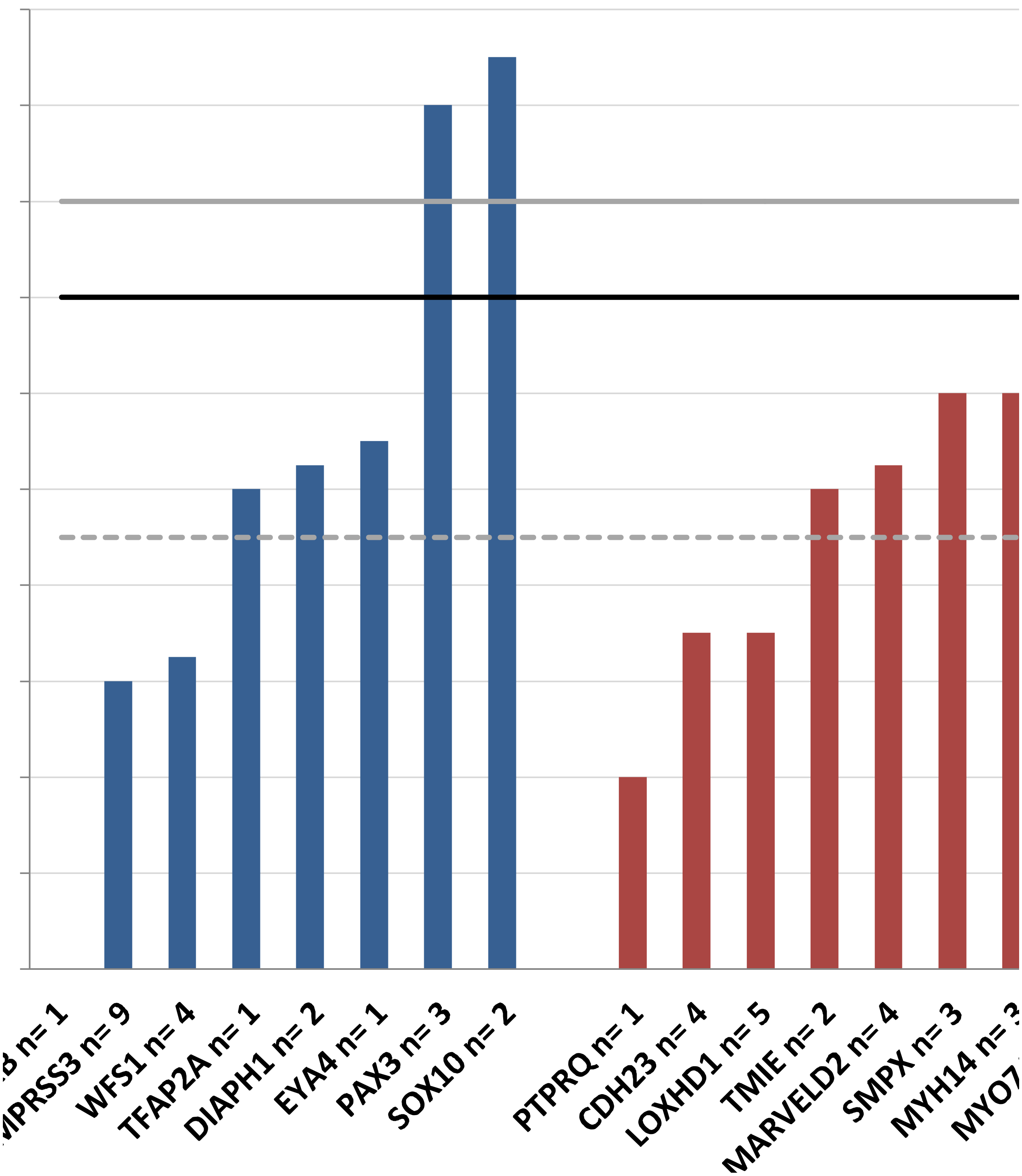
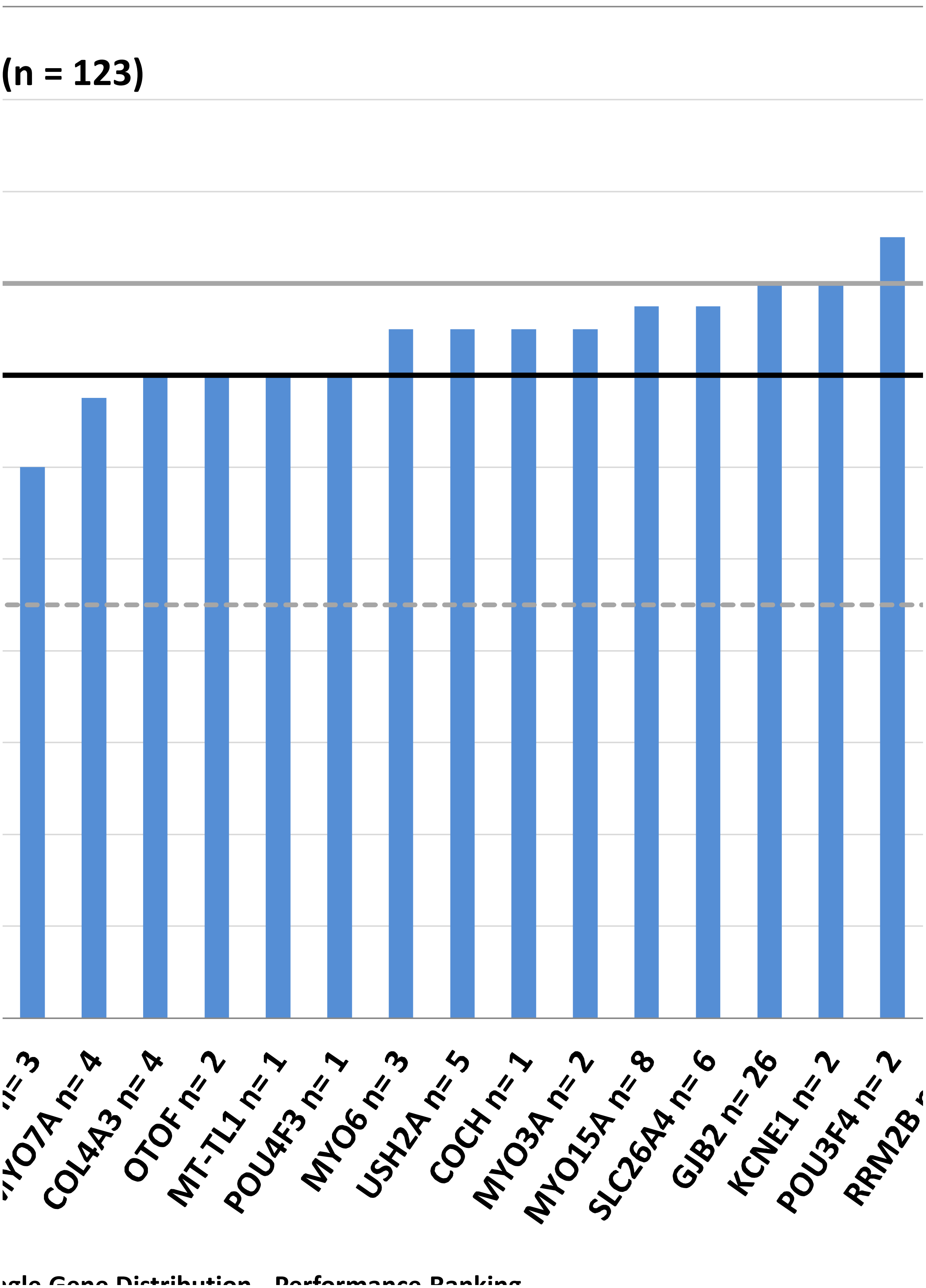
90
90
90
90
90


Cochlear Implant Performance - Single Genes (
.00
90
80
70
60
50
40
30
20
10
0
11A1 n= 1
EDNRB n= 1
PTPRQ n= 1
TMPRSS3 n= 9
WFS1 n= 4
CDH23 n= 4
LOXHD1 n= 5
TMIE n= 2
TFAP2A n= 1
DIAPH1 n= 2
MARVELD2 n= 4
EYA4 n= 1
SMPX n= 3
COL2A1 n= 1
MYH14 n
M
Sin

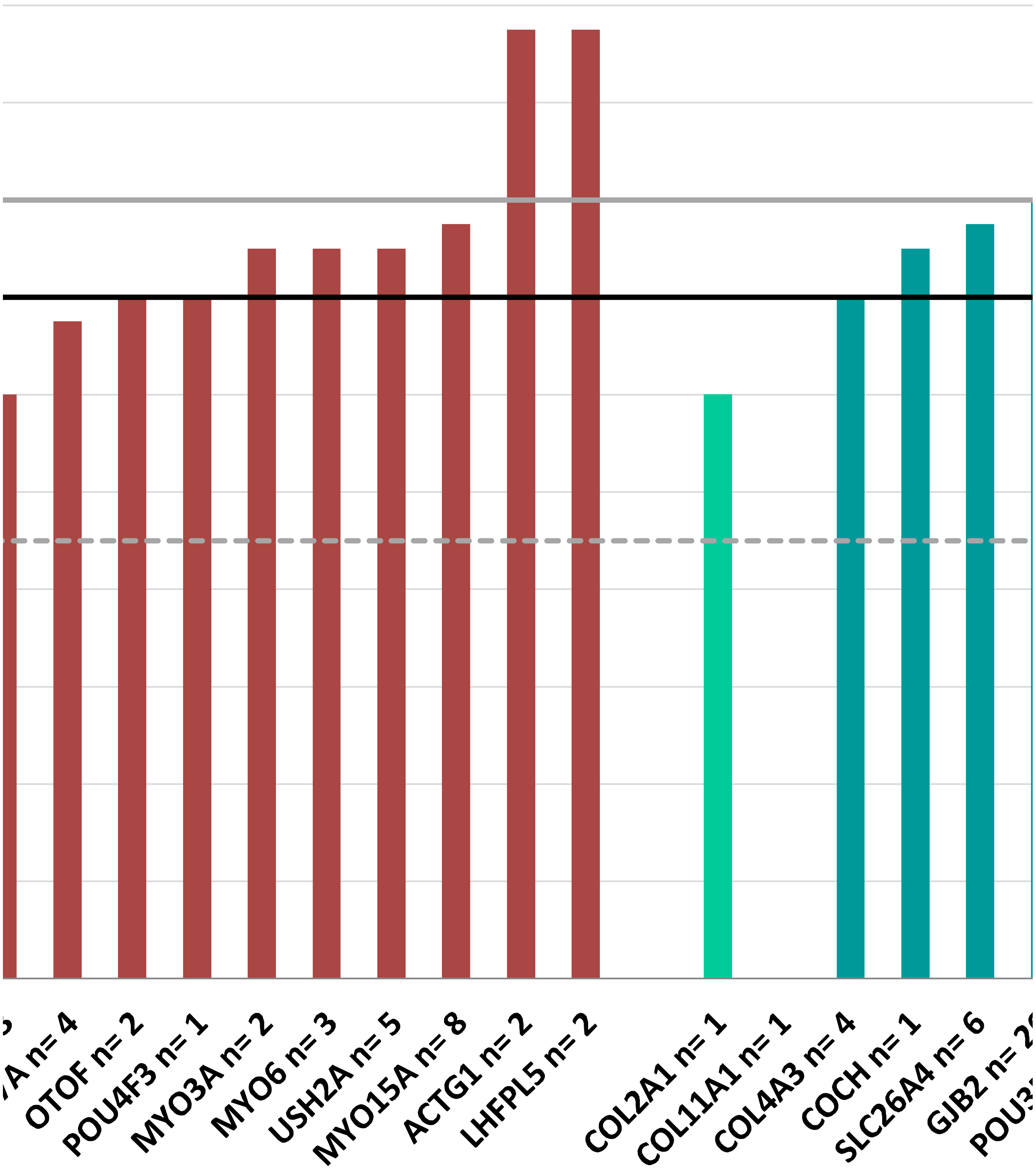
Cochlear Implant Performance - Gene Expression (n=1



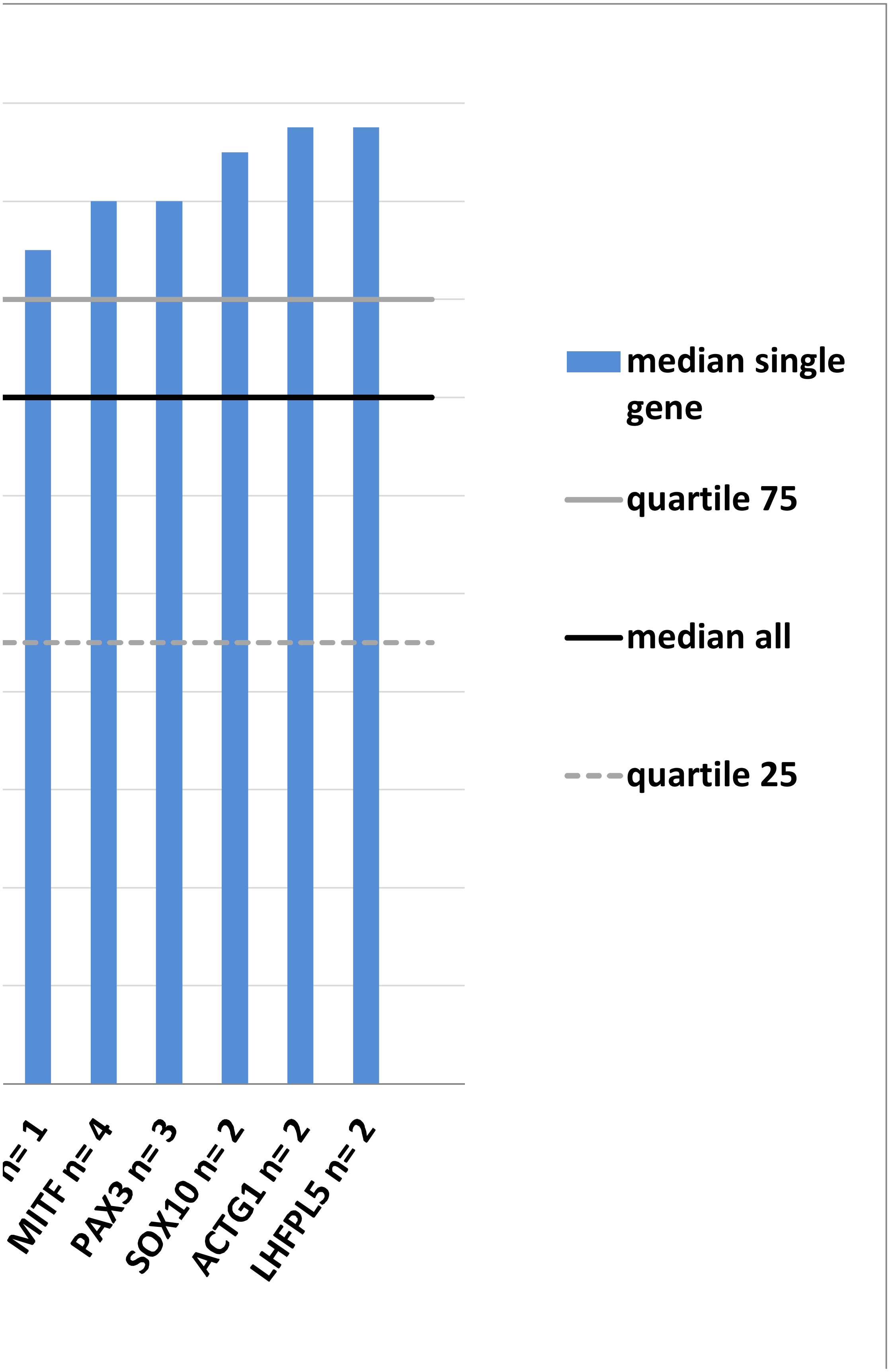

(n = 123)
n= 3
MYO7A n= 4
COL4A3 n= 4
OTOF n= 2
MT-TL1 n= 1
POU4F3 n= 1
MYO6 n= 3
USH2A n= 5
COCH n= 1
MYO3A n= 2
MYO15A n= 8
SLC26A4 n= 6
GJB2 n= 26
KCNE1 n= 2
POU3F4 n= 2
RRM2B n
gle Gene Distribution – Performance Ranking

igle Gene Distribution - Performance Ranking

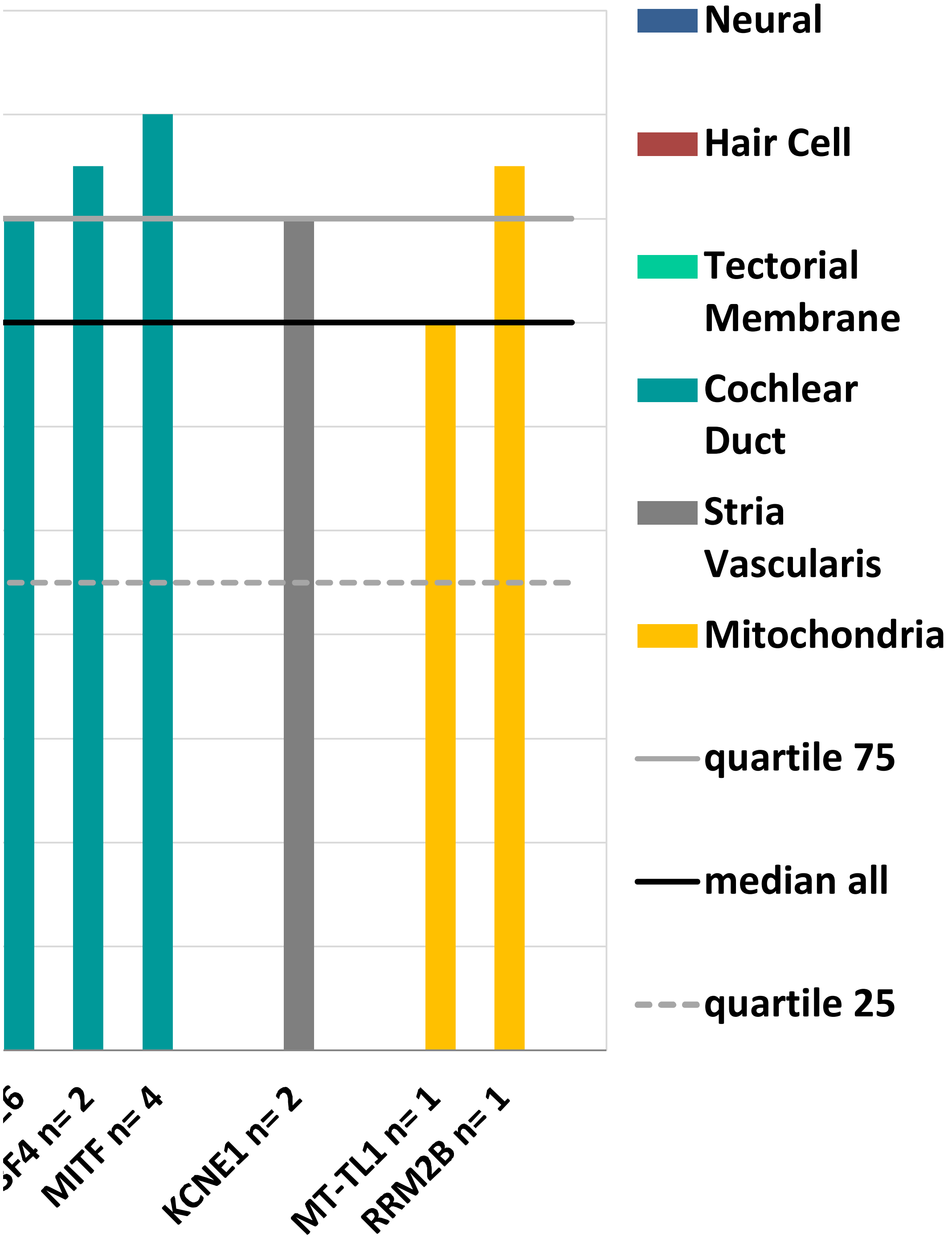
23)



ngle Gene Distribution - Gene Expression Groups



n= 1
MITF n= 4
PAX3 n= 3
SOX10 n= 2
ACTG1 n= 2
LHFPL5 n= 2
median single gene
quartile 75
median all
quartile 25


6
F4 n= 2
MITF n= 4
KCNE1 n= 2
MT-TL1 n= 1
RRM2B n= 1
Neural
Hair Cell
Tectorial Membrane
Cochlear Duct
Stria Vascularis
Mitochondria
quartile 75
median all
quartile 25

			Median 65 both sides
gene cat.	Neural (23)	Neural	45
	Hair Cell (51)	HC	70
	TM and CD (45)	Structural	80
	Stria Vascularis (2)	SV	80
	Mitochondrial (2)	Mito	77.5
Inheritance	AR (44)	AR	70
	AD (19)	AD	70
	Sporadic (57)	sporadic	75
	X-linked (3)	x-linked	57.5
impl age (IA)			
	0-2 (31)	0-2	80
	3-6 (14)	3-6	80
	7-19 (21)	7-19	55
	20-59 (45)	20-59	55
	> 60 (12)	> 60	62.5
onset (O)	Congenital (63)	congenital	80
	Pre-/Peri-lingual (20)	peri-lingual	65
	Post-lingual (40)	post-lingual	60
gap O / IA	<=2 (33)	<=2	80
	3-5 (14)	3-5	80
	6-10 (8)	6-10	60
	>10 (68)	>10	55
hearing loss	severe (6)	severe	42.5
	profound (24)	profound	55
	complete (93)	complete	70
laterality	unilateral (4)	unilateral	0
	asymmetric (2)	asymmetric	62.5
	bilateral sym. (117)	bilateral sym.	70
sequence of impl	first ear (61)	**first ear**	60
	second ear (32)	second ear	67.5
	simultaneous (30)	simultaneous	80

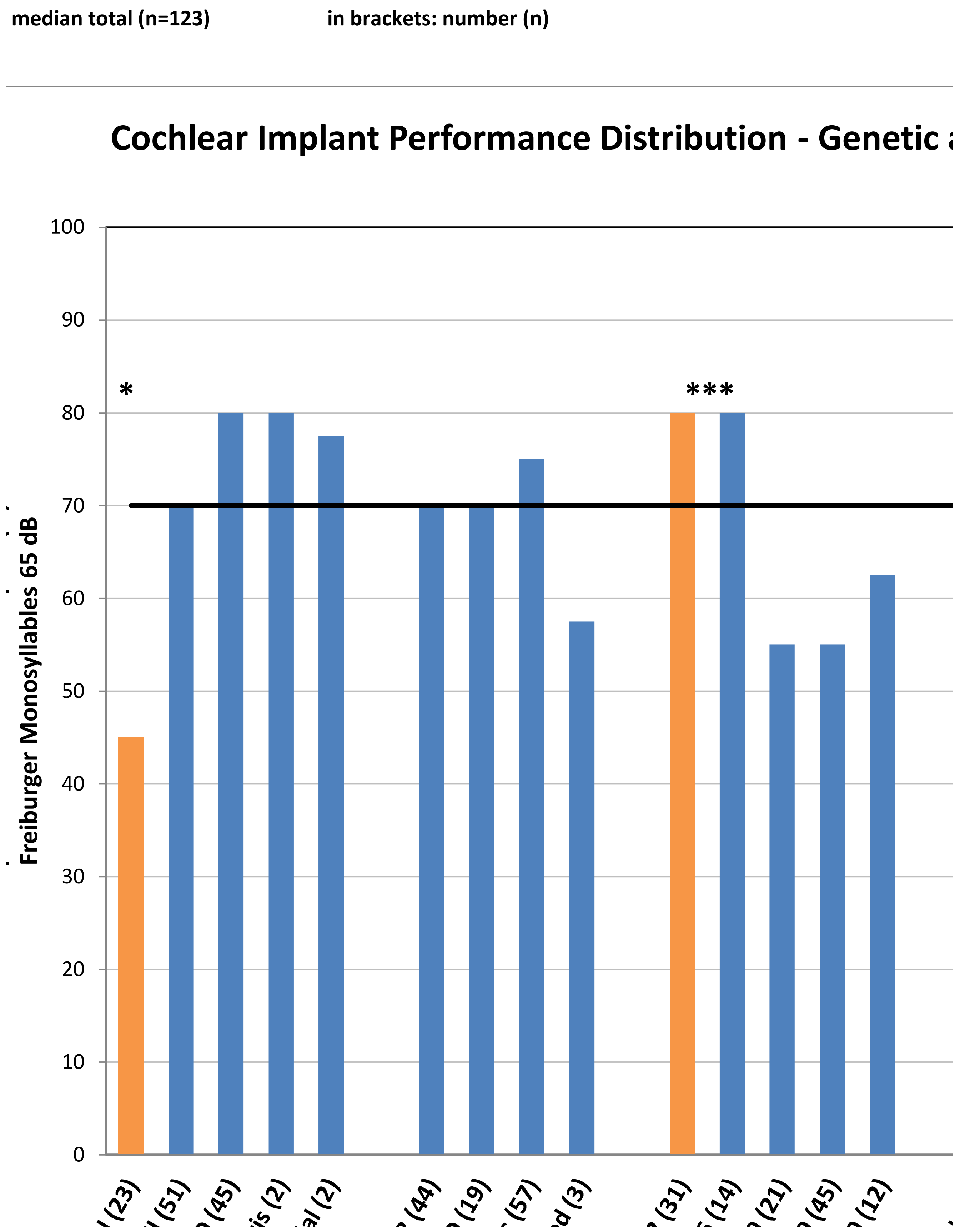
first ear = first ear of 2 implants + single ea

	first ear	single ears
median	**72.5**	**55**
n	**32**	**29**

number	sum	total median	statistics	
23		70	0.014	<0.05*
51		70	n.s.	
45		70	n.s.	
2		70	n.s.	
2	123	70	n.s.	
		70		
44		70	n.s.	
19		70	n.s.	
57	120	70	n.s.	
3	123	70	n.s.	
		70		
31		70	0.000183	<0.001***
14		70	n.s.	
21		70	n.s.	
45		70	n.s.	
12	123	70	n.s.	
		70		
63		70	0.008	<0.01**
20		70	n.s.	
40	123	70	0.023	<0.05*
		70		
33		70	0.002	<0.01**
14		70	n.s.	
8		70	n.s.	
68	123	70	0.023	<0.05*
		70		
6	(1 ear WHO 3)	70	n.s.	
24		70	n.s.	
93	123	70	n.s.	
		70		
4		70	n.s.	0.053
2		70	n.s.	
117	123	70	n.s.	
		70		
61		70	n.s.	
32		70	n.s.	
30	123	70	0.032	<0.05*

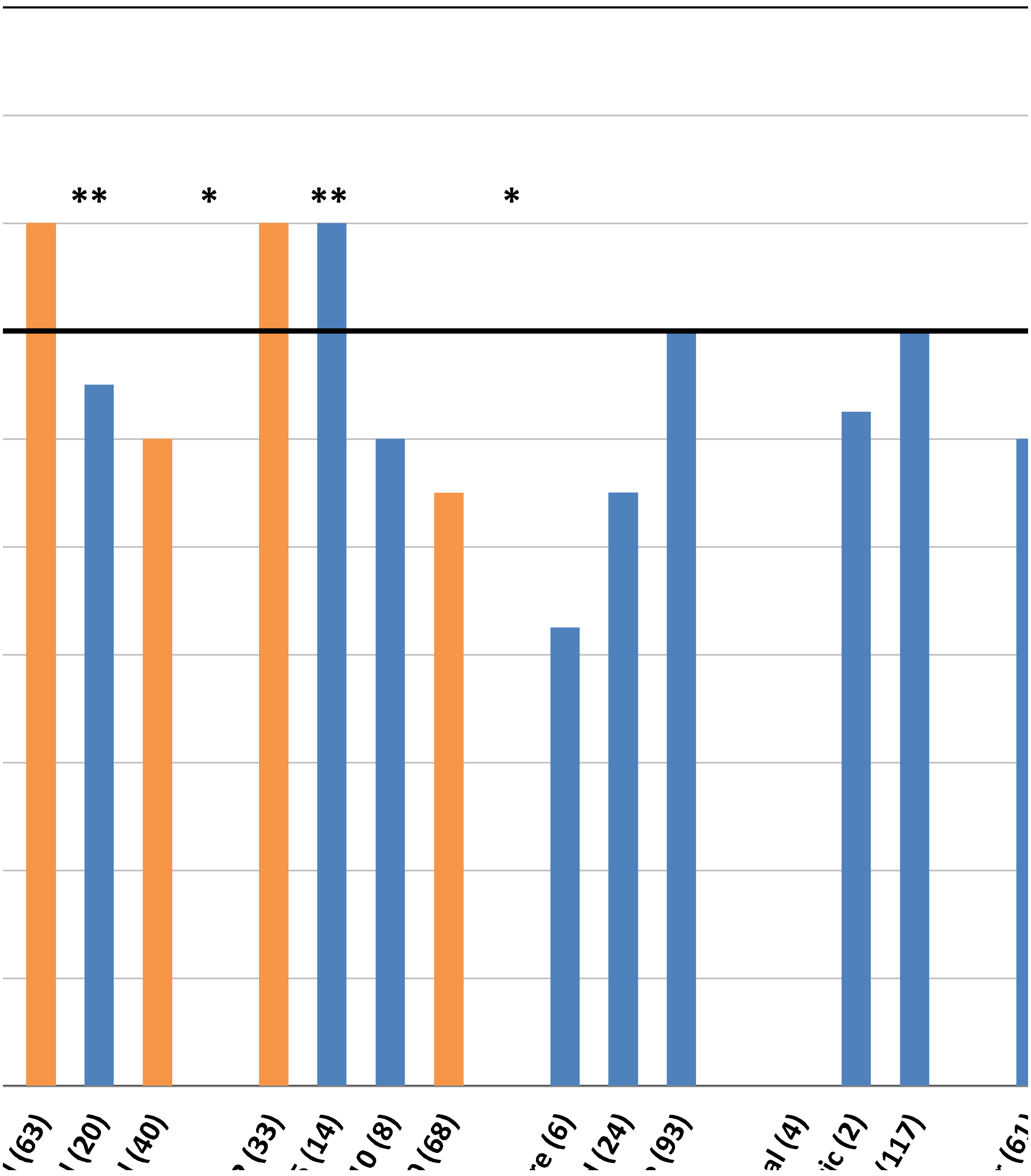
Speech discrimination in quiet (%)

rs

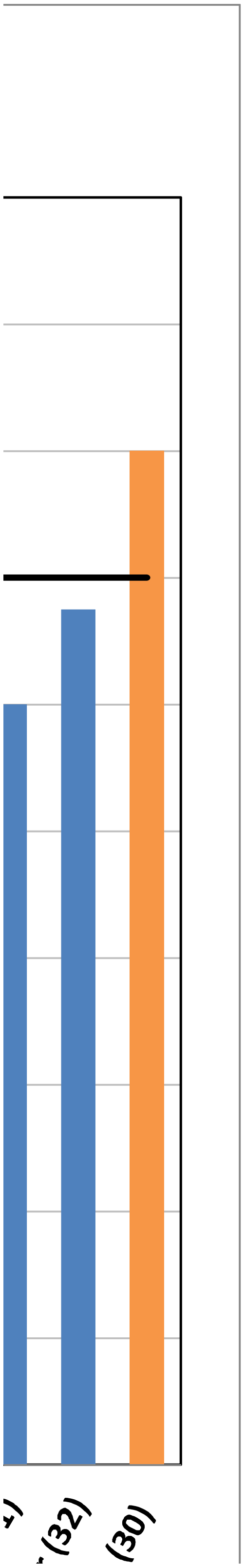

median total (n=123)
in brackets: number (n)
Cochlear Implant Performance Distribution - Genetic a
Freiburger Monosyllables 65 dB
100
90
80
70
60
50
40
30
20
10
0
*
***
(23)
(51)
(45)
is (2)
al (2)
(44)
(19)
(57)
d (3)
(31)
(14)
(21)
(45)
(12)

Neura	Hair Cel	TM and CD	Stria Vascular	Mitochondri	AR	AD	Sporadic	X-linke	0-2	3-6	7-19	20-59	> 60	Congenit	Pre-/P
Gene Expression					Inheritance (Family History)				Age at Implantation					H	

and Clinical Parameters (n=123)



Onset of earing loss (HL)			Delay (years) HL-Onset - Implantation				Grades of Hearing loss			Laterality of hearing loss			Se Im	
al	eri-lingual	Post-lingual	<=2	3-5	6-1	>10	sever	profound	complete	unilatera	asymmetri	bilateral sym. (	first ear	secon


(32)
(30)

d ear

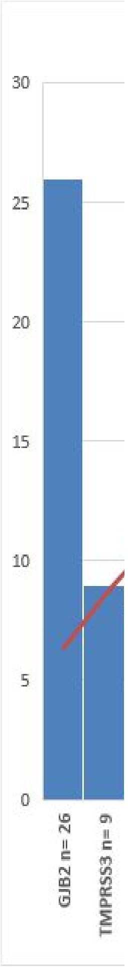
simultaneous

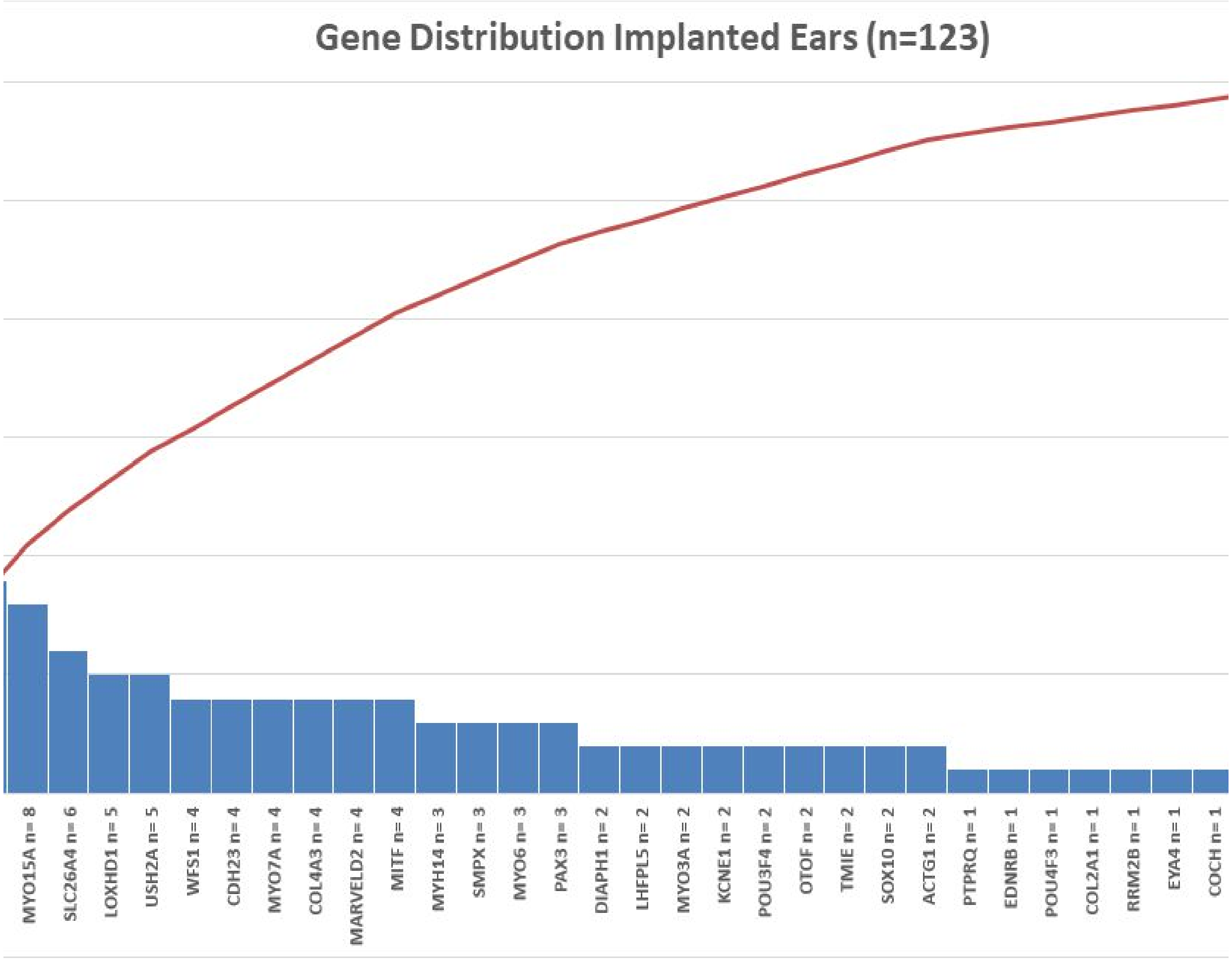
equence of
nplantation

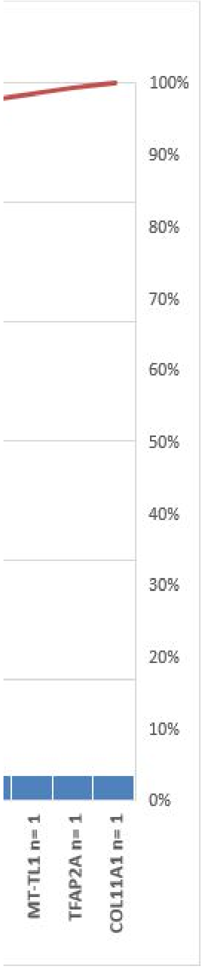
SDC 3 Figure

SDC fig.3

Gen	Anzahl Ohren	Genes	
COL11A1	1	COL11A1 n= 1	1
EDNRB	1	EDNRB n= 1	1
PTPRQ	1	PTPRQ n= 1	1
TMPRSS3	9	TMPRSS3 n= 9	9
WFS1	4	WFS1 n= 4	4
CDH23	4	CDH23 n= 4	4
LOXHD1	5	LOXHD1 n= 5	5
TMIE	2	TMIE n= 2	2
TFAP2A	1	TFAP2A n= 1	1
DIAPH1	2	DIAPH1 n= 2	2
MARVELD2	4	MARVELD2 n= 4	4
EYA4	1	EYA4 n= 1	1
SMPX	3	SMPX n= 3	3
COL2A1	1	COL2A1 n= 1	1
MYH14	3	MYH14 n= 3	3
MYO7A	4	MYO7A n= 4	4
COL4A3	4	COL4A3 n= 4	4
OTOF	2	OTOF n= 2	2
MT-TL1	1	MT-TL1 n= 1	1
POU4F3	1	POU4F3 n= 1	1
MYO6	3	MYO6 n= 3	3
USH2A	5	USH2A n= 5	5
COCH	1	COCH n= 1	1
MYO3A	2	MYO3A n= 2	2
MYO15A	8	MYO15A n= 8	8
SLC26A4	6	SLC26A4 n= 6	6
GJB2	26	GJB2 n= 26	26
KCNE1	2	KCNE1 n= 2	2
POU3F4	2	POU3F4 n= 2	2
RRM2B	1	RRM2B n= 1	1
MITF	4	MITF n= 4	4
PAX3	3	PAX3 n= 3	3
SOX10	2	SOX10 n= 2	2
ACTG1	2	ACTG1 n= 2	2
LHFPL5	2	LHFPL5 n= 2	2




Gene Distribution Implanted Ears (n=123)
MYO15A n= 8
SLC26A4 n= 6
LOXHD1 n= 5
USH2A n= 5
WFS1 n= 4
CDH23 n= 4
MYO7A n= 4
COL4A3 n= 4
MARVELD2 n= 4
MITF n= 4
MYH14 n= 3
SMPX n= 3
MYO6 n= 3
PAX3 n= 3
DIAPH1 n= 2
LHFPL5 n= 2
MYO3A n= 2
KCNE1 n= 2
POU3F4 n= 2
OTOF n= 2
TMIE n= 2
SOX10 n= 2
ACTG1 n= 2
PTPRQ n= 1
EDNRB n= 1
POU4F3 n= 1
COL2A1 n= 1
RRM2B n= 1
EYA4 n= 1
COCH n= 1



100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
MT-TL1 n= 1
TFAP2A n= 1
COL11A1 n= 1

SDC 4 Figure

	80 dB
Genes	median single gene
EDNRB n= 1	15
PTPRQ n= 1	30
CDH23 n= 4	30
COL11A1 n=	50
TMPRSS3 n=	50
MARVELD2 n	52.5
SLC26A4 n= 4	57.5
OTOF n= 2	60
WFS1 n= 4	70
POU4F3 n= 1	70
TFAP2A n= 2	72.5
SMPX n= 3	75
LOXHD1 n= 5	80
DIAPH1 n= 2	80
EYA4 n= 1	80
MYH14 n= 2	80
COL4A3 n= 4	85
MYO6 n= 3	85
GJB2 n= 26	85
TMIE n= 2	90
COL2A1 n= 1	90
MYO7A n= 4	90
MT-TL1 n= 1	90
USH2A n= 5	90
COCH n= 1	90
MYO3A n= 2	90
MYO15A n=	90
PAX3 n= 3	95
SOX10 n= 2	95
ACTG1 n= 2	95
LHFPL5 n= 2	95
POU3F4 n= 2	100
RRM2B n= 1	100

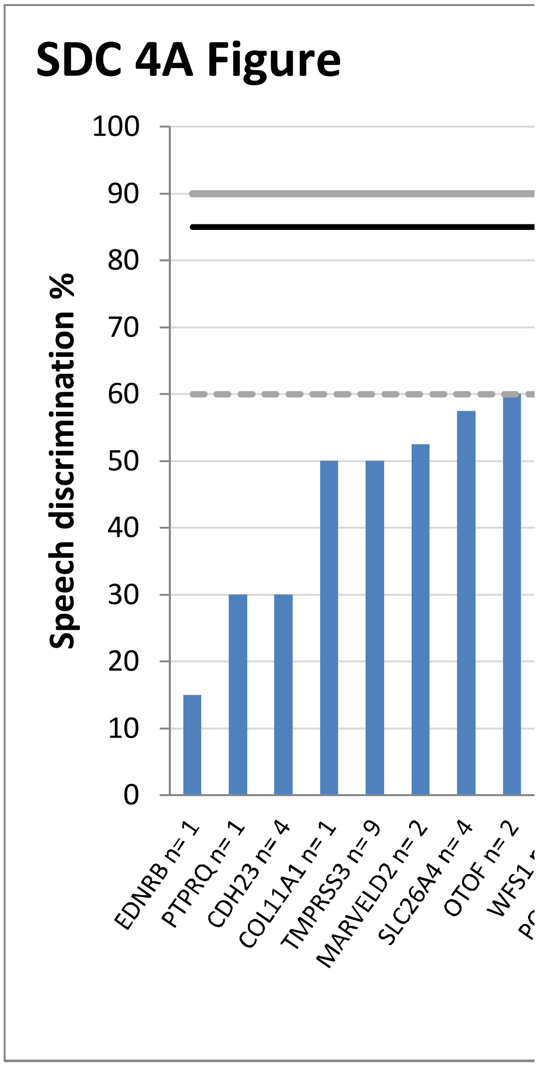
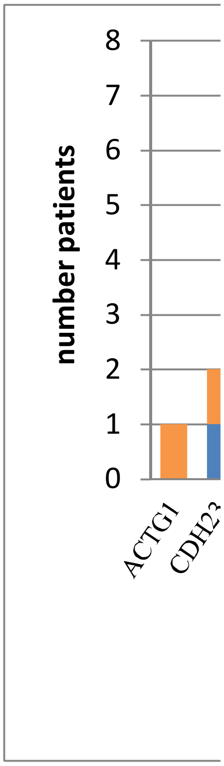


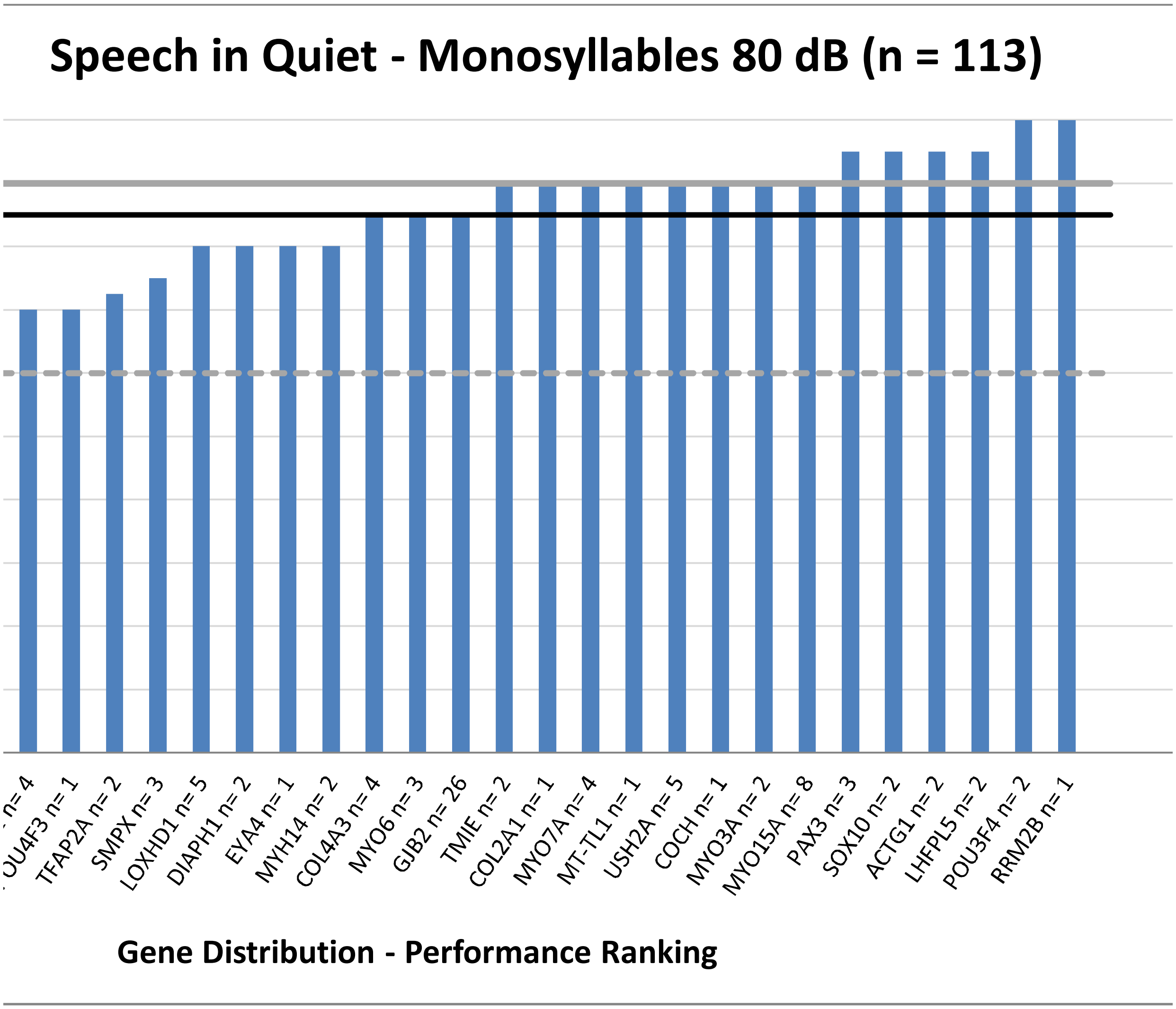
fig. Suppl. 1B

		median 80 dB		Str	SH	TM
	Gen	Neural	HC	Stru-TM	Stru-CD	SV
EDNRB n= 1	EDNRB	15				
TMPRSS3 n=	TMPRSS3	50				
TFAP2A n= 2	TFAP2A	72.5				
WFS1 n= 4	WFS1	70				
DIAPH1 n= 2	DIAPH1	80				
EYA4 n= 1	EYA4	80				
PAX3 n= 3	PAX3	95				
SOX10 n= 2	SOX10	95				
PTPRQ n= 1	PTPRQ		30			
CDH23 n= 4	CDH23		30			
MARVELD2 n	MARVELD2		52.5			
OTOF n= 2	OTOF		60			
POU4F3 n= 1	POU4F3		70			
SMPX n= 3	SMPX		75			
LOXHD1 n= 5	LOXHD1		80			
MYH14 n= 2	MYH14		80			
MYO6 n= 3	MYO6		85			
TMIE n= 2	TMIE		90			
MYO7A n= 4	MYO7A		90			
MYO3A n= 2	MYO3A		90			
USH2A n= 5	USH2A		90			
MYO15A n=	MYO15A		90			
ACTG1 n= 2	ACTG1		95			
LHFPL5 n= 2	LHFPL5		95			
COL2A1 n= 1	COL2A1			90		
COL11A1 n=	COL11A1				50	
SLC26A4 n=	SLC26A4				57.5	
COL4A3 n= 4	COL4A3				85	
GJB2 n= 26	GJB2				85	
COCH n= 1	COCH				90	
POU3F4 n= 2	POU3F4				100	
MT-TL1 n= 1	MT-TL1					
RRM2B n= 1	RRM2B					

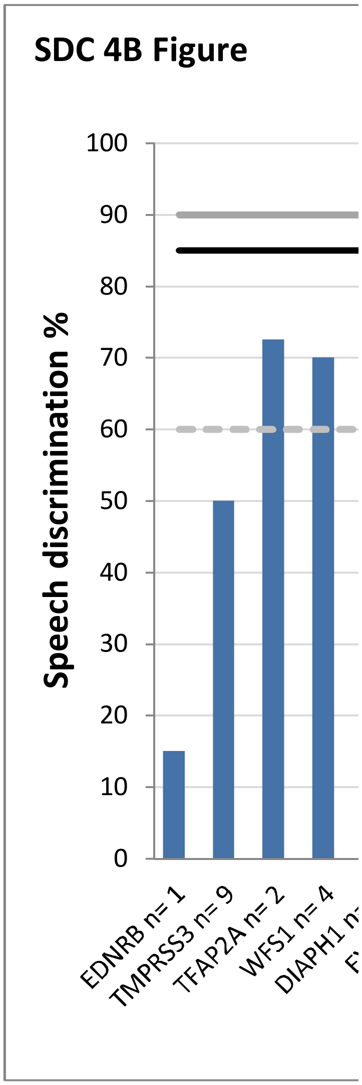
Impl. Age 6-17 y. 18+ y.

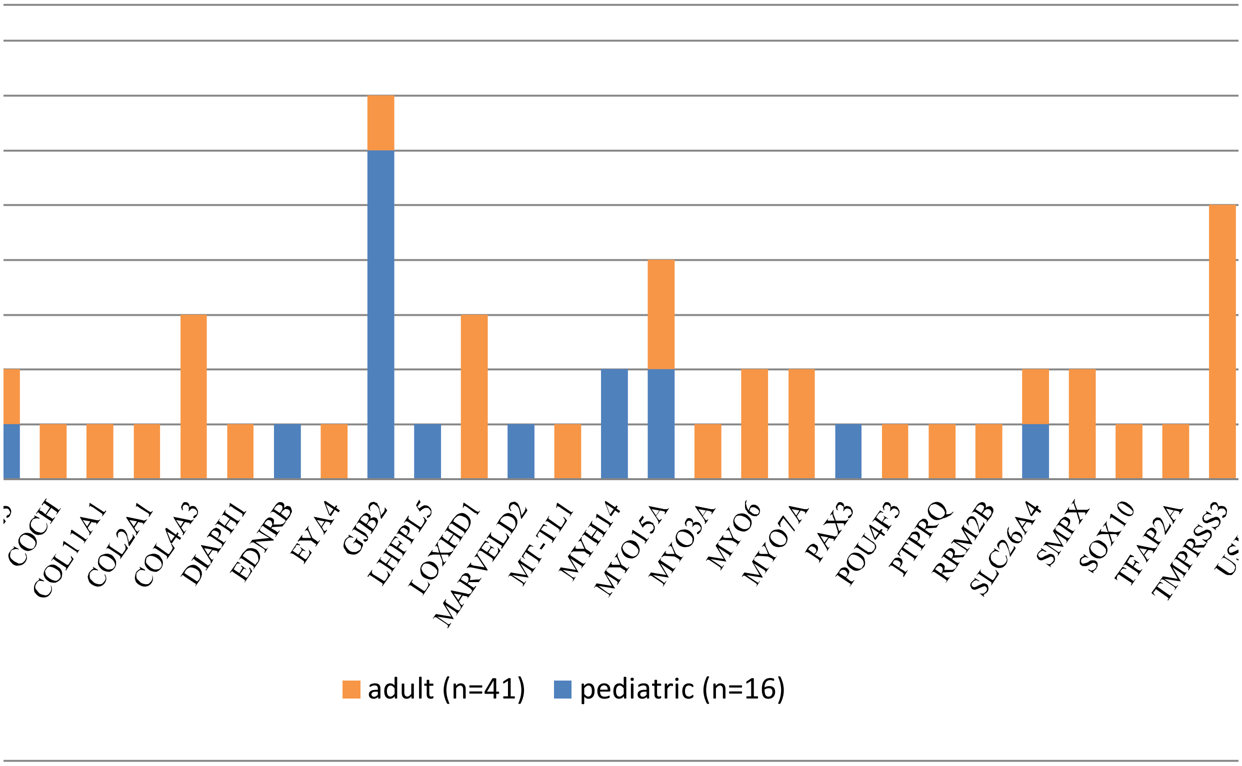
Gen	pediatric (n=16)	adult (n=41)	
ACTG1		1	
CDH23	1	1	
COCH		1	
COL11A1		1	
COL2A1		1	
COL4A3		3	
DIAPH1		1	
EDNRB	1		
EYA4		1	
GJB2	6	1	**Pat. 297: ped.+ adult**
LHFPL5	1		
LOXHD1		3	
MARVELD2	1		
MT-TL1		1	
MYH14	2		
MYO15A	2	2	
MYO3A		1	
MYO6		2	
MYO7A		2	
PAX3	1		
POU4F3		1	
PTPRQ		1	
RRM2B		1	
SLC26A4	1	1	
SMPX		2	
SOX10		1	
TFAP2A		1	
TMPRSS3		5	
USH2A		3	
WFS1		3	

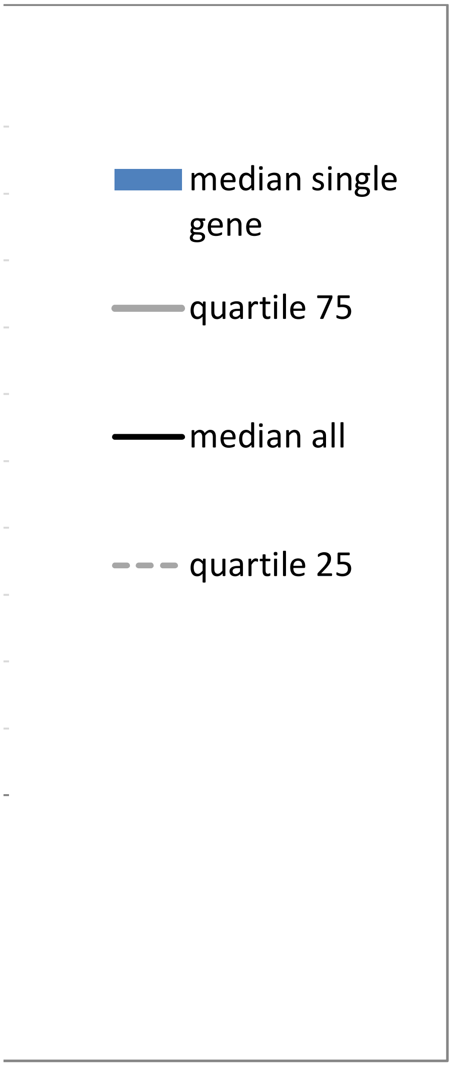


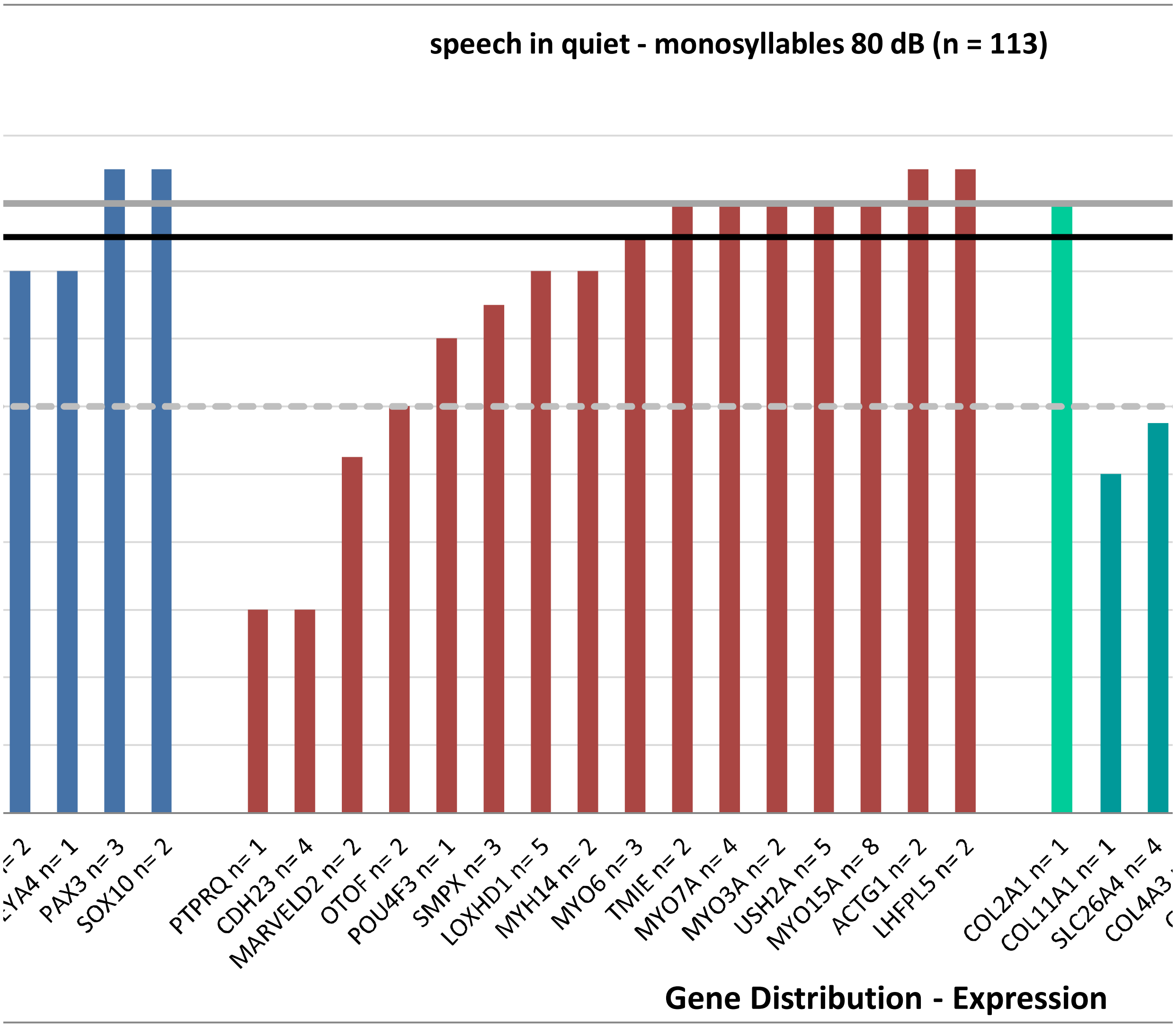

Speech in Quiet - Monosyllables 80 dB (n = 113)
n= 4
OU4F3 n= 1
TFAP2A n= 2
SMPX n= 3
LOXHD1 n= 5
DIAPH1 n= 2
EYA4 n= 1
MYH14 n= 2
COL4A3 n= 4
MYO6 n= 3
GJB2 n= 26
TMIE n= 2
COL2A1 n= 1
MYO7A n= 4
MT-TL1 n= 1
USH2A n= 5
COCH n= 1
MYO3A n= 2
MYO15A n= 8
PAX3 n= 3
SOX10 n= 2
ACTG1 n= 2
LHFPL5 n= 2
POU3F4 n= 2
RRM2B n= 1
Gene Distribution - Performance Ranking

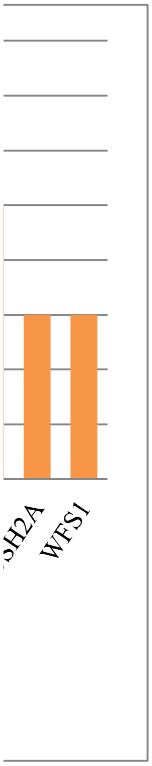
S			
Mito	median all	quartile 25	quartile 75
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
	85	60	90
90	85	60	90
100	85	60	90
	85	60	90

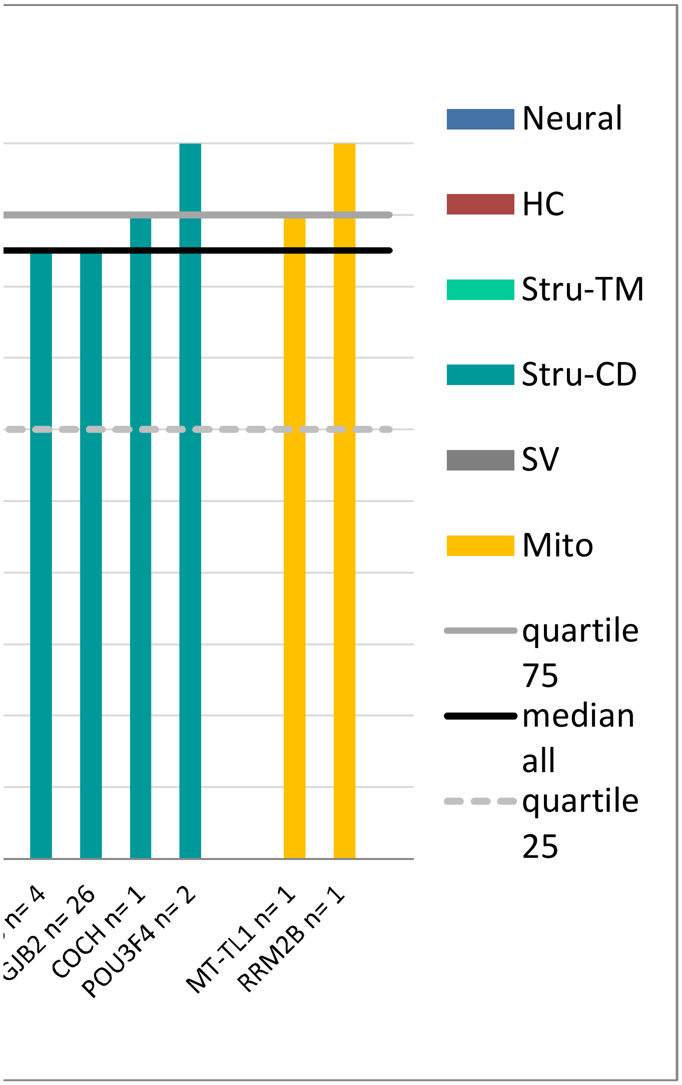



COCH
COL11A1
COL2A1
COL4A3
DIAPH1
EDNRB
EYA4
GJB2
LHFPL5
LOXHD1
MARVELD2
MT-TL1
MYH14
MYO15A
MYO3A
MYO6
MYO7A
PAX3
POU4F3
PTPRQ
RRM2B
SLC26A4
SMPX
SOX10
TFAP2A
TMPRSS3
US
adult (n=41)
pediatric (n=16)


median single gene
quartile 75
median all
quartile 25


speech in quiet - monosyllables 80 dB (n = 113)
= 2
YA4 n= 1
PAX3 n= 3
SOX10 n= 2
PTPRQ n= 1
CDH23 n= 4
MARVELD2 n= 2
OTOF n= 2
POU4F3 n= 1
SMPX n= 3
LOXHD1 n= 5
MYH14 n= 2
MYO6 n= 3
TMIE n= 2
MYO7A n= 4
MYO3A n= 2
USH2A n= 5
MYO15A n= 8
ACTG1 n= 2
LHFPL5 n= 2
COL2A1 n= 1
COL11A1 n= 1
SLC26A4 n= 4
COL4A3
Gene Distribution - Expression


SH2A
WFS1


n= 4
GJB2 n= 26
COCH n= 1
POU3F4 n= 2
MT-TL1 n= 1
RRM2B n= 1
Neural
HC
Stru-TM
Stru-CD
SV
Mito
quartile 75
median all
quartile 25

SPSS 27: exploratory data analysis

Case Processing Summary

		Cases			
		Valid		Missing	
	group	N	Percent	N	Percent
Fb_all	age_gt6	78	100.0%	0	0.0%
	age0_6	45	100.0%	0	0.0%
	congenital	47	100.0%	0	0.0%
	pp_lingual	76	100.0%	0	0.0%
	gap_gt5	76	100.0%	0	0.0%
	gap0_5	47	100.0%	0	0.0%
	neural_genes	23	100.0%	0	0.0%
	other_genes	100	100.0%	0	0.0%
	first_sec_ears	93	100.0%	0	0.0%
	simult_ears	30	100.0%	0	0.0%

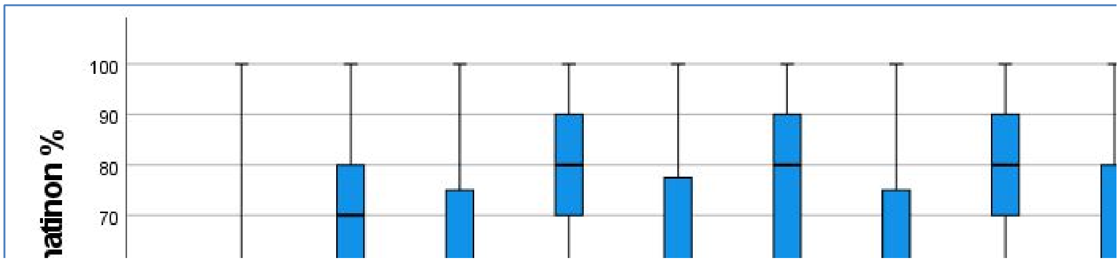
Tests of Normality[a] **all groups besides neural genes show significant differen**

		Kolmogorov-Smirnov[b]			
	group	Statistic	df	Sig.	Statistic
Fb_all	age_gt6	0.111	78	0.019	0.941
	age0_6	0.263	45	0.000	0.811
	congenital	0.184	47	0.000	0.926
	pp_lingual	0.144	76	0.000	0.915
	gap_gt5	0.111	76	0.021	0.943
	gap0_5	0.251	47	0.000	0.808
	neural_genes	0.137	23	**,200***	0.916
	other_genes	0.176	100	0.000	0.909
	first_sec_ears	0.129	93	0.001	0.935
	simult_ears	0.245	30	0.000	0.792

*. This is a lower bound of the true significance.

a. There are no valid cases for Fb_all when group = ,000. Statistics cannot be computed for this level.

b. Lilliefors Significance Correction



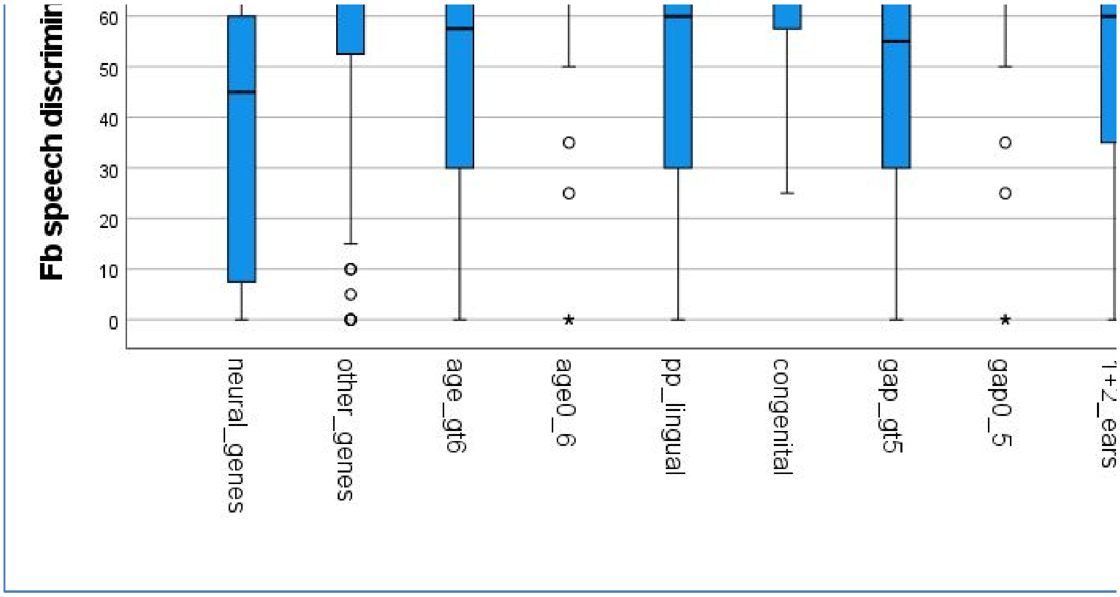


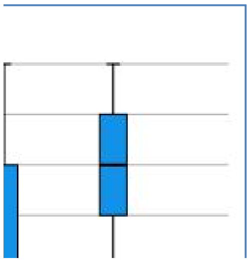
fig. Boxplots:

° outliers (outside of whiskers)
* extreme outliers (>3x interquartile range)
box: upper line 75% percentile
middle line median
lower line 25% percentile
whiskers: total length = 1.5x interquartile range

Total	
N	Percent
78	100.0%
45	100.0%
47	100.0%
76	100.0%
76	100.0%
47	100.0%
23	100.0%
100	100.0%
93	100.0%
30	100.0%

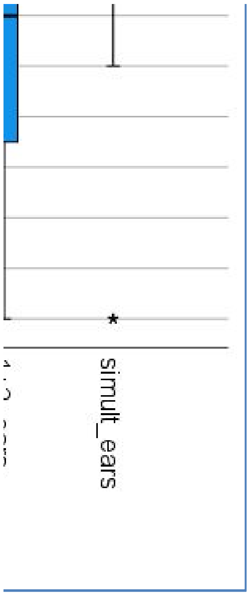
ce to normal distribution

Shapiro-Wilk	
df	Sig.
78	0.001
45	0.000
47	0.005
76	0.000
76	0.002
47	0.000
23	**0.054**
100	0.000
93	0.000
30	0.000



Descriptives[a]

group			
Fb_all	age_gt6	Mean	
		95% Confidence Interval for Mean	Lower Bound
			Upper Bound
		5% Trimmed Mean	
		Median	
		Variance	
		Std. Deviation	
		Minimum	
		Maximum	
		Range	
		Interquartile Range	
		Skewness	
		Kurtosis	
	age0_6	Mean	
		95% Confidence Interval for Mean	Lower Bound
			Upper Bound
		5% Trimmed Mean	
		Median	
		Variance	
		Std. Deviation	
		Minimum	
		Maximum	
		Range	
		Interquartile Range	
		Skewness	
		Kurtosis	
	congenit	Mean	
		95% Confidence Interval for Mean	Lower Bound
			Upper Bound
		5% Trimmed Mean	
		Median	
		Variance	
		Std. Deviation	
		Minimum	
		Maximum	
		Range	
		Interquartile Range	
		Skewness	
		Kurtosis	



first_se	Mean	
	95% Confidence Interval for Mean	Lower Bound
		Upper Bound
	5% Trimmed Mean	
	Median	
	Variance	
	Std. Deviation	
	Minimum	
	Maximum	
	Range	
	Interquartile Range	
	Skewness	
	Kurtosis	
gap_gt5	Mean	
	95% Confidence Interval for Mean	Lower Bound
		Upper Bound
	5% Trimmed Mean	
	Median	
	Variance	
	Std. Deviation	
	Minimum	
	Maximum	
	Range	
	Interquartile Range	
	Skewness	
	Kurtosis	
gap0_5	Mean	
	95% Confidence Interval for Mean	Lower Bound
		Upper Bound
	5% Trimmed Mean	
	Median	
	Variance	
	Std. Deviation	
	Minimum	
	Maximum	
	Range	
	Interquartile Range	
	Skewness	
	Kurtosis	
neural_g	Mean	
	95% Confidence Interval for Mean	Lower Bound
		Upper Bound

	5% Trimmed Mean	
	Median	
	Variance	
	Std. Deviation	
	Minimum	
	Maximum	
	Range	
	Interquartile Range	
	Skewness	
	Kurtosis	
other_ge	Mean	
	95% Confidence Interval for Mean	Lower Bound
		Upper Bound
	5% Trimmed Mean	
	Median	
	Variance	
	Std. Deviation	
	Minimum	
	Maximum	
	Range	
	Interquartile Range	
	Skewness	
	Kurtosis	
pp_lingu	Mean	
	95% Confidence Interval for Mean	Lower Bound
		Upper Bound
	5% Trimmed Mean	
	Median	
	Variance	
	Std. Deviation	
	Minimum	
	Maximum	
	Range	
	Interquartile Range	
	Skewness	
	Kurtosis	
simult_e	Mean	
	95% Confidence Interval for Mean	Lower Bound
		Upper Bound
	5% Trimmed Mean	
	Median	
	Variance	
	Std. Deviation	

	Minimum
	Maximum
	Range
	Interquartile Range
	Skewness
	Kurtosis

a. There are no valid cases for Fb_all when group = ,000. Statistics cannot be

Statistic	Std. Error
53.14	3.178
46.81	
59.47	
53.63	
57.50	
787.733	
28.067	
0	
100	
100	
45	
-0.476	0.272
-0.726	0.538
75.56	3.565
68.37	
82.74	
78.24	
80.00	
571.843	
23.913	
0	
100	
100	
20	
-1.708	0.354
3.080	0.695
74.36	2.963
68.40	
80.33	
75.48	
80.00	
412.627	
20.313	
25	
100	
75	
35	
-0.649	0.347
-0.377	0.681

56.94	2.944
51.09	
62.78	
57.80	
60.00	
805.996	
28.390	
0	
100	
100	
45	
-0.566	0.250
-0.653	0.495
52.37	3.211
45.97	
58.77	
52.76	
55.00	
783.649	
27.994	
0	
100	
100	
45	
-0.446	0.276
-0.740	0.545
75.85	3.425
68.96	
82.75	
78.52	
80.00	
551.434	
23.483	
0	
100	
100	
20	
-1.756	0.347
3.331	0.681
42.17	6.957
27.75	
56.60	

41.34	
45.00	
1,113.241	
33.365	
0	
100	
100	
60	
0.199	0.481
-1.058	0.935
65.75	2.568
60.66	
70.84	
67.33	
70.00	
659.280	
25.676	
0	
100	
100	
29	
-0.947	0.241
0.276	0.478
53.29	3.461
46.39	
60.18	
53.79	
60.00	
910.368	
30.172	
0	
100	
100	
49	
-0.509	0.276
-0.950	0.545
75.00	4.624
65.54	
84.46	
77.78	
80.00	
641.379	
25.325	

0	
100	
100	
20	
-1.796	0.427
3.590	0.833

e computed for this level.

Hypothesis Test Summary				
	Null Hypothesis	Test	Sig.^{a,b}	Decision
1	The distribution of Fb_all is the same across categories of group.	**Independent-Samples Kruskal-Wallis Test**	0.000	Reject the null hypothesis.
a. The significance level is ,050.				
b. Asymptotic significance is displayed.				

Pairwise Comparisons of group, sorted by effect size in descending o

	Sample 1-Sample 2	**Test Statistic**	**Std. Error**	**Std. Test Statistic (z)**	**Sig.**
1	neural_genes-simult_ears	-203.181	49.060	-4.141	0.000
2	neural_genes-gap0_5	208.550	45.045	4.630	0.000
3	neural_genes-age0_6	206.959	45.373	4.561	0.000
4	neural_genes-congenital	186.848	45.045	4.148	0.000
5	gap_gt5-gap0_5	164.597	32.848	5.011	0.000
6	gap_gt5-age0_6	163.006	33.296	4.896	0.000
7	age_gt6-gap0_5	-159.459	32.687	-4.878	0.000
8	age_gt6-age0_6	157.868	33.137	4.764	0.000
9	pp_lingual-gap0_5	151.176	32.848	4.602	0.000
10	pp_lingual-age0_6	149.585	33.296	4.493	0.000
11	gap_gt5-simult_ears	-159.228	38.168	-4.172	0.000
12	gap_gt5-congenital	142.895	32.848	4.350	0.000
13	age_gt6-simult_ears	-154.090	38.029	-4.052	0.000
14	age_gt6-congenital	-137.756	32.687	-4.214	0.000
15	pp_lingual-simult_ears	-145.807	38.168	-3.820	0.000
16	pp_lingual-congenital	129.474	32.848	3.942	0.000
17	first_sec_ear-gap0_5	-132.777	31.680	-4.191	0.000
18	first_sec_ear-age0_6	131.186	32.144	4.081	0.000
19	first_sec_ear-simult_ears	-127.409	37.168	-3.428	0.001
20	first_sec_ear-congenital	111.075	31.680	3.506	0.000

21	gap_gt5-other_genes	-87.470	26.938	-3.247	0.001
22	neural_genes-	-131.423	40.936	-3.210	0.001
23	age_gt6-other_genes	-82.331	26.741	-3.079	0.002
24	pp_lingual-other_genes	74.049	26.938	2.749	0.006
25	other_genes-gap0_5	77.127	31.306	2.464	0.014
26	other_genes-age0_6	75.536	31.776	2.377	0.017
27	neural_genes-gap_gt5	43.953	42.127	1.043	0.297
28	neural_genes-age_gt6	49.091	42.001	1.169	0.242
29	neural_genes-pp_lingual	-57.374	42.127	-1.362	0.173
30	neural_genes-first_sec_ear	75.773	41.223	1.838	0.066
31	gap_gt5-age_gt6	5.138	28.531	0.180	0.857
32	gap_gt5-pp_lingual	-13.421	28.716	-0.467	0.640
33	gap_gt5-first_sec_ear	31.819	27.372	1.162	0.245
34	age_gt6-pp_lingual	-8.283	28.531	-0.290	0.772
35	age_gt6-first_sec_ear	-26.681	27.178	-0.982	0.326
36	pp_lingual-first_sec_ear	18.398	27.372	0.672	0.501
37	first_sec_ear-other_genes	-55.650	25.501	-2.182	0.029
38	other_genes-congenital	55.425	31.306	1.770	0.077
39	other_genes-simult_ears	-71.758	36.849	-1.947	0.051
40	congenital-simult_ears	-16.333	41.367	-0.395	0.693
41	congenital-age0_6	20.111	36.919	0.545	0.586
42	congenital-gap0_5	-21.702	36.516	-0.594	0.552
43	simult_ears-age0_6	3.778	41.723	0.091	0.928
44	simult_ears-gap0_5	5.369	41.367	0.130	0.897
45	age0_6-gap0_5	-1.591	36.919	-0.043	0.966

Each row tests the null hypothesis that the Sample 1 and Sample 2 distributions are the same.
Asymptotic significances (2-sided tests) are displayed. The significance level is ,050.

a. Significance values have been adjusted by the Bonferroni correction for multiple tests.

Independent-Samples Kruskal-Wallis Test Summary	
Total N	615
Test Statistic	85,399[a]
Degree Of Freedom	9
Asymptotic Sig.(2-sided test)	0.000

a. The test statistic is adjusted for ties.

rder

Adj. Sig.[a]	n	effect size r*	effect type
0.002	53	0.57	strong
0.000	70	0.55	strong
0.000	68	0.55	strong
0.002	70	0.50	strong
0.000	123	0.45	middle
0.000	121	0.45	middle
0.000	125	0.44	middle
0.000	123	0.43	middle
0.000	123	0.41	middle
0.000	121	0.41	middle
0.002	106	0.41	middle
0.001	123	0.39	middle
0.003	108	0.39	middle
0.001	125	0.38	middle
0.007	106	0.37	middle
0.004	123	0.36	middle
0.002	140	0.35	middle
0.002	138	0.35	middle
0.033	123	0.31	middle
0.025	140	0.30	middle

group
age_gt6
age0_6
congenital
pp_lingual
gap_gt5
gap0_5
neural_genes
other_genes
first_sec_ears
simult_ears

0.064
0.073
0.114
0.329
0.756
0.960
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000

* effect size Cohen's d   r=z/sqrt(n)

Cohen, J. (1992). A power primer. *Psychological Bulletin, 122* (1), 155-1

N
78
45
47
76
76
47
23
100
93
30

SPSS 27: univariate analysis of variance

Descriptive Statistics

Dependent Variable:

group_std	Mean	Std. Deviation	N
age 0-6	75.56	23.913	45
age gt6	53.14	28.067	78
congenital	74.36	20.313	47
first_sec_ears	56.94	28.390	93
gap 0-5	75.85	23.483	47
gap gt5	52.37	27.994	76
neural genes	42.17	33.365	23
other genes	65.75	25.676	100
peri-post-lingual	53.29	30.172	76
simult_ears	75.00	25.325	30
Total	61.34	28.558	615

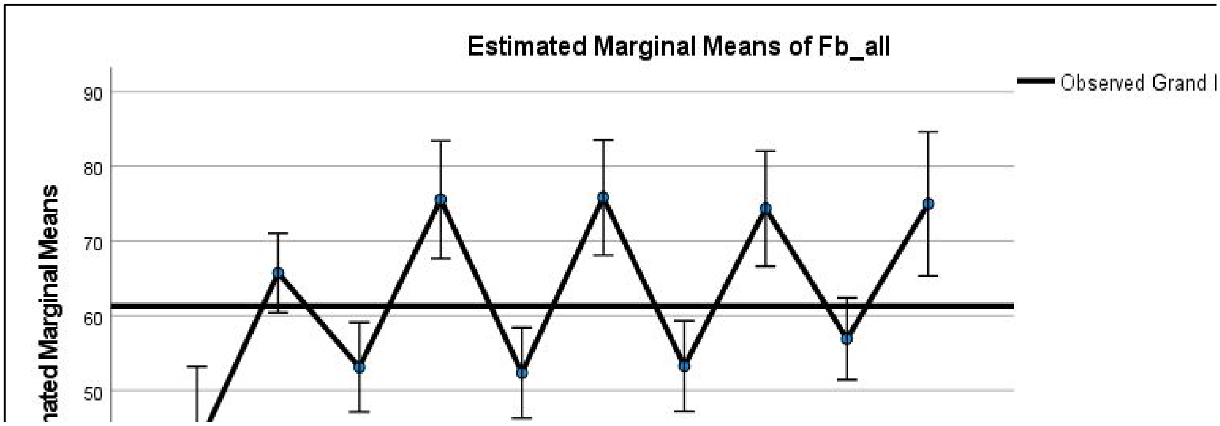
Levene's Test of Equality of Error Variances: variances not homogeneous

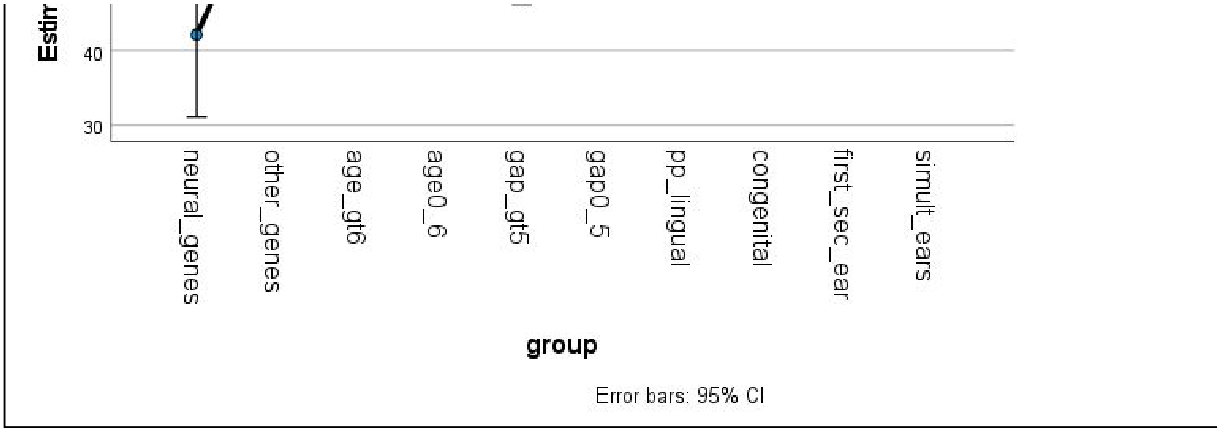
		Levene Statistic	df1	df2	Sig.	
Fb_all	Based on Mean	2.870	9	605	**0.003**	**no valid ANOVA; s**
	Based on Median	3.040	9	605	**0.001**	
	Based on Median and with adjusted df	3.040	9	590.695	0.001	
	Based on trimmed mean	3.226	9	605	0.001	

Tests the null hypothesis that the error variance of the dependent variable is equal across groups.

a. Dependent variable: Fb_all

b. Design: Intercept + group





Tests of Between-Subjects Effects

Dependent Variable:

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	61041,941[a]	9	6,782.438	9.332	0.000	0.122
Intercept	1,935,260.926	1	1,935,260.926	2,662.640	0.000	0.815
group	61,041.941	9	6,782.438	9.332	0.000	0.122
Error	439,726.351	605	726.820			
Total	2,814,875.000	615				
Corrected Total	500,768.293	614				

a. R Squared = .122 (Adjusted R Squared = .109)

b. Computed using alpha = .05

Parameter Estimates

Dependent Variable:

Parameter	B	Std. Error	t	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Intercept	75.000	4.922	15.237	0.000	65.333	84.667
[group_std=age 0-6]	0.556	6.354	0.087	0.930	-11.924	13.035
[group_std=age gt6]	-21.859	5.792	-3.774	0.000	-33.234	-10.484
[group_std=congenital]	-0.638	6.300	-0.101	0.919	-13.011	11.734
[group_std=first_sec_ears]	-18.065	5.661	-3.191	0.001	-29.181	-6.948
[group_std=gap 0-5]	0.851	6.300	0.135	0.893	-11.522	13.224
[group_std=gap gt5]	-22.632	5.813	-3.893	0.000	-34.048	-11.216

[group_std=neural genes]	-32.826	7.472	-4.393	0.000	-47.500	-18.152
[group_std=other genes]	-9.250	5.612	-1.648	0.100	-20.272	1.772
[group_std=peri-post-lingual]	-21.711	5.813	-3.735	0.000	-33.127	-10.294
[group_std=simult_ears]	0[a]					

a. This parameter is set to zero because it is redundant.

b. Computed using alpha = .05

Welch-ANOVA (variances inhomogeneou

Robust Tests of Equal

Fb_all

	Statistic[a]	df1
Welch	9.784	9

a. Asymptotically F distributed.

ee Welch-Anova for results

		Mean Difference (I-J)
neural	**other**	-23,576*
	age0_6	-33,382*
	age_gt6	-10.967
	congenital	-32,188*
	pp_lingual	-11.116
	gap0_5	-33,677*
	gap_gt5	-10.195
	simult_ears	-32,826*
	first-sec_ears	-14.762
other	neural	23,576*
	age0_6	-9.806
	age_gt6	12.609
	congenital	-8.612
	pp_lingual	12.461
	gap0_5	-10.101
	gap_gt5	13.382
	simult_ears	-9.250
	first-sec_ears	8.815
age0_6	neural	33,382*
	other	9.806
	age_gt6	22,415*
	congenital	1.194
	pp_lingual	22,266*
	gap0_5	-0.296

Mean

Noncent. Parameter	Observed Power[b]
83.985	1.000
2,662.640	1.000
83.985	1.000

Partial Eta Squared	Noncent. Parameter	Observed Power[b]
0.277	15.237	1.000
0.000	0.087	0.051
0.023	3.774	0.965
0.000	0.101	0.051
0.017	3.191	0.890
0.000	0.135	0.052
0.024	3.893	0.973

	gap_gt5	23,187*
	simult_ears	0.556
	first-sec_ears	18,620*
age_gt6	neural	10.967
	other	-12.609
	age0_6	-22,415*
	congenital	-21,221*
	pp_lingual	-0.148
	gap0_5	-22,710*
	gap_gt5	0.773
	simult_ears	-21,859*
	first-sec_ears	-3.794
congenital	neural	32,188*
	other	8.612
	age0_6	-1.194
	age_gt6	21,221*
	pp_lingual	21,072*
	gap0_5	-1.489
	gap_gt5	21,993*
	simult_ears	-0.638
	first-sec_ears	17,426*
pp_lingual	neural	11.116
	other	-12.461
	age0_6	-22,266*
	age_gt6	0.148
	congenital	-21,072*
	gap0_5	-22,562*
	gap_gt5	0.921
	simult_ears	-21,711*
	first-sec_ears	-3.646
gap0_5	neural	33,677*
	other	10.101
	age0_6	0.296
	age_gt6	22,710*
	congenital	1.489
	pp_lingual	22,562*
	gap_gt5	23,483*

0.031	4.393	0.992
0.004	1.648	0.377
0.023	3.735	0.962

	simult_ears	0.851
	first-sec_ears	18,916*
gap_gt5	neural	10.195
	other	-13.382
	age0_6	-23,187*
	age_gt6	-0.773
	congenital	-21,993*
	pp_lingual	-0.921
	gap0_5	-23,483*
	simult_ears	-22,632*
	first-sec_ears	-4.567
simult_ears	neural	32,826*
	other	9.250
	age0_6	-0.556
	age_gt6	21,859*
	congenital	0.638
	pp_lingual	21,711*
	gap0_5	-0.851
	gap_gt5	22,632*
	first-sec_ears	18.065
first-sec_ears	neural	14.762
	other	-8.815
	age0_6	-18,620*
	age_gt6	3.794
	congenital	-17,426*
	pp_lingual	3.646
	gap0_5	-18,916*
	gap_gt5	4.567
	simult_ears	-18.065

*. The mean differe

s)

lity of Means

df2	Sig.
189.053	**0.000**

Multiple Comparisons

Std. Error	Sig.	95% Confidence Interval	
		Lower Bound	Upper Bound
6.235	**0.008**	-44.00	-3.15
6.910	**0.000**	-56.02	-10.74
6.397	1.000	-31.93	9.99
6.860	**0.000**	-54.67	-9.71
6.416	1.000	-32.14	9.91
6.860	**0.000**	-56.16	-11.20
6.416	1.000	-31.22	10.83
7.472	**0.001**	-57.31	-8.34
6.278	0.856	-35.33	5.81
6.235	**0.008**	3.15	44.00
4.839	1.000	-25.66	6.05
4.073	0.092	-0.74	25.95
4.768	1.000	-24.23	7.01
4.103	0.112	-0.98	25.90
4.768	1.000	-25.72	5.52
4.103	0.053	-0.06	26.82
5.612	1.000	-27.64	9.14
3.884	1.000	-3.91	21.54
6.910	**0.000**	10.74	56.02
4.839	1.000	-6.05	25.66
5.047	**0.000**	5.88	38.95
5.623	1.000	-17.23	19.62
5.071	**0.001**	5.65	38.88
5.623	1.000	-18.72	18.13

mean Fb
42.2
75.6
53.1
74.4
75.9
52.4
53.3

5.071	**0.000**	6.57	39.80
6.354	1.000	-20.26	21.38
4.896	**0.007**	2.58	34.66
6.397	1.000	-9.99	31.93
4.073	0.092	-25.95	0.74
5.047	**0.000**	-38.95	-5.88
4.978	**0.001**	-37.53	-4.91
4.345	1.000	-14.39	14.09
4.978	**0.000**	-39.02	-6.40
4.345	1.000	-13.46	15.01
5.792	**0.008**	-40.84	-2.88
4.139	1.000	-17.36	9.77
6.860	**0.000**	9.71	54.67
4.768	1.000	-7.01	24.23
5.623	1.000	-19.62	17.23
4.978	**0.001**	4.91	37.53
5.003	**0.001**	4.68	37.46
5.561	1.000	-19.71	16.73
5.003	**0.001**	5.60	38.38
6.300	1.000	-21.28	20.00
4.825	**0.015**	1.62	33.24
6.416	1.000	-9.91	32.14
4.103	0.112	-25.90	0.98
5.071	**0.001**	-38.88	-5.65
4.345	1.000	-14.09	14.39
5.003	**0.001**	-37.46	-4.68
5.003	**0.000**	-38.95	-6.17
4.373	1.000	-13.41	15.25
5.813	**0.009**	-40.76	-2.66
4.169	1.000	-17.31	10.01
6.860	**0.000**	11.20	56.16
4.768	1.000	-5.52	25.72
5.623	1.000	-18.13	18.72
4.978	**0.000**	6.40	39.02
5.561	1.000	-16.73	19.71
5.003	**0.000**	6.17	38.95
5.003	**0.000**	7.09	39.87

other
age0_6
congenital
gap0_5
simult_ears

age_gt6
pp_lingual
gap_gt5
first-sec_ears

congenital
gap0_5
simult_ears

pp_lingual
gap_gt5

gap_gt5
first-sec_ears

simult_ears

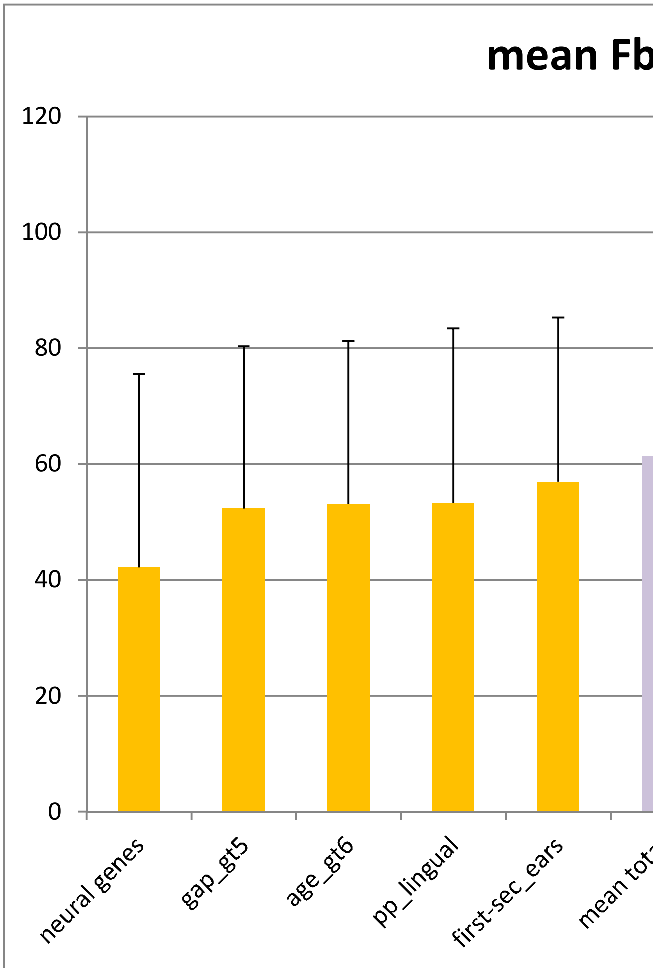
simult_ears

6.300	1.000	-19.79	21.49
4.825	**0.004**	3.11	34.72
6.416	1.000	-10.83	31.22
4.103	0.053	-26.82	0.06
5.071	0.000	-39.80	-6.57
4.345	1.000	-15.01	13.46
5.003	**0.001**	-38.38	-5.60
4.373	1.000	-15.25	13.41
5.003	**0.000**	-39.87	-7.09
5.813	**0.005**	-41.68	-3.59
4.169	1.000	-18.23	9.09
7.472	**0.001**	8.34	57.31
5.612	1.000	-9.14	27.64
6.354	1.000	-21.38	20.26
5.792	**0.008**	2.88	40.84
6.300	1.000	-20.00	21.28
5.813	**0.009**	2.66	40.76
6.300	1.000	-21.49	19.79
5.813	**0.005**	3.59	41.68
5.661	0.067	-0.48	36.61
6.278	0.856	-5.81	35.33
3.884	1.000	-21.54	3.91
4.896	**0.007**	-34.66	-2.58
4.139	1.000	-9.77	17.36
4.825	**0.015**	-33.24	-1.62
4.169	1.000	-10.01	17.31
4.825	**0.004**	-34.72	-3.11
4.169	1.000	-9.09	18.23
5.661	0.067	-36.61	0.48

nce is significant at the 0.05 level.

mean Fb	**65.8**	**75.6**	**53.1**	**74.4**	**53.3**	**75.9**	**52.4**
	other	age0_6	age_gt6	congenital	pp_lingual	gap0_5	gap_gt5
neural	*	*		*		*	
age0_6			*		*		*
age_gt6				*		*	
congenital					*		*
gap0_5							*
gap_gt5							
pp_lingual							

factor	**mean Fb**	**SD**
neural genes	**42.2**	**33.4**
gap_gt5	**52.4**	**28.0**
age_gt6	**53.1**	**28.1**
pp_lingual	**53.3**	**30.2**
first-sec_ears	**56.9**	**28.4**
mean total	**61.3**	**28.6**
other genes	**65.8**	**25.7**
congenital	**74.4**	**20.3**
simult_ears	**75.0**	**25.3**
age0_6	**75.6**	**23.9**
gap0_5	**75.9**	**23.5**



neural	**Effektstärke Cohens d**	
*	0.87	groß
*	1.22	groß
*	1.27	groß
*	1.24	groß
*	1.13	groß

Ref.:

Hemmerich, W. (2015). StatistikGuru: Cohen's d berech

Cohen, J. (1988). *Statistical power an*

d ≥ 0.8	großer Effekt
d ≥ 0.5	mittel
d ≥ 0.2	klein

age0_6		
*	0.84	groß
*	0.80	groß
*	0.87	groß
*	0.69	mittel

group_std	Mean	Std. Deviation	N
age 0-6	75.56	23.913	45
age gt6	53.14	28.067	78
congenital	74.36	20.313	47
first_sec_ears	56.94	28.390	93
gap 0-5	75.85	23.483	47
gap gt5	52.37	27.994	76
neural genes	42.17	33.365	23
other genes	65.75	25.676	100
peri-post-lingual	53.29	30.172	76
simult_ears	75.00	25.325	30
Total	61.34	28.558	615

age_gt6		
*	0.83	groß
*	0.86	groß
*	0.80	groß

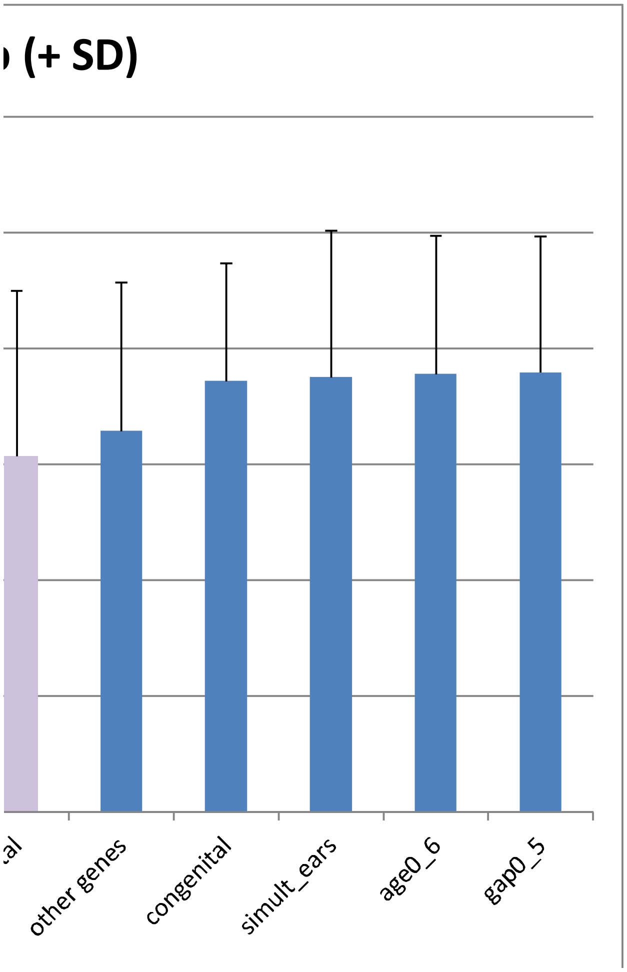
congenital		
*	0.79	mittel
*	0.87	groß

gap0_5		
*	0.89	groß
*	0.70	mittel

gap_gt5		
*	0.83	groß

pp_lingual		
*	0.76	mittel

75.0	56.9	
simult_ears	first-sec_ears	number of sign.
*		5
	*	4
*		3
		2
	*	2
*		1
*		1
		18



ANOVA: standard

Dependent Variable:

group_std
age 0-6
age gt6
congenital
first_sec_ears
gap 0-5
gap gt5
neural genes
other genes
peri-post-lingual
simult_ears
Total

std_Fb_all

Tests the null hypothesis t

a. Dependent variable: std

b. Design: Intercept + grou

Dependent Variable:

Source
Corrected Model
Intercept
group_std
Error
Total

nen. Retrieved from https://statistikguru.de/rechner/cohens-d.html

alysis for the behavioral sciences *(2nd ed). Hillsdale, N.J: L. Erlbaum Associates.*

Corrected Total

a. R Squared = .122 (Adju

b. Computed using alpha

Dependent Variable:

Parameter
Intercept
[group_std=age 0-6]
[group_std=age gt6]
[group_std=congenital]
[group_std=first_sec_ears]
[group_std=gap 0-5]
[group_std=gap gt5]
[group_std=neural genes]
[group_std=other genes]
[group_std=peri-post-lingual]
[group_std=simult_ears]

a. This parameter is set to

b. Computed using alpha

ised, minus all-over median (70)

Descriptive Statistics

std_Fb_all

Mean	Std. Deviation	N
5.56	23.913	45
-16.86	28.067	78
4.36	20.313	47
-13.06	28.390	93
5.85	23.483	47
-17.63	27.994	76
-27.83	33.365	23
-4.25	25.676	100
-16.71	30.172	76
5.00	25.325	30
-8.66	28.558	615

Levene's Test of Equality of Error Variances[a,b]

	Levene Statistic	df1	df2	Sig.
Based on Mean	2.870	9	605	**0.003**
Based on Median	3.040	9	605	**0.001**
Based on Median and with adjusted df	3.040	9	590.695	0.001
Based on trimmed mean	3.226	9	605	0.001

see Welch-Anova (same results

:hat the error variance of the dependent variable is equal across groups.

_Fb_all

ıp_std

Tests of Between-Subjects Effects

Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared	Noncent. Parameter
61041,941[a]	9	6,782.438	9.332	0.000	0.122	83.985
28,347.461	1	28,347.461	39.002	0.000	0.061	39.002
61,041.941	9	6,782.438	9.332	0.000	**0.122**	83.985
439,726.351	605	726.820				
546,875.000	615					

500,768.293	614					

sted R Squared = .109)

= .05

Parameter Estimates

B	Std. Error	t	Sig.	95% Confidence Interval		Partial Eta Squared
				Lower Bound	Upper Bound	
5.000	4.922	1.016	**0.310**	-4.667	14.667	**0.002**
0.556	6.354	0.087	0.930	-11.924	13.035	0.000
-21.859	5.792	-3.774	0.000	-33.234	-10.484	0.023
-0.638	6.300	-0.101	0.919	-13.011	11.734	0.000
-18.065	5.661	-3.191	0.001	-29.181	-6.948	0.017
0.851	6.300	0.135	0.893	-11.522	13.224	0.000
-22.632	5.813	-3.893	0.000	-34.048	-11.216	0.024
-32.826	7.472	-4.393	0.000	-47.500	-18.152	0.031
-9.250	5.612	-1.648	0.100	-20.272	1.772	0.004
-21.711	5.813	-3.735	0.000	-33.127	-10.294	0.023
0[a]						

zero because it is redundant.

= .05

)

Observed Power[b]
1.000
1.000
1.000

Fb normal

Noncent. Parameter	Observed Power[b]		Sig.	Partial Eta Squared
1.016	0.174	Intercept	**0.000**	**0.277**
0.087	0.051	[group_std=age 0-6]	0.930	0.000
3.774	0.965	[group_std=age gt6]	0.000	0.023
0.101	0.051	[group_std=congenital]	0.919	0.000
3.191	0.890	[group_std=first_sec_ears]	0.001	0.017
0.135	0.052	[group_std=gap 0-5]	0.893	0.000
3.893	0.973	[group_std=gap gt5]	0.000	0.024
4.393	0.992	[group_std=neural genes]	0.000	0.031
1.648	0.377	[group_std=other genes]	0.100	0.004
3.735	0.962	[group_std=peri-post-lingual]	0.000	0.023
		[group_std=simult_ears]		

Descriptive Statistics

Dependent Variable:

Analysis - Category	Mean	Std. Deviation	N
Bilateral SSNHL	0.5762	0.66952	13
Menieres Disease	0.1667	0.61513	6
Neural - Genetic	-0.4171	0.98715	24
Other	-0.5922	0.97511	9
Otosclerosis	0.6460	0.42395	5
Sensory - Genetic	0.5208	0.81391	12
Single Sided Deafness	-0.5923	0.89798	26
Unknown	-0.1120	0.86824	60
Total	-0.1257	0.93459	155

Post-hoc tests				**Sig.**
Bilateral SSNHL	Single Sided Deafness	1,1685*	0.29375	**0.003**
Single Sided Deafness	Bilateral SSNHL	-1,1685*	0.29375	**0.003**
Bilateral SSNHL	Neural - Genetic	,9932*	0.29780	**0.030**
Neural - Genetic	Bilateral SSNHL	-,9932*	0.29780	**0.030**
Sensory - Genetic	Single Sided Deafness	1,1131*	0.30180	**0.009**
Single Sided Deafness	Sensory - Genetic	-1,1131*	0.30180	**0.009**
Bilateral SSNHL	Other	1.1684	0.37499	0.062
Other	Bilateral SSNHL	-1.1684	0.37499	0.062
Neural - Genetic	Sensory - Genetic	-0.9379	0.30575	0.072
Sensory - Genetic	Neural - Genetic	0.9379	0.30575	0.072
Otosclerosis	Single Sided Deafness	1.2383	0.42229	0.109
Single Sided Deafness	Otosclerosis	-1.2383	0.42229	0.109
Other	Sensory - Genetic	-1.1131	0.38133	0.114

Sensory - Genetic	Other	1.1131	0.38133	0.114
Bilateral SSNHL	Unknown	0.6882	0.26456	0.287
Unknown	Bilateral SSNHL	-0.6882	0.26456	0.287
Other	Otosclerosis	-1.2382	0.48235	0.315
Otosclerosis	Other	1.2382	0.48235	0.315
Neural - Genetic	Otosclerosis	-1.0631	0.42512	0.378
Otosclerosis	Neural - Genetic	1.0631	0.42512	0.378
Single Sided Deafness	Unknown	-0.4803	0.20304	0.541
Unknown	Single Sided Deafness	0.4803	0.20304	0.541
Sensory - Genetic	Unknown	0.6328	0.27347	0.617
Unknown	Sensory - Genetic	-0.6328	0.27347	0.617
Bilateral SSNHL	Menieres Disease	0.4095	0.42681	1.000
Bilateral SSNHL	Otosclerosis	-0.0698	0.45508	1.000
Bilateral SSNHL	Sensory - Genetic	0.0553	0.34619	1.000
Menieres Disease	Bilateral SSNHL	-0.4095	0.42681	1.000
Menieres Disease	Neural - Genetic	0.5838	0.39472	1.000
Menieres Disease	Other	0.7589	0.45578	1.000
Menieres Disease	Otosclerosis	-0.4793	0.52365	1.000
Menieres Disease	Sensory - Genetic	-0.3542	0.43239	1.000
Menieres Disease	Single Sided Deafness	0.7590	0.39167	1.000
Menieres Disease	Unknown	0.2787	0.37028	1.000
Neural - Genetic	Menieres Disease	-0.5838	0.39472	1.000
Neural - Genetic	Other	0.1751	0.33801	1.000
Neural - Genetic	Single Sided Deafness	0.1752	0.24479	1.000
Neural - Genetic	Unknown	-0.3051	0.20886	1.000
Other	Menieres Disease	-0.7589	0.45578	1.000
Other	Neural - Genetic	-0.1751	0.33801	1.000
Other	Single Sided Deafness	0.0001	0.33445	1.000
Other	Unknown	-0.4802	0.30912	1.000

Otosclerosis	Bilateral SSNHL	0.0698	0.45508	1.000
Otosclerosis	Menieres Disease	0.4793	0.52365	1.000
Otosclerosis	Sensory - Genetic	0.1252	0.46031	1.000
Otosclerosis	Unknown	0.7580	0.40253	1.000
Sensory - Genetic	Bilateral SSNHL	-0.0553	0.34619	1.000
Sensory - Genetic	Menieres Disease	0.3542	0.43239	1.000
Sensory - Genetic	Otosclerosis	-0.1252	0.46031	1.000
Single Sided Deafness	Menieres Disease	-0.7590	0.39167	1.000
Single Sided Deafness	Neural - Genetic	-0.1752	0.24479	1.000
Single Sided Deafness	Other	-0.0001	0.33445	1.000
Unknown	Menieres Disease	-0.2787	0.37028	1.000
Unknown	Neural - Genetic	0.3051	0.20886	1.000
Unknown	Other	0.4802	0.30912	1.000
Unknown	Otosclerosis	-0.7580	0.40253	1.000

Levene's Test of Equality of Error Variances[a,b]

		Levene Statistic	df1	df2	Sig.
Z Score Avg	Based on Mean	1.465	7	147	**0.184**
	Based on Median	1.431	7	147	0.197
	Based on Median and with adjusted df	1.431	7	138.381	0.198
	Based on trimmed mean	1.472	7	147	0.181

Variances homogene:

Tests the null hypothesis that the error variance of the dependent variable is equal across groups.

a. Dependent variable: Z Score Avg

b. Design: Intercept + AnalysisCategory

Tests of Between-Subjects Effects

Dependent Variable:

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared	Noncent. Parameter
Corrected Model	24,579[a]	7	3.511	4.695	0.000	0.183	32.866
Intercept	0.052	1	0.052	0.070	0.792	0.000	0.070
AnalysisCategory	24.579	7	3.511	4.695	0.000	**0.183**	32.866
Error	109.933	147	0.748				
Total	136.962	155					
Corrected Total	134.511	154					

a. R Squared = ,183 (Adjusted R Squared = ,144)

b. Computed using alpha = .05

Parameter Estimates

Dependent Variable:

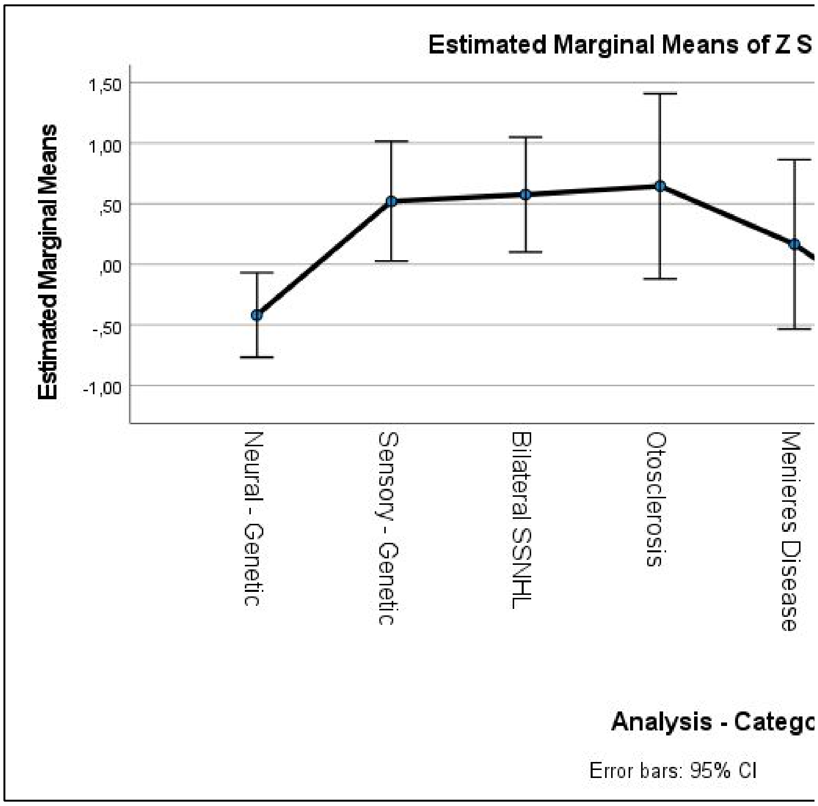
Parameter	B	Std. Error	t	Sig.	95% Confidence Interval		**Partial Eta Squared**
					Lower Bound	Upper Bound	

Intercept	-0.112	0.112	-1.003	0.317	-0.333	0.109	**0.007**
[AnalysisCategory= Bilateral SSNHL]	0.688	0.265	2.601	**0.010**	0.165	1.211	**0.044**
[AnalysisCategory= Menieres Disease]	0.279	0.370	0.753	0.453	-0.453	1.010	0.004
[AnalysisCategory= Neural - Genetic]	-0.305	0.209	-1.461	0.146	-0.718	0.108	0.014
[AnalysisCategory= Other]	-0.480	0.309	-1.553	0.122	-1.091	0.131	0.016
[AnalysisCategory= Otosclerosis]	0.758	0.403	1.883	0.062	-0.037	1.553	0.024
[AnalysisCategory= Sensory - Genetic]	0.633	0.273	2.314	**0.022**	0.092	1.173	**0.035**
[AnalysisCategory= Single Sided Deafness]	-0.480	0.203	-2.366	**0.019**	-0.882	-0.079	**0.037**
[AnalysisCategory= Unknown]	0[a]						

a. This parameter is set to zero because it is redundant.

b. Computed using alpha = .05

Neural-genetic nicht signifikant, daher kann part. Eta-Quadrat nicht verwendet werden !

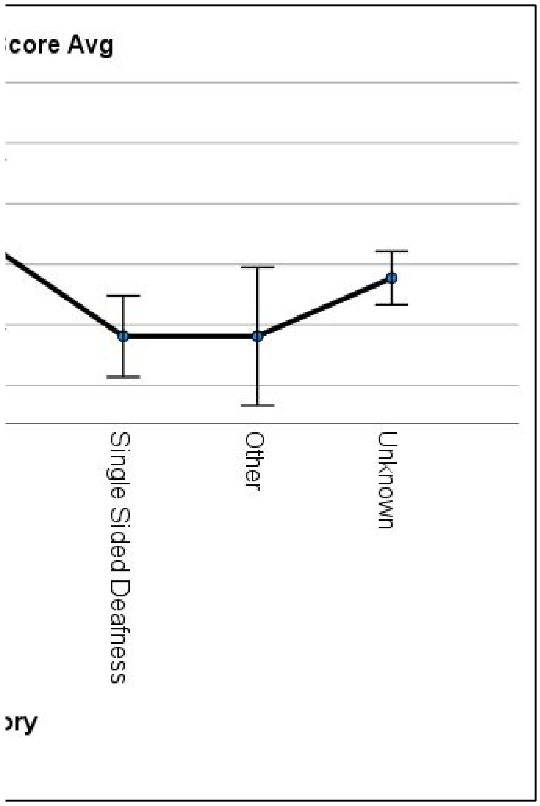


ANOVA valid

Observed Power[b]
0.994
0.058
0.994

Noncent. Parameter	Observed Power[b]

1.003	0.169
2.601	0.734
0.753	0.116
1.461	0.306
1.553	0.339
1.883	0.465
2.314	0.633
2.366	0.652



core Avg
Single Sided Deafness
Other
Unknown
ory