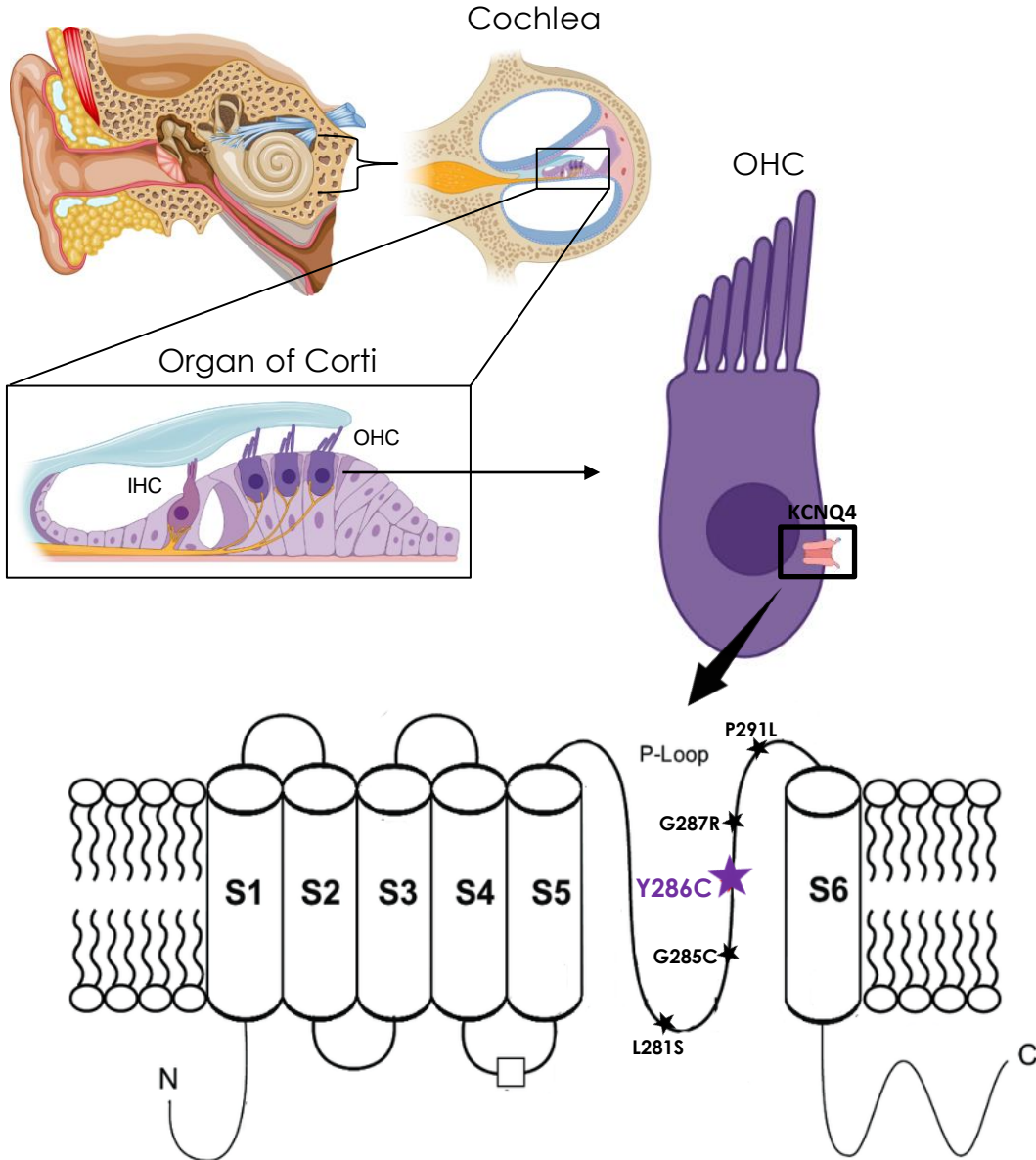




MISSENSE MUTATION OF KCNQ4 GENE ASSOCIATED TO DFNA2: VIRAL VECTOR TO RECOVER HEARING FUNCTIONS

C. Argento
B. Citro
F. De Iuliis
A. Di Pace

Background



KCNQ4 ASSOCIATED TO DFNA2



Autosomal dominant disease due to **KCNQ4** channel mutation present on the **outer hair cells** in the inner ear



Gene nucleotide substitutions in the portion coding for the **P-loop** that generate **loss of function**



- **cell death** due to cytotoxicity
- progressive **hearing loss (ipoacusis)**
- Worsens **every 10 years** till total compromise at 70

AGING



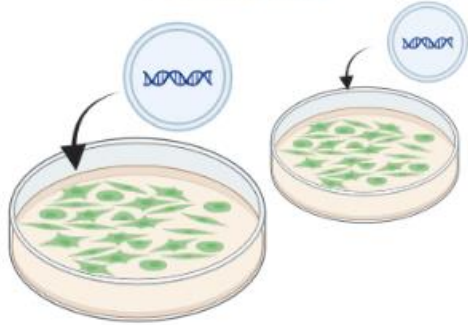
AIM OF THE PROJECT

IN VITRO

1

HEK transfection

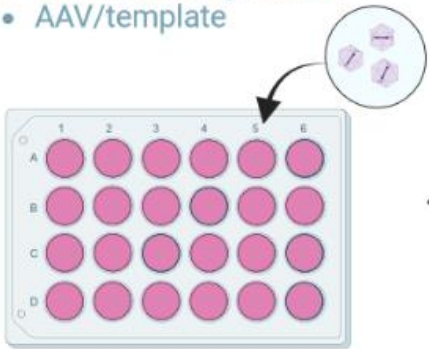
- KCNQ4⁺
- KCNQ4^{Y286C}



FACS
WB
Whole-cell
patch clamp

2

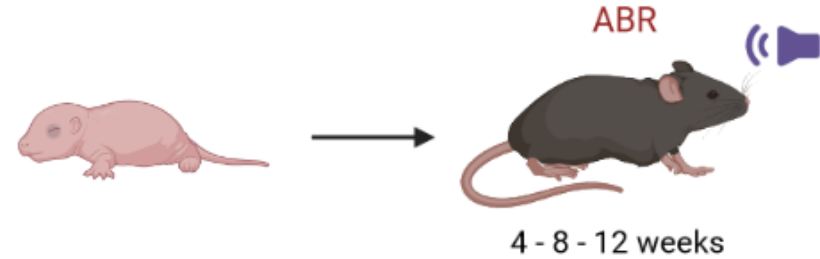
- AAV/Cas9n/sgRNA5+6
- AAV/template



FACS
WB
Whole-cell
patch clamp
CIRCLE-seq

IN VIVO

1

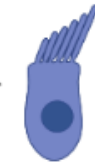


2

- AAV/Cas9n/sgRNA5+6
- AAV/template



OHCs explant



Thallium-based
imaging
Whole-cell
patch clamp
NGS



Vector design

**AAV9
Cas9n**



**AAV9
template**



Possible sgRNAs

CCGCCCTGCAGACTTCA TCGTGTTTCGTGGCCTCGGTGGCCGTCAT CGCCGCGGGTACCCAGG

GCAGACTTCATCGTGTTTCGTGGCCTCGGTGGCCGTCATCGCCGCGGGTACCCAGGGCAACATCTTCGC

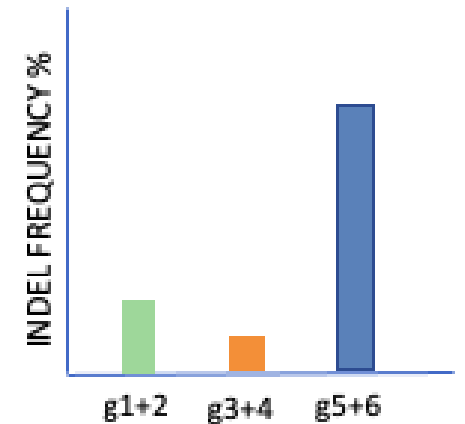
CCGCCCCGCCCTGCAGACTTCATCGTGTTTCGTGGCCTCGGTGGCCGTCATCGCCGCGGGTACCCAGGG

PAM CGG

g1 + g2

g3 + g4

g5 + g6 ←

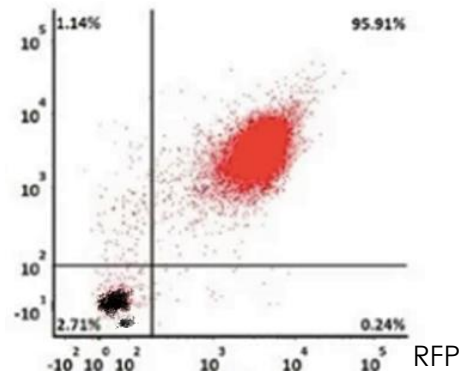


MODEL CONSTRUCTION IN VITRO

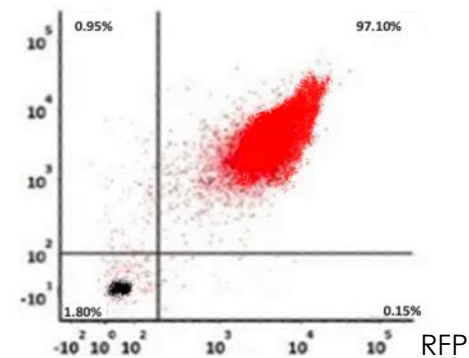
① Creation of **HEK293** cell lines: **WT** and **KCNQ4_{Y286C}**

FACS

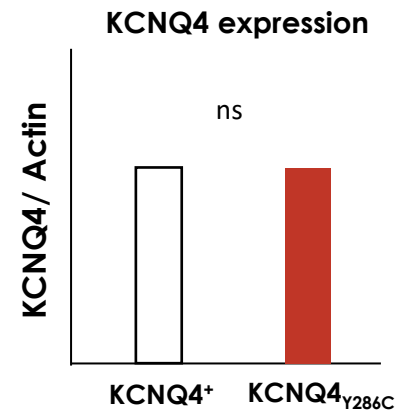
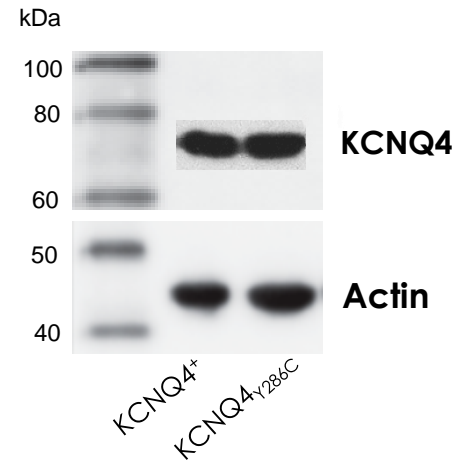
HEK293 cells+RFP labelled **KCNQ4⁺**



HEK293 cells+RFP labelled **KCNQ4_{Y286C}**

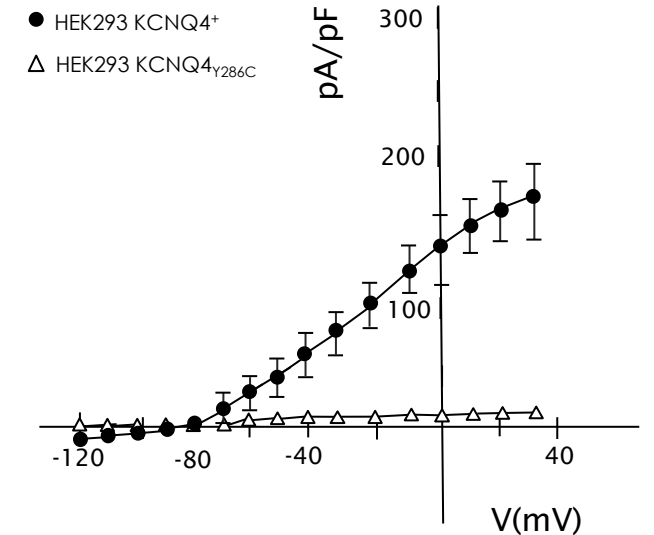
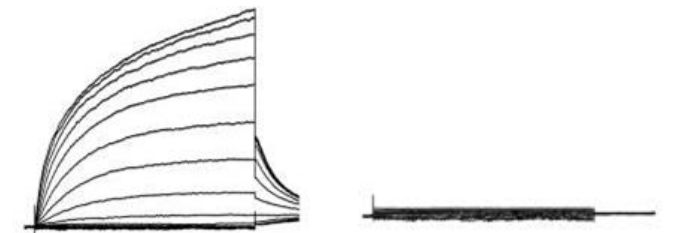


WB



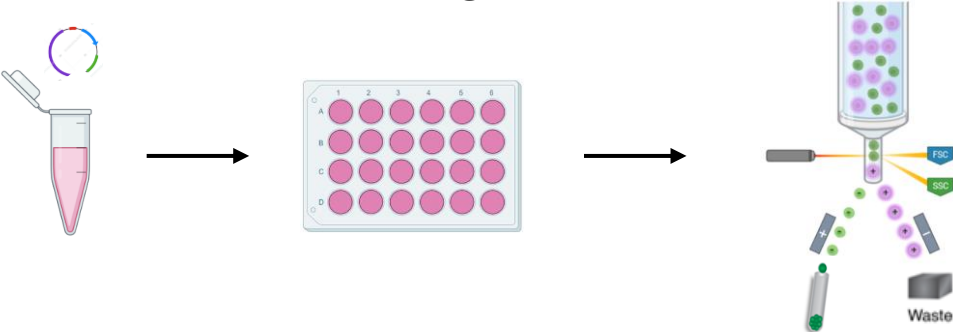
Whole-cell patch clamp

● HEK293 **KCNQ4⁺** △ HEK293 **KCNQ4_{Y286C}**

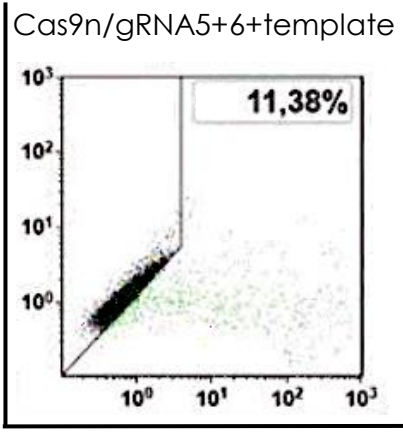


EXPECTED RESULTS IN VITRO

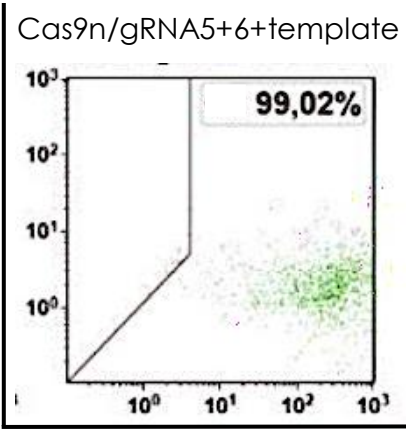
② HEK **KCNQ4**_{Y286C} transduction with **AAV** vectors



FACS

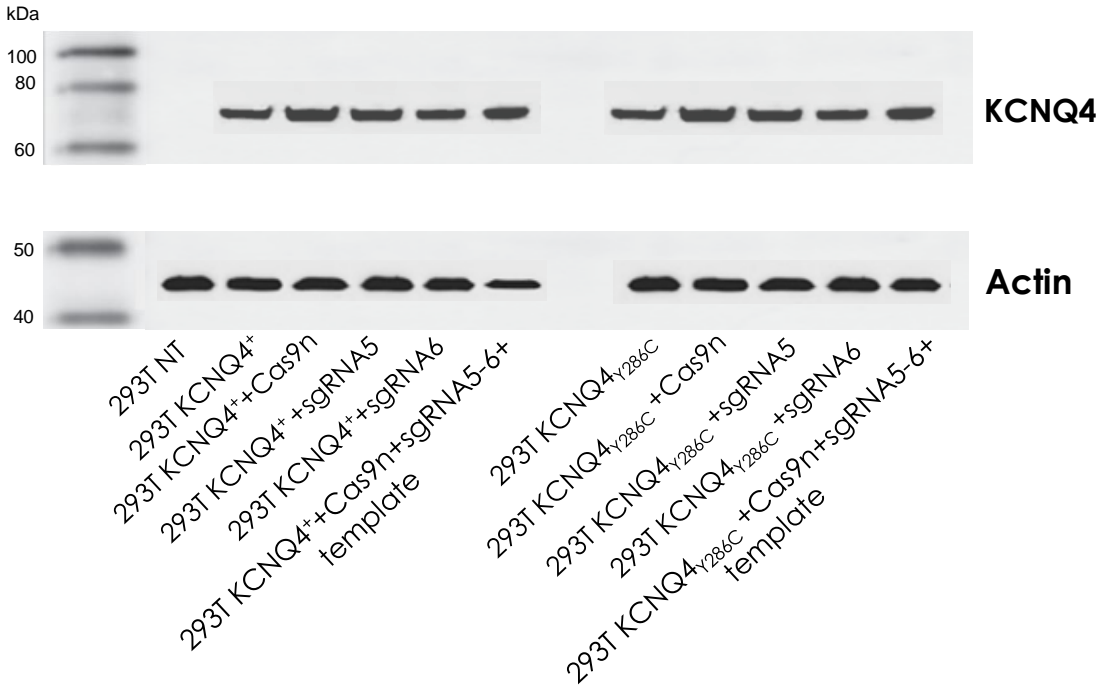


GFP – one day post transduction



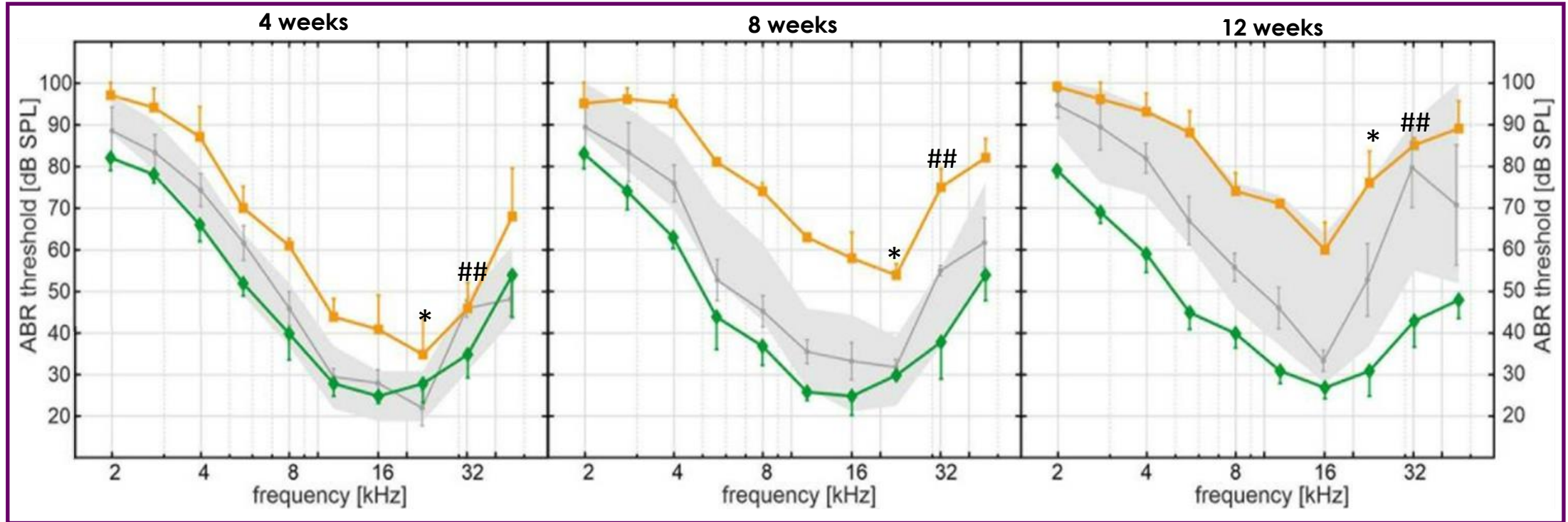
GFP – 14 day post transduction

WB



EXPECTED RESULTS IN VIVO

① ABR in WT e KI before AAV injection



■ ABR → KI (C57BL/6-tg KCNQ4^{Y286C}) n=7

◆ ABR → WT (C57BL/6) n=8

■ Baseline threshold

* $p < 0.05$ WT vs KI, two-way ANOVA

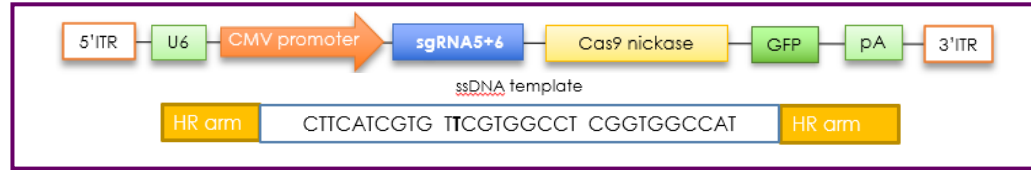
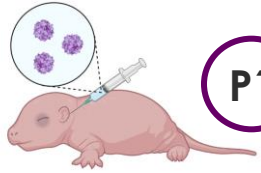
$p < 0.05$ KI 4 weeks vs KI 8 weeks vs KI 12 weeks, two-way ANOVA

n obtained with G*power

EXPECTED RESULTS IN VIVO



② AAV intracochlear injection into KI (C57BL/6-tg KCNQ4^{Y286C})



EXPERIMENTAL GROUP:

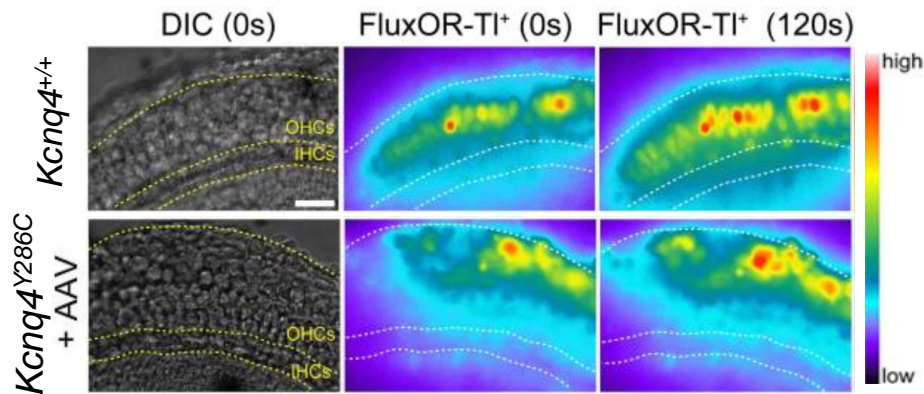
1. KI (C57BL/6-tg KCNQ4^{Y286C}) AAV double system injected (n=17)

CONTROL GROUPS:

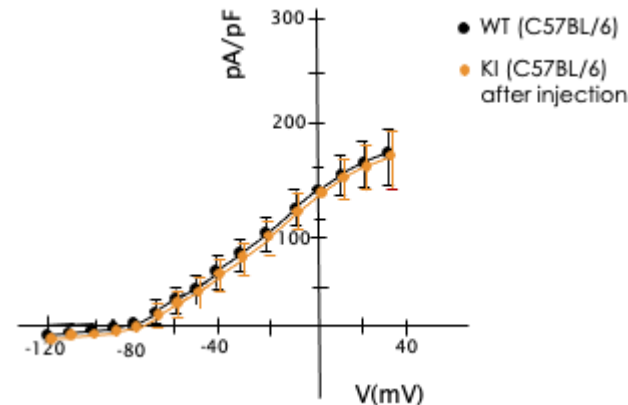
1. WT (C57BL/6) (n=12)
2. KI (C57BL/6-tg KCNQ4^{Y286C}) blank vector injected (n=8)

OHCs explant

Thallium-based imaging



Whole-cell patch clamp



NGS

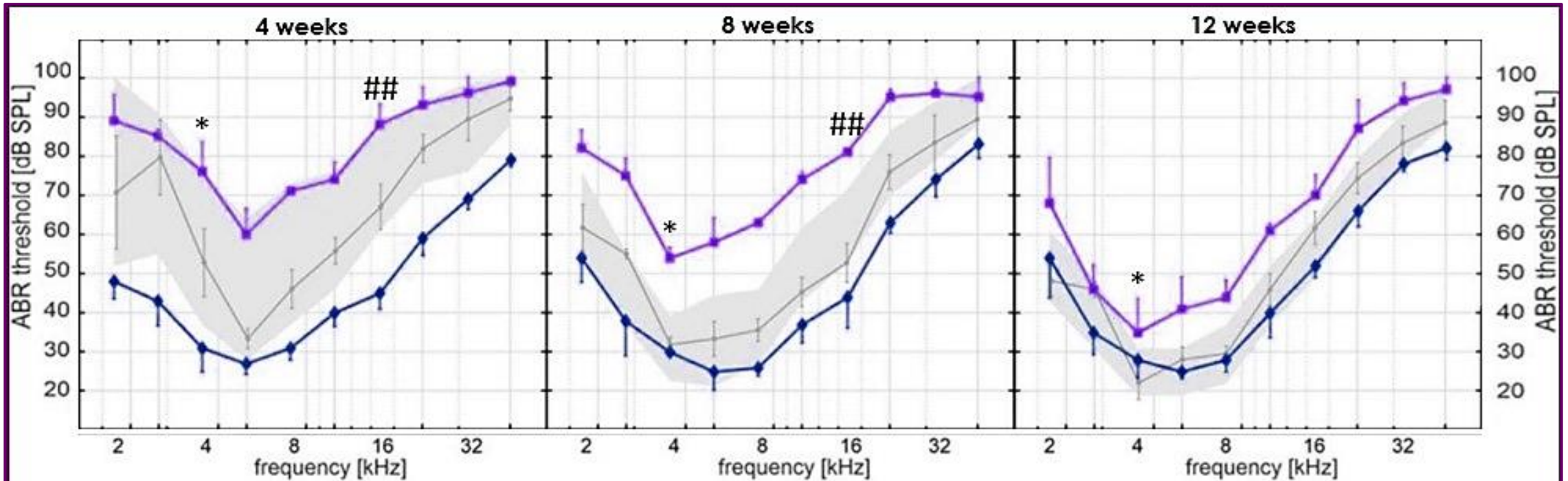
1 week after the injection:

Genotyping of OHC

- 68,8% efficiency of AAV double-system integration
- No Off-Target effects

EXPECTED RESULTS IN VIVO

 **ABR** → evaluation of hearing restoration



■ KI + AAV (n=12)

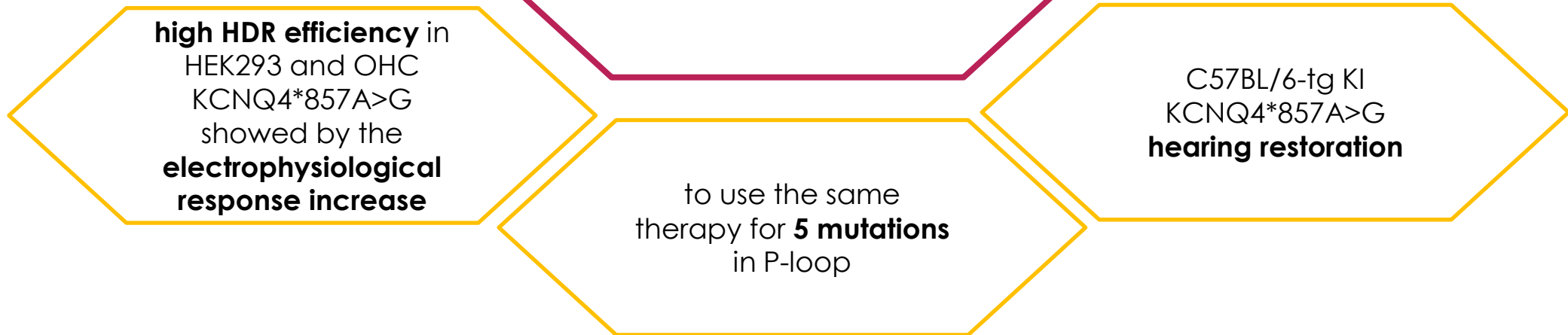
◆ WT (n=8)

p<0.05 KI vs WT

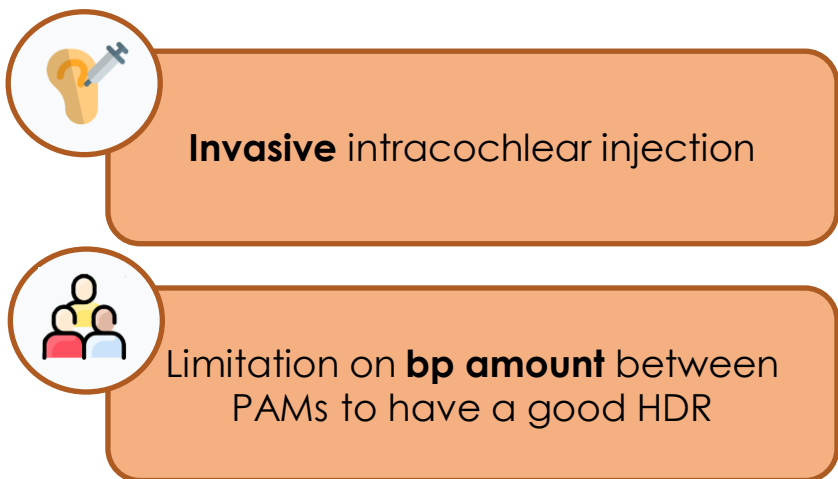
n obtained with G*power

* p<0.05 4 weeks vs 8 weeks vs 12 weeks, two-way ANOVA

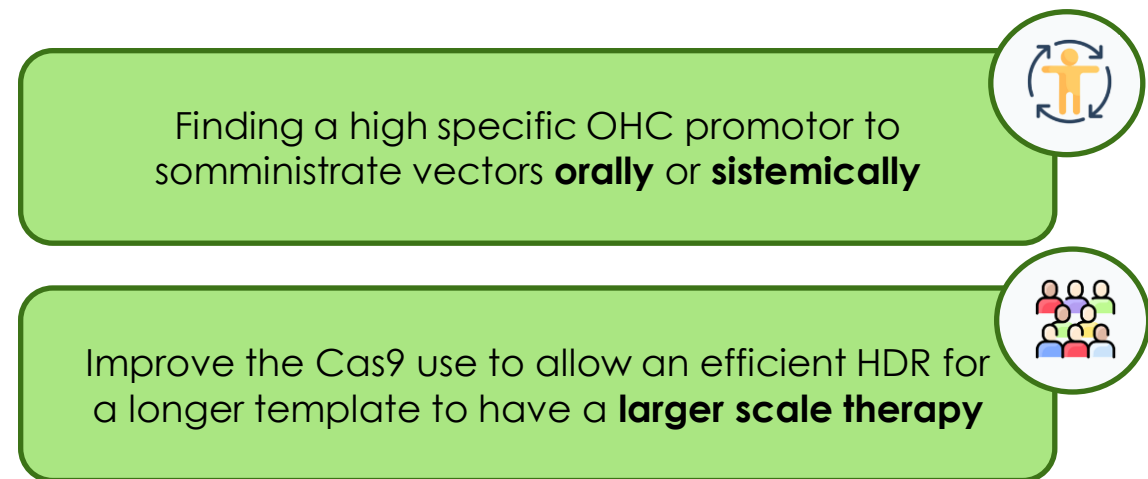
CONCLUSIONS



PITFALLS



SOLUTIONS



BUDGET AND MATERIALS



2 YEARS



<i>In Vitro</i>	Cell line HEK293 + culture medium supplements (DMEM, FBS, GlutaMAX, Penicillin + Streptomycine, ViraDuctin AAV Transduction Kit + PEI)	3.495€
	WB Analysis kit + Antibody (Anti-KCNQ4, Anti-IgG, Anti Actin)	312€ (1y) + 125€ (1y) + 550€ = 3.500€
	AssayLite Mutli-color Conjugated Antibodies Flow Cytometry (FACS Analysis kit)	595€
<i>In Vivo</i>	Mice: C57BL/6 C57BL/6-tg(KCNQ4*857A>G)	22€ (ca) = 220€ 540€ (ca) = 5.400€
	Animal Housing	10.000€ (1y) = 20.000€
	AAV9 + packaging	1200€
	Lipofectamine 2000 tranfection reagent	479€
	Crispr/Cas9 Nickase	1500€
sgRNAs	400€	
Cas9 protein	200€	
ABR kit	350€	
<i>OHC Analysis</i>	Culture medium OHC (DMEM, FBS, N2 supplement, B27 supplement)	635€
	NGS kit	1.000€ (1y) = 2000€
	Staff Salary: 1 PI, 2 PhD, 1 Technician	120.000€ (1y) = 240.000€


TOT: 279.662€

References

KCNQ4 MUTATION

- 1) John Hoon Rim, Jae Young Choi, Jinsei Jung, and Heon Yung Gee. **“Activation of KCNQ4 as a Therapeutic Strategy to Treat Hearing Loss”**. Srdjan M Vlaiskovic, Academic Editor 2021. Mar 2.
- 2) Liping Nie. **“Mutations of KCNQ4 Channels Associated with Nonsyndromic Progressive Sensorineural Hearing Loss”**. Curr Opin Otolaryngol Head Neck Surg. 2008 Oct; 16(5): 441–444.
- 3) Jinsei Jung, Haiyue Lin, Young Ik Koh, Kunhi Ryu, Joon Suk Lee, John Hoon Rim, Hye Ji Choi, Hak Joon Lee, Hye-Youn Kim, Seyoung Yu, Hyunsoo Jin, Ji Hyun Lee, Min Goo Lee, Wan Namkung, Jae Young Choi, and Heon Yung Gee **“Rare KCNQ4 variants found in public databases underlie impaired channel activity that may contribute to hearing impairment”**. Exp Mol Med. 2019 Aug; 51(8): 99.
- 4) Hyo Jeong Kim, Ping Lv, Choong-Ryoul Sihm, and Ebenezer N. Yamoah. **“Cellular and Molecular Mechanisms of Autosomal Dominant Form of Progressive Hearing Loss, DFNA2”**. J Biol Chem. 2011 Jan 14; 286(2): 1517–1527. Published online 2010 Oct 21.
- 5) Byunghwa Noh, John Hoon Rim, Ramu Gopalappa, Haiyue Lin, Kyu Min Kim, Min Jin Kang, Heon Yung Gee, Jae Young Choi, Hyongbum Henry Kim, and Jinsei Jung **“In vivo outer hair cell gene editing ameliorates progressive hearing loss in dominant-negative Kcnq4 murine model”**. Theranostics. 2022; 12(5): 2465–2482. Published online 2022 Feb 28.
- 6) Tatjana Kharkovets, Karin Dedek, Hannes Maier, Michaela Schweizer, Darina Khimich, Régis Nouvian, Vitya Vardanyan, Rudolf Leuwer, Tobias Moser, and Thomas J Jentsch **“Mice with altered KCNQ4 K channels implicate sensory outer hair cells in human progressive deafness”** EMBO J. 2006 Feb 8; 25(3): 642–652. Published online 2006 Jan 26.
- 7) **KCNQ4 potassium voltage-gated channel subfamily Q member 4 [Homo sapiens (human)]**. Gene ID: 9132, updated on 8-Dec-2022

CRISPR

- 8) Chong Cui, Daqi Wang, Bowei Huang, Fang Wang, Yuxin Chen, Jun Lv, Luping Zhang, Lei Han, Dong Liu, Zheng-Yi Chen, Geng-Lin Li, Huawei Li, and Yilai Shu **“Precise detection of CRISPR-Cas9 editing in hair cells in the treatment of autosomal dominant hearing loss”**. Mol Ther Nucleic Acids. 2022 Sep 13; 29: 400–412. Published online 2022.
- 9) F. Ann Ran, Patrick D. Hsu, Chie-Yu Lin, Jonathan S. Gootenberg, Silvana Konermann, Alexandro E. Trevino, David A. Scott, Azusa Inoue, Shogo Matoba, Yi Zhang and Feng Zhang **“Double Nicking by RNA-Guided CRISPR Cas9 for Enhanced Genome Editing Specificity”** Harvard Medical School, Boston, MA 02115, USA 2013/08/21
- 10) Thomas Kocher, Roland N. Wagner, Alfred Klausegger, Christina Guttman-Gruber, Stefan Hainzl, Johann W. Bauer, Julia Reichelt, and Ulrich Koller **“Improved Double-Nicking Strategies for COL7A1-Editing by Homologous Recombination”**. Mol Ther Nucleic Acids. 2019 Dec 6; 18: 496–507. Published online 2019 Sep 20.
- 11) Xi A. Ge and Craig P. Hunter. **“Efficient Homologous Recombination in Mice Using Long Single Stranded DNA and CRISPR Cas9 Nickase”**. Department of Molecular and Cellular Biology, Harvard University, Cambridge, MA 02138
- 12) Zhili Rong, Shengyun Zha, Yang Xu, Xuemei Fu **“Homologous recombination in human embryonic stem cells using CRISPR/Cas9 nickase and a long DNA donor template”**. Protein Cell 2014, 5(4):258–260.
- 13) Matthew T. N. Yarnall, Eleonora I. Ioannidi, Cian Schmitt-Ulms, Rohan N. Krajcski, Justin Lim, Lukas Villiger, Wenyan Zhou, Kaiyi Jiang, Sofya K. Garushyants, Nathaniel Roberts, Liyang Zhang, Christopher A. Vakulskas, John A. Walker II, Anastasia P. Kadina, Adrianna E. Zepeda, Kevin Holden, Hong Ma, Jun Xie, Guangping Gao, Lander Foquet, Greg Bial, Sara K. Donnelly, Yoshinari Miyata, Daniel R. Radloff, Jordana M. Henderson, Andrew Ujita, Omar O. Abudayyeh & Jonathan S. Gootenberg **“Drag-and-drop genome insertion of large sequences without double-strand DNA cleavage using CRISPR-directed integrases”**. Epub 2022 Jun 3.
- 12) Ngoc Tung Tran, Eric Danner, Xun Li, Robin Graf, Mikhail Lebedin, Kathrin de la Rosa, Ralf Kuhn, Klaus Rajewsky, Van Trung Chu. **“Precise CRISPR-Cas-mediated gene repair with minimal off-target and unintended on-target mutations in human hematopoietic stem cells”**. Published online 2022/11/24