1 Title:

2 USH2A gene mutations in rabbits lead to progressive retinal degeneration and

- 3 hearing loss
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23 Abstract

24	Mutations in USH2A gene are responsible for the greatest proportion of hearing and
25	vision loss among individuals with Usher Syndrome (USH) and for autosomal
26	recessive non-syndromic retinitis pigmentosa. Mutations on USH2A exon 13 account
27	for more than 35% of the disease causing USH2A variants including the most
28	prevalence point mutation, c.2299delG, a frameshift mutation. The lack of a clinically
29	relevant animal model has been a bottleneck for the development of therapeutics for
30	USH2A related vision loss. Using CRSPR/Cas9 technology, this study establishes a
31	rabbit line carrying an USH2A frameshift mutation on exon12 (equivalent to human
32	USH2A Exon 13) as a novel mammalian animal model of USH2A. The bi-allelic
33	mutant rabbits exhibit hyper reflective signals in FAF indicating RPE damage and
34	OCT changes indicating photoreceptor degeneration as early as 4 months of age.
35	ERG signals of both rod and cone function were reduced in the USH2A mutant rabbits
36	starting from 7 months old and further decreased at 15-22 months old, indicating
37	progressive retinal photoreceptor degeneration, which is further confirmed by retinal
38	histopathology examination. ABR examination showed moderate to server hearing
39	loss in the USH2A mutant rabbits. These results indicated that disruption of USH2A
40	gene in rabbits is sufficient to induce hearing loss and progressive photoreceptor
41	degeneration. To our knowledge, this is the first mammalian animal model of USH2
42	which closely recapitulates the phenotype of retinitis pigmentosa in human patients.
43	This study supports the use of rabbits as a clinically relevant animal model to
44	understand the pathogenesis and to develop novel therapeutics for Usher Syndrome.

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45 Introduction

46	Usher syndrome (USH) is an autosomal recessive genetic disorder resulting in
47	hearing loss, progressive visual impairment and, in some types, balance issues ¹ . The
48	major ocular symptom of patients with USH is a disease called retinitis pigmentosa
49	(RP). RP causes the light-sensing photoreceptor cells in the retina to gradually
50	deteriorate, initially resulting in night blindness, followed by tunnel vision, and severe,
51	permanent, progressive vision loss. More than 400,000 people are affected by USH
52	worldwide, accounting for about 50 percent of all hereditary deaf-blindness cases ² .
53	USH is classified into three subtypes (I, II, and III), which are distinguished by severity
54	and age of onset of deafness, presence or absence of vestibular dysfunction, and age
55	at onset of RP. Among them, type II (USH2) is the most common subtype,
56	characterized by hearing loss from birth and progressive vision loss that begins in
57	adolescence or adulthood. USH2 may be caused by mutations in any of three genes:
58	USH2A, GPR98, and DFNB31, with USH2A mutations being the most prevalent,
59	present in approximately 70% of USH2 cases 3 . Mutations in the USH2A gene are
60	also a cause of some forms of RP without hearing loss (i.e., non-syndromic RP) ⁴ .
61	More than 700 pathogenic USH2A mutations have been identified, as reported in the
62	LOVD database (http://www.lovd.nl). Mutations in exon 13 account for approximately
63	35% of all USH2A cases, including the two most recurrent mutations in USH2A,
64	c.2299delG (p. Glu767fs*21) and c.2276G>T (p. Cys759Phe) 5 . Despite extensive
65	research, there is no cure for USH2 yet. Hearing aids provide benefits to USH2
66	patients who have moderate to severe hearing loss; however, efforts to mitigate the

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67	progressive visual loss caused by RP have been disappointing. Most individuals with
68	USH2 RP will eventually suffer from severe, progressive vision loss. Therefore, there
69	is a pressing unmet clinical need to develop novel therapeutics for USH2.
70	
71	Mouse and zebrafish models of USH2A have been developed. Unfortunately,
72	phenotypes observed in retinas of USH2A-USH2 patients are not faithfully replicated
73	in mouse models carrying USH2A mutations ⁶⁻⁸ . USH2A knock out mice suffer from
74	hearing loss but only manifested weak and very late onset retina degeneration
75	phenotype. The zebrafish models exhibit early retinal degeneration phenotypes.
76	However, their features of adult photoreceptor regeneration as well as the distance
77	from humans may pose problems in translational studies ⁹ . Therefore, development of
78	an alternative mammalian model of USH2, which more closely approximates human
79	physiology, function, and anatomy, and importantly RP pathogenesis is of prime
80	importance and may accelerate translating discoveries from animal models into
81	clinical therapies and interventions for the disease.
82	
83	Rabbits, compared with mice, are closer to humans in terms of phylogenesis,
84	anatomical features, physiology, and pathophysiological responses ¹⁰⁻¹⁴ , and are used
85	as a classic lab animal species to develop novel therapeutics for humans and refine
86	medical and surgical equipment ^{13,15-19} . Historically, retinal degeneration has been
87	studied in rhodopsin Pro347Leu transgenic rabbits, a model of RP ²⁰⁻³¹ . Recently, the

88 emerging gene editing technology in rabbits has greatly increased their value to

- 89 biomedicine, motivating our efforts to develop rabbits that carry the disease causing
- 90 mutations found in human patients, as models to replicate human diseases more
- 91 precisely³²⁻³⁴. In this study, we report the development of USH2A rabbits by
- 92 CRISPR/Cas9. This novel model is expected to greatly facilitate both the basic and
- 93 translational studies of USH.
- 94

95 Materials and Methods

96 <u>Animals</u>

97 New Zealand White (NZW) rabbits were purchased from Covance or Charles River. 98 The animal maintenance, care and use procedures were reviewed and approved by 99 the Institutional Animal Care and Use Committee (IACUC) of the University of 100 Michigan. All procedures were carried out in accordance with the approved guidelines 101 and were performed in accordance with the ARVO (The Association for Research in 102 Vision and Ophthalmology) Statement for the Use of Animals in Ophthalmic and 103 Vision Research. All efforts were made to minimize suffering. All the methods were 104 carried out in accordance with the approved guidelines.

105 <u>Reverse transcription polymerase chain reaction (RT-PCR) and real time PCR</u>

106 analysis.

Total RNA from retina, sclera, brain, liver, kidney, and bone marrow were isolated
using the RNeasy kit (Qiagen). Reverse transcription was used to generate cDNA
(SuperScript® III First-Strand Synthesis System, Thermo Fisher Scientific, 18080-05)

110	as template for RT-PCR and real time PCR. For real time PCR analysis, samples
111	were analyzed on a BioRad CFX Connect™ Real-Time PCR Detection System and
112	amplification was detected using the SYBR green method (BioRad, SYBR green
113	supermix). PCR primers are as following: RTF1: 5'-aattcaggccagtgcaagtg-3', RTR1:
114	5'-gcccagaaagaggattgcag-3'; RTF2:5'-ggagaagaagagggtgtgct -3'; RTR2: 5'-
115	gactctccactggaagctga-3'. Rabbit 18S rRNA or GAPDH expression was used as
116	internal control. The RT-PCR products were purified and subject to Sanger
117	sequencing.

118 Scanning electron microscopy

The neuroretinas obtained from perfused rabbits were postfixed by immersion in 2.5% glutaraldehyde in 0.1 M cacodylate buffer (pH 7.3) for 2 h at room temperature. The samples were dehydrated in ethanol, dried to critical point, and fractured along a plane passing through the long axis of the photoreceptors. The fragments were mounted on aluminum stubs with double-adhesive carbon tape and examined under a scanning electron microscope.

125 Histopathology

To euthanize the rabbits, euthanasia solution (Euthanasia, 0.22 mg/kg, 50 mg/mL,
VetOne, ID, USA) was injected into the rabbit intravenously through the marginal ear
vein. The eyeballs were harvested and fixed in Davidson's fixative solution for 24 h.
The sample was then cut into 5 mm pieces and embedded in paraffin. The sample
was sectioned to a thickness of 4 µm using a Leica Autostainer XL (Leica Biosystems,

- 131 Nussloch, Germany) and stained with hematoxylin and eosin (H&E). The H&E slides
- 132 were observed using a Leica DM600 light microscope (Leica Biosystems, Nussloch,
- 133 Germany) and the images were captured using a BF450C camera.

134 CRISPR reagents

135	The Cas9 expression plasmid JDS246 was obtained from Addgene. Cas9 mRNA was
136	transcribed in vitro, capped and polyadenylated using the T7 mScript [™] Standard
137	mRNA Production System (C-MSC100625, CELLSCRIPT, Madison, WI). Guide
138	RNA (gRNA) was designed using CRISPOR software ³⁵ , synthesized as chemically
139	modified (2'-O-Methyl at 3 first and last bases, 3' phosphorothioate bonds between
140	first 3 and last 2 bases) single strand gRNA (sgRNA EZ Kit, Synthego). The target
141	sequence on rbUSH2A is shown in Fig. 2A. Cas9 mRNA and sgRNA were diluted in
142	RNase-free TE buffer (1mM Tris-Cl pH 8.0, 0.1mM EDTA), stored at -80 °C in 10 μl
143	aliquots, and were thawed and kept on ice before microinjection.

144 Rabbit genome editing

Methods of rabbit genome editing has been described previously in detail³⁶. Briefly, pronuclear stage rabbit embryos were injected with approximately 2-5 pL RNase-free TE buffer (1mM Tris-Cl pH 8.0, 0.1mM EDTA) containing 150 ng/µl Cas9 mRNA, 50 ng/µl sgRNA and 50 ng/µl donor oligo. Injected embryos were washed three times in embryo culture medium, which consisted of Earle's Balanced Salt Solution (E2888, Sigma) supplemented with non-essential amino acids (M7145, Sigma), essential amino acids (B-6766, Sigma), 1 mM L-glutamine (25030-081, Life Technologies), 0.4 mM sodium pyruvate (11360-070, Life Technologies) and 10% FBS. Twenty to thirty
embryos were surgically transferred to oviducts of each synchronized recipient doe.
For gRNA validation, instead of transferring to recipients, the injected embryos were
washed and cultured in the medium at 38.5 °C in 5% CO2 for additional 2-3 days until
they reach blastocyst stage.

157 Detection of gene editing events

For gRNA *in vitro* validation, PCR products amplified the targeted USH2A gene region were purified with a PCR purification kit. The purified PCR products were mixed in a Eppendorf tube with Cas9 protein and gRNA to be tested as following: 10XNEBuffer 3.1, gRNA (30 nM final), Cas9 Nuclease, S. pyogenes (M0386S) (~30 nM final), substrate PCR products (3 nM final), and Nuclease-free water to total reaction volume of 30 µl. The reaction solution was incubated at 37°C for 30 minutes and analyzed by gel electrophoresis.

165 For *in vivo* testing, injected embryos developed to blastocyst stage in culture were 166 collected in 1.5 ul water individually and the whole genome was replicated using a 167 REPLI-g® Mini Kit (Qiagen, Germantown, MD) following the manufacturer's protocol. 168 For rabbit genotyping, genomic DNA was isolated from the newborn kits ear skin. 169 Genomic DNA was then amplified by PCR using corresponding primers: Primers for 170 indels detection: forward (F), 5'-tctgcagtagcattgtttgtgatt-3', reverse (R), 171 5'-gtcccagtctcatcacagttacaa-3'; Primers for NGS F, sequencing: 172 5'-agccctgccagtgtaacctc-3', R, 5'-agtgactgagcctgctgtgttg-3'; Primers for OT1 detection:

173 F, 5'-gaggtacaagcagggtaagaaggg-3', R, 5'-gaatgaaacatggcctgggacct-3'; Primers for 174 OT2 detection: F, 5'-gagagctggactggaagaggag-3'; R, 5'-agggtacttctgtgcgttcg-3'; 175 Primers for OT3 detection: F, 5'-tcaggagtgaatcagcagatacaa-3', R. 176 5'-ttcggcttattcaggaaagaaatg-3'. PCR products were purified and subjected to T7E1 assay, Sanger sequencing, and NGS (MGH CCIB DNA core). NGS data were 177 178 analyzed using CRISPResso2 software³⁷.

179 **Rabbit eye examination and imaging procedure**

180 A comprehensive examination of the eyelids, conjunctiva, cornea, anterior chamber, 181 iris, and lens was performed using before imaging by slit lamp bio-microscopy 182 (SL120, Carl Zeiss, Germany). Fundus photography, fundus autofluorescence (FAF), 183 fluorescein angiography (FA), and indocyanine green angiography (ICGA) were 184 employed to evaluate the vascular network of the retina and choroid. Briefly, after pupil dilation, a clinical fundus camera (TRC-50EX, Topcon Corporation, Tokyo, 185 186 Japan) was used to acquire fundus photography, FAF, FA, and ICGA. Fluorescein 187 sodium (0.2mL, 10% solution) (Akorn, Lake Forest, IL, USA) and indocyanine green 188 (0.5 mg/kg, 5 mg/mL, HUB Pharmaceuticals LLC, Patheon, Italy) were injected in the 189 rabbit marginal ear vein. Photographs were captured immediately after injection up to 190 10 minutes to capture early, middle, and late phase angiography images. There was a 191 5-minute interval between the two kinds of angiography tests.

Spectral domain optical coherence tomography (OCT) imaging was performed as
 described previously³⁸. Briefly, two superluminescent light emitting diodes with a

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194 center wavelength of 905 nm were used to illuminate the surface of the cornea and 195 focused on the fundus by the rabbit eye optics. The average power of the OCT 196 probing light was 0.8 mW. The lateral and axial resolutions are 3.8 µm and 4.0 µm, 197 respectively. The system can achieve an imaging depth of 1.9 mm. The rabbits were 198 put on a custom-built platform, and the eye position was adjusted under the 199 ophthalmic lens using a CCD camera to visualize the region of interest.

200 Electroretinography (ERG)

201 Full field ERG (ff-ERG) was performed after pupillary dilation. After 60 minutes of dark 202 adaptation, rabbits were anesthetized. After topical anesthesia, ERG-Jet contact lens 203 electrodes (The Electrode Store, Enumclaw, WA, USA) were applied. Corneal 204 hydration was maintained with a 2.5% hypromellose ophthalmic demulcent solution 205 (Akorn Inc, Lake Forest, IL, USA). A pair of reference electrodes and a ground 206 electrode (needle electrodes, The Electrode Store) were placed subcutaneously 207 behind the bilateral ears and in the scruff, respectively. All animal handling was done 208 under dim red light. ERGs were recorded with a Ganzfeld configuration using the LKC 209 UTAS 3000 electrophysiology system (LKC Technologies, Gaithersburg, MD, USA). 210 ERG responses were amplified at 2500 gain at 0.312-500 Hz and digitized at a rate of 211 2000 Hz. Scotopic ERGs were recorded at a dim flash intensity of 0.01 cd.s/m2 to 212 obtain the rod isolated ERG and at 3.0 cd.s/m2 to obtain the combined rod-cone ERG. 213 After 10 minutes of light adaptation to a white 32 cd/m2 rod suppressing background, 214 photopic ERGs were recorded at a flash intensity of 3.0 cd.s/m2. For ERG analyses, 215 the a-wave amplitude was measured from the pre-stimulus baseline to the trough of -10-

216	the a-wave, and the implicit time of the a-wave was measured from flash onset to the
217	trough of the a-wave. The b-wave amplitude was measured from the trough of the
218	a-wave to the peak of the b-wave, and the b-wave implicit time was measured from
219	flash onset to the peak of the b-wave. ERG recording was performed using a xenon
220	white flash, 1000 Hz sampling frequency, 0.312 - 300 Hz cut off filter, 500 ms
221	recording time, 10 ms baseline prior to flash, and no notch filter was used.

222 Acoustic auditory brainstem responses (ABR)

223 Auditory sensitivity of the animals is evaluated by recording auditory brainstem 224 responses to acoustic stimuli. Rabbits are anesthetized with xylazine and ketamine 225 (and butorphanol to prolong anesthesia) and placed on a warm water-circulating 226 heating in a sound attenuated chamber. Needle electrodes are placed under each 227 pinna: test ear (reference) and contralateral ear (ground) and at the vertex (active) of 228 the animal's head to record the neural output. Tucker Davis Technologies (TDT) 229 System III hardware and SigGen/BioSig software (TDT, Alachua, FL USA) is used to 230 present the stimulus and record responses. Tones are delivered through an EC1 231 driver (TDT, aluminum-shielded enclosure made in house), with the speculum placed 232 just inside the tragus. Stimulus presentation is 15 ms tone bursts, with 1 ms rise/fall 233 times, presented 10 per second. Up to 1024 responses are averaged for each 234 stimulus level. Responses are collected for stimulus levels in 10 dB steps at higher 235 stimulus levels, with additional 5 dB steps near threshold. Thresholds are interpolated 236 between the lowest stimulus level where a response was observed, and 5 dB lower,

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- 237 where no response is observed. ABR thresholds and suprathresholds will be tested at
- 3 or 4 frequencies (between 4 24 kHz). ABR sessions may last 45 60 min.

239

240 Results

241 Usherin is highly conserved in rabbit and human

- 242 The rabbit USH2A gene has two isoforms: (i) the short transcript containing 23 exons
- that encodes 1543 amino acids (Ensemble transcript ID: ENSOCUT00000014751.4);
- and (ii) the long transcript contains 74 exons encodes 5202 amino acids (NCBI
- 245 Reference Sequence: XM_008268426.2). Analysis of protein sequences of usherin
- revealed that Usherin is highly conserved in human and rabbit, with 84% identify
- score for long isoforms and 85% identity score for short isoforms, and 91% positive
- score for both isoforms (**Fig.1A**). To our interest, as shown in **Fig. 1B**, rabbit exon12
- of USH2A is of the same length of human exon13, both are 642 bp long, which
- notably is an in-frame length that is suitable for exon deletion-based therapy³⁹. We
- 251 examined the expression profiles of USH2A gene in rabbits by real-time PCR using
- two pairs of primers: (i) Pair 1 on exon11 and exon12, that detects both short and long
- isoforms; and (ii) Pair 2 on exon50 and exon51, that detects only the long isoform. As
- shown in Fig. 1C, both isoforms of USH2A are exclusively expressed in the rabbit
- 255 retina, but not in any other organs/tissues examined.
- 256

257 Calyceal processes like structures in rabbits

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258	It has been reported that photoreceptor calyceal processes (CPs) are present in the
259	retina of primates but absent from mice, suggesting that the presence/absence of CPs
260	maybe the cause of the difference in visual phenotype between USH1 human patients
261	and mice models ⁴⁰ . It is possible that this structure (i.e. CPs) is also critical to the eye
262	pathogenesis in USH2, as USH1 and USH2 proteins function together in higher order
263	protein complexes ⁴¹ . Electron microscopy imaging results indicate that CP-like
264	structures exist in rabbit retina (Fig. 1D).
265	
266	Production of USH2A mutant rabbits
267	In efforts to model USH2 in rabbits, we chose to knock in the USH2A c.2299delG
268	mutation, the most prevalent USH2A frameshift mutation found in human USH
269	patients ⁵ , into rabbit genome. We designed four gRNAs targeting exon 12 of the rabbit
270	USH2A gene (Fig.2A). All four sgRNAs could cut their target in test tubes efficiently
271	with Cas9 protein (Fig.2B). T7E1 and Sanger sequencing assay showed that sgRNA1
272	achieved high efficiency of cleavage in rabbit embryos (Fig.2B). The guide RNA1
273	selected was co-introduced to rabbit embryos with Cas9 mRNA and a donor single
274	stranded DNA harboring the intended c.2299delG mutation and 50 nucleotides
275	homologue arms on each side. Totally 60 injected embryos were surgically
276	transferred into the oviduct of two synchronized recipients. All 9 term kits were
277	identified as USH2A mutant animals with 1 of them carrying 15.08% of the
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c.2299delG mutation detected by ear skin deep sequencing (**Fig.2 C&D**,

279 supplementary Fig.1). these data demonstrate that USH2A mutant founder rabbits

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280	can be produced by CRISPR/Cas9 very efficiently. Sperm DNA analysis by targeted
281	deep sequencing in founder that carries the c.2299delG mutation show a high
282	percentage of presence of this mutant allele (10.22% HDR, Fig.2D). Among the
283	knockout founders, one male (Founder#2) was mated with two wildtype rabbits
284	producing 19 kits, 9 of which carried frameshift indels mutations predicted to cause
285	premature stop codon (+14bp, -11bp, and -1 bp, Fig.3B). these data show that both
286	knock-in and knockout USH2A rabbits are germline transmitting.
287	
288	Off target analysis
288 289	Off target analysis To test the off-target effects, we chose the top three potential off-target sites predicted
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289 290	To test the off-target effects, we chose the top three potential off-target sites predicted by the gRNA design software to test off-target effects, in which the predicted off-target
289 290 291	To test the off-target effects, we chose the top three potential off-target sites predicted by the gRNA design software to test off-target effects, in which the predicted off-target sites were PCR amplified and analyzed with T7E1 assay and confirmed by Sanger

- site (Fig.3C, Supplementary Fig.2). As this region is an intergenic region, it is more
- likely a natural polymorphism. Nevertheless, to avoid the potential adverse effects,
- these two F1 rabbits carrying the OT1 site indels were excluded from the breeding
- 298 program.

299

300 Exon 12 mutation in rabbits result in nonsense-mediated mRNA decay

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301	Upon sexual maturation, one of the F1 rabbit carrying del11 mutation was used to
302	establish the USH2A KO (USH2A-/-) line. This mutation is predicted to cause a
303	premature stop codon, which may lead to the nonsense-mediated mRNA decay and
304	the production of non-functional truncated Usherin. Real time PCR detection of the
305	USH2A transcripts in the retina tissue isolated from a founder animal carrying high
306	percentage of indels mutation (Founder #2 in Fig.2D.) and a USH2A KO homozygous
307	rabbit. As shown in Figure 4, the expression of USH2A transcripts was decreased
308	more than 50% in the founder animal retina compared with wildtype controls, and the
309	expression level further decreased to less than 30% that of wildtype controls in the
310	USH2A KO retina, indicate nonsense-mediated mRNA decay did happened in the
311	USH2A KO rabbits. We expect that the introduced mutation results in decreased
312	mRNA level and the residual mRNA carrying the mutation leading to premature
313	termination of usherin translation.

314 Eye phenotype of the USH2A rabbits

As shown in **Figure 5A**, USH2A KO rabbits had normal retinal and choroidal vasculature. In addition, ophthalmic examination confirmed that all USH2A rabbits had ophthalmoscopically normal and healthy corneas, anterior chambers, and clear lenses. There was no difference in the fundus appearance between WT and USH2A KO rabbits. It should be noted that these USH2A KO animals were on an albino background, and the characteristic bone spicule pigmentation of the retina seen in RP eyes would therefore not be expected. FA and ICGA imaging shows normal retinal and choroidal vascular morphology. In contrast, hyper-FAF spots were detected in the
retina of the USH2A KO rabbits as early as 4 months old. OCT images also indicated
changes at the photoreceptor layer with hyper-reflective foci at the level of the
photoreceptor IS and OS segments as early as 4 months old.

326 OCT imaging was performed on both WT and USH2A KO rabbits as illustrated in 327 Figure 5B. B-scan OCT image obtained from WT rabbits show normal and healthy 328 retina with the different retinal layers such as the nuclear layers, plexiform layers, 329 photoreceptors, retinal vessels (RVs), choroidal vessels (CVs), RPE, inner limiting 330 membrane, and sclera. No evidence of photoreceptor or RPE disruption or damaged 331 was observed in WT rabbits. On the other hand, hyper-reflective foci were noted at 332 the level of the photoreceptor inner and outer segments and RPE in USH2A rabbits at 333 4 months old as marked by red dotted circle, which increased over time with more 334 disruptions at 8 and 12 months old.

335 Loss of retinal function in USH2A KO rabbits

To investigate whether the disruption of USH2A gene causes retinal abnormalities, visual function of USH2A KO and WT control rabbits were compared by ERG analyses at different ages under scotopic and photopic conditions. At age 7 months, the USH2A KO rabbits displayed rod response (scotopic 24 dB), scotopic combined rod and cone response (scotopic 0dB), and photopic response b-wave amplitudes (**Fig.6A,B Fig. S3**) and 32 Hz flicker amplitudes (**Fig. 6C,D**) significantly lower than WT counterparts. The responses of USH2A KO rabbits were 10% to 20% lower than

those of WT control (P=0.0456 and 0.042 respectively by t-test) as shown in **Figures**. **6B**, **6D** and **Fig. S3**. At age 15-22 months, scotopic b-wave amplitudes and 32 Hz flicker amplitudes became further reduced with the responses of USH2A KO more than 50% lower than those of WT controls (P =0.0073 and 0.0031 respectively by t-test). This age dependent decline suggests progressively loss of photoreceptor function in USH2A KO rabbits. Implicit time did not show a significant difference between WT and USH2A KO over time (**Fig. S4**).

350

351 USH2A rabbit histopathology showed reduced photoreceptor nuclei in the ONL

352 To look for photoreceptor degeneration characteristics of Usher-associated retinitis 353 pigmentosa, the number of photoreceptor nuclei in the outer nuclear layer (ONL), 354 which represents the rod and cone cell bodies, of a 16 months USH2A KO rabbit was 355 compared with age matched control rabbits. Figure 6A shows the H&E image of WT 356 (left) and USH2A KO (right). These H&E images clearly show thinner ONL layer in the 357 USH2A KO rabbit retina compared with the age matched wildtype control. Figure 7B 358 represent the overview of a rabbit retinal section illustrating the locations of optic 359 nerve (Myelinated region) and visual streak as well as the 10 spots for ONL nuclear 360 number counting in Figure 7C. We found that the USH2A KO rabbit has reduced 361 photoreceptor nuclear numbers throughout the whole retina compared to the age 362 matched controls, indicating photoreceptor cell degeneration which explained the 363 reduced ERG signals in Figure 6.

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365 USH2A KO rabbits showed moderate to severe hearing loss

366	USH2 affects both hearing and vision. In this study, auditory brainstem response
367	(ABR) was tested in three USH2A KO rabbits at 5 months old. As shown in figure 7,
368	ABR threshold at three different frequencies tested (4 kHz, 12 kHz, and 16 kHz) were
369	all increased by 2-3 times in the USH2A KO rabbits compared with wildtype control
370	rabbits (p=0.0465, n=3) (Fig. 7), indicating moderate to severe hearing loss in these
371	rabbits.

372

373 Discussion

374 Usher syndrome type 2 is characterized by hearing loss and early adulthood-onset of 375 RP. Retinal degeneration in patients is apparent by fundus examination and the 376 progressive reduction in ERG amplitudes over the course of the disorder. A targeted 377 Ush2a knock-out mouse demonstrates only mild retinal degeneration with late age of 378 onset⁶. A spontaneous mutant mouse model, Kunming, shows a rapid, early-onset 379 retinal degeneration, but contains mutations in two genes known to be involved in inherited retinal dystrophies: Ush2a and Pde6b⁴⁷. Recently, bright light induction has 380 381 been reported to be able to induce the damage of the rod photoreceptors in several of 382 the USH1 and USH2 mouse models. However, these experiments were in a 129 Sv/j 383 background, which is inherently more sensitive to light-induced photoreceptor cell damage ^{48,49}. Overall, these models only showed slightly reduced rod function 384

385 indicated by reduced scotopic b wave amplitude, but no cone function reduction was 386 detected. This is probably due to their late onset features, as cones are affected later 387 in the disease course compared with rods. Due to the short life span of the mice, it is 388 very difficult to study USH2 disease in mouse models. Here, we have successfully 389 established USH2A KO rabbit line. We found that targeted disruption of the USH2A 390 gene in rabbits resulted in hearing loss and severe retinal degeneration starting as 391 early as 4 months of age, which is equivalent to human adolescence, and showed 392 progressive retinal degeneration mimicking the RP in USH2 patients. To our 393 knowledge, it is the first genetic preclinical large animal model that manifest eye 394 phenotype of USH2.

395 In humans, the location of highest acuity in the retina is a circular area termed the 396 fovea which boasts the highest concentration of cones, the lowest concentration of 397 rods, and much smaller receptive field sizes for all cells. The area of greatest acuity in 398 rabbit retina is not a single point, but rather an elongated "streak" running across the 399 retina. The present of the visual streak made rabbits very useful for studying retinal 400 degenerative diseases in contrast to mice. As shown in figure 6, the reduction of the 401 ONL nuclear numbers in USH2A KO rabbits were more apparent in the visual streak 402 area (point 6), suggesting loss of cone photoreceptors. It is reported that severe visual 403 phenotype seen in syndromic USH2A patients compared with the non-syndromic 404 USH2A patients could relate to a greater extent of cone dysfunction indicated by significantly reduced 30Hz-ficker ERG amplitudes⁵⁰. In this study, in addition to the 405 406 reduced rod function detected by the reduced scotopic b wave amplitudes in ERG, our

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407 USH2A KO rabbit models also showed significantly reduced 32Hz-ficker ERG

408 amplitudes, which mimicking the cone function reduction in human patients.

409	In conclusion, we have succeeded in generating a rabbit model of USH2. Although
410	further studies are needed to fully characterize the natural history of hearing loss and
411	retinal degeneration phenotype in USH2A KO rabbits and to determine the exact
412	mechanism of photoreceptor dysfunction observed in this model, we believe that this
413	USH2A mutant rabbit model will serve as a useful large animal model with which to
414	study the pathophysiology of RP in USH and develop novel treatments. The
415	successful replication of the RP phenotype in USH2A rabbit models in this study as
416	well as the extension of gene targeting technology to rabbits by CRISPR/Cas9
417	technology motivating efforts to develop rabbit models for other types of Usher
418	Syndrome as well as other hereditary retinal diseases.

419

420 Figure legends

Figure 1. USH2A is conserved in rabbit and human. (A). Rabbit vs human Usherin protein long isoform sequence alignment using BlastP program. (B). Genomic DNA sequence alignment of rabbit exon 12 vs human exon 13 using BlastN program. (C). Real-time PCR detection of USH2A variants in adult rabbit organs. Primer pair 1(RTF1,RTR1) detects both variant 1 and variant 2 (v1+v2, blue bar); Primer pair 2(RTF2,RTR2) detects variant 2 only (orange bar). Values were normalized to18S rRNA expression. Y axes show the fold change relative to the expression level in

428	brain. Error bars represent Standard Deviation. (D). Scanning electron microscopy
429	shown Calyceal Processes like structures (CPLs) in rabbit photoreceptors. IS/OS:
430	inner and outer segments of rod and cone photoreceptor cells.

431

432 Figure 2. Production of USH2A mutant rabbits. (A). Illustration of CRISPR/Cas9 mediated targeting strategy to produce rbUSH2A mutant rabbits. (B). Four candidate 433 434 sgRNA were designed and tested in vitro (left panel). sgRNA1 was validated in rabbit 435 embryos using T7E1 analysis (right panel). In right panel, each lane representative 436 one injected embryos. The PCR product of 479 bp will be cleaved into 238 bp and 241 437 bp bands if the embryos have indels generated at the gRNA target. M, NEB 100 bp 438 DNA ladder. (C). Production of the USH2A mutant founder rabbits through embryo 439 transfer. (D). Representative NGS analysis of the founder rabbits ear biopsy showed 440 high frequencies of both indels (NHEJ) and knock-in (HDR) mutations (left and mid 441 panel). The germline transmission of the mutations was confirmed by targeted deep 442 sequencing in semen collected from the knock in founder.

443

444 Figure 3. USH2A KO line establishment and off-target analysis

(A). Breeding of the founder male rabbit mated with two female wildtype rabbits. (B).
Mutated USH2A DNA sequence and the predicted protein sequence found in the F1
generation USH2A KO rabbits. (C). Detection of off-target indels using T7E1 analysis
in F1 generation USH2A mutant rabbits with a wild-type rabbit as control. Red arrow

449	heads showing the indels detected at off-target 1 locus in F1 generation kits #2 and #6.
450	M, NEB 100 bp ladder DNA marker; On, on-target sequences; Off, off-target
451	sequences; Nucleotides in red color indicate the mismatches of the gRNA and the
452	potential off-target sequence. NGG/NGA PAMs were highlighted by underlines.
453	
454	Figure 4. USH2A expression in USH2A KO rabbit retina. Real-time PCR detection
454 455	Figure 4 . USH2A expression in USH2A KO rabbit retina. Real-time PCR detection of USH2A variants in retina tissue of a USH2A KO rabbit using the primer pair 1 in
455	of USH2A variants in retina tissue of a USH2A KO rabbit using the primer pair 1 in
455 456	of USH2A variants in retina tissue of a USH2A KO rabbit using the primer pair 1 in Fig.1, which detects both long and short variants of USH2A. Values were normalized

459

460	Figure 5. Retinal imaging in USH2A KO rabbit. A). Fundus photographs
461	(Fundus), fundus autofluorescence (FAF), indocyanine green angiography (ICGA),
462	and fluorescein angiography (FA) images obtained from a USH2A KO rabbit at
463	4-month-old to 12-month-old demonstrating hyper-FAF spots (arrows). B). Spectral
464	domain optical coherence tomography (OCT) images of a USH2A KO rabbit at
465	4-month-old to 12-month-old demonstrating hyper-reflective foci at the level of the
466	photoreceptor IS and OS segments in the photoreceptor layer (red dotted circles).
467	

468 Figure 6. Progressive retinal degeneration in USH2A KO rabbits

-22-

469	A). Representative rod ERGs recorded at scotopic -24 dB flash from a 15-month-old
470	USH2A KO rabbit with an age matched wild-type rabbit as Control. B). Full field
471	electroretinography (ERG) demonstrated a significant reduction in rod response
472	amplitude at 7 months that is further reduced at 15-22 months in USH2A KO rabbits
473	compared with age matched wildtype (WT) rabbits. C). Representative ERGs
474	recorded at 0 dB 32Hz flicker demonstrating cone response from a 15-month-old
475	USH2A KO rabbit with an age matched wild-type rabbit as control. D). A significant
476	reduction in amplitude of cone ERGs by 7 months that is consistent and further
477	reduced at 15-22 months were recorded in USH2A KO rabbits compared with age
478	matched wildtype (WT) rabbits. ICGA: indocyanine green angiography, FA:
479	fluorescein angiography, RVs: Retinal vessels. ILM: Inner Limiting Membrane. RPE:
480	Retinal pigment epithelium. CVs: Choroidal Vessels. OD: Right eye; OS: Left eye.
481	Data analyzed by unpaired t-test, * p<0.05, ** p<0.01.
482	
483	Figure 7. Histopathology analysis of USH2A KO rabbit retina. A). Representative

484	retinal section prepared from a 16 months USH2A KO rabbit stained with H&E show
485	reduced retinal layer thickness compared with age-matched wildtype (WT). Scale
486	bars 75 μ m. B). overview of a rabbit retinal section illustrating the locations for ONL
487	nuclear number counting in Panel C. C). Counting of ONL layer nuclei numbers in a
488	defined field of view (150 μm along the retina layer) at different locations on the retina
489	indicated in panel B. Error bars represent SD. RGC: Retinal Ganglion cell layer; IPL:
490	Inner plexiform layer; INL: Inner nuclear layer; OPL: Outer plexiform layer; ONL: Outer -23-

- 491 nuclear layer; IS/OS: Inner and Outer segments of rod and cone photoreceptor cells;
- 492 RPE: Retinal pigment epithelium; CL: Choroid layer.

493 Figure 8. Hearing loss in USH2A KO rabbits. Auditory brainstem response (ABR) test

- 494 demonstrating significant hearing loss in the USH2A KO rabbits at 5 months old compared
- 495 with wildtype (WT) control rabbits (p=0.0139, n=3).

496

497

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633

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641 Author contributions statement

- 642 D.Y, Y.M.P., Y.P and Y.E.C conceived the experiments. D.Y, Y.M.P, V.P. N, J.S, Y. L,
- 643 D.P, D.D, J.X, and J.Z, conducted the experiments. D.Y, Y.M.P, K.T.J and Y.E.C
- analyzed the results and wrote the manuscript. All authors critically reviewed the
- 645 manuscript.

646 Additional information

647 **Competing financial interests**: The authors declare no competing financial interests.

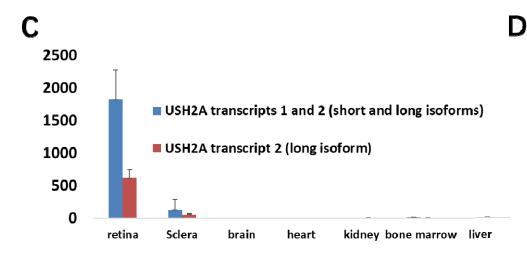
Figure 1. USH2A gene is highly conserved in rabbits and humans

В

Usherin, rabbit vs human (84% identities)

Α

Score		Expect	Method	Identities	Positives	Gaps	Frame
9171 bits(237	99)	0.0()	Compositional matrix adjust.	4382/5205(8	<mark>84%)</mark> 4743/5205(91%)6/5205(0%)	
Rabbit	1	MNCL	ALSMGFGFLFQVIETLIFG LS+G GFLFQVIE LIF	YFASISLADSR		NVSVVPSQATCGL	60
Human	1	MNCP	VLSLGSGFLFQVIEMLIFA	YFASISLTESR	GLFPRLENVGAFK	KVSIVPTQAVČGL	60
Rabbit	5038	YSEL	FIVLMAVLGLILLAIFLS	LILORKIHREP	YIRERPPLVPVQK	RMSALSVYPPGEP	5097
Human	5038	YSEL	NFIVLMAVLGLILLAIFLS NFIVLMA+LGLILLAIFLS NFIVLMAMLGLILLAIFLS	LILQRKIHKEP	YIRERPPLVPLQK	RMSPLNVYPPGEN	5097
Rabbit	5098	HMGL	ADTKIPQSGTPVSIRSNRS ADTKIP+SGTPVSIRSNRS	LSVLRIPSOSO	VSRTCSQGSLHRS	VSQLLDLQDKKVV	5157
Human	5098	HMGL	ADTKIPTSGTPVSIRSNRS	ACVLRIPSQHQ	TSLTYSQGSLHRS	VSQLHDIQDKKVL	5157
Rabbit	5158		LWETIMGHSSGLYVDEEDL			5202	
Human	5158		LWEAIMGHNSGLYVDEEDL			5202	



Rabbit exon 12 vs human xon13 (88% identities)

Score		Expect	Identities	Gaps	Strand	Frame
765 bits(4	414)	0.0()	566/642(88%)	0/642(0%)	Plus/Plus	
Rabbit	1	GGCTTCGATGTGA	TCATTGCAATTTTG	GATTTAAATTTCTTC	GAAGTTTAAATGAT	GATG 60
Human	1	GGCTTAGGTGTGA	TCATTGCAATTTTG	GATTTAAATTTCTCC	GAAGCTTTAATGAT	IGTTG 60
Rabbit Human	61 61		1	ATGGCTCAGTGAACA ATGGCTCAGTGAACA		TCTTT 120
Rabbit	541	ACTCCTTGGGGAG	ATTACCTGGGACTG	TGTGCGACCCAGTCA		ATGCT 600
Human	541	ATTCCTTGGGGA	ATTACCTGGGACCA	TTTGTGACCCAATCA	GTGGCCAGTGCCT	STGTG 600
Rabbit	601	TGCCTAATCGTC	AGGAAGAAGGTGTA		642	
Human	601	TGCCTAATCGTC	AGGAAGAAGGTGTA	ATCAGTGTCAACCAG	642	

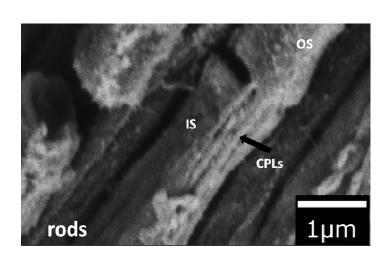
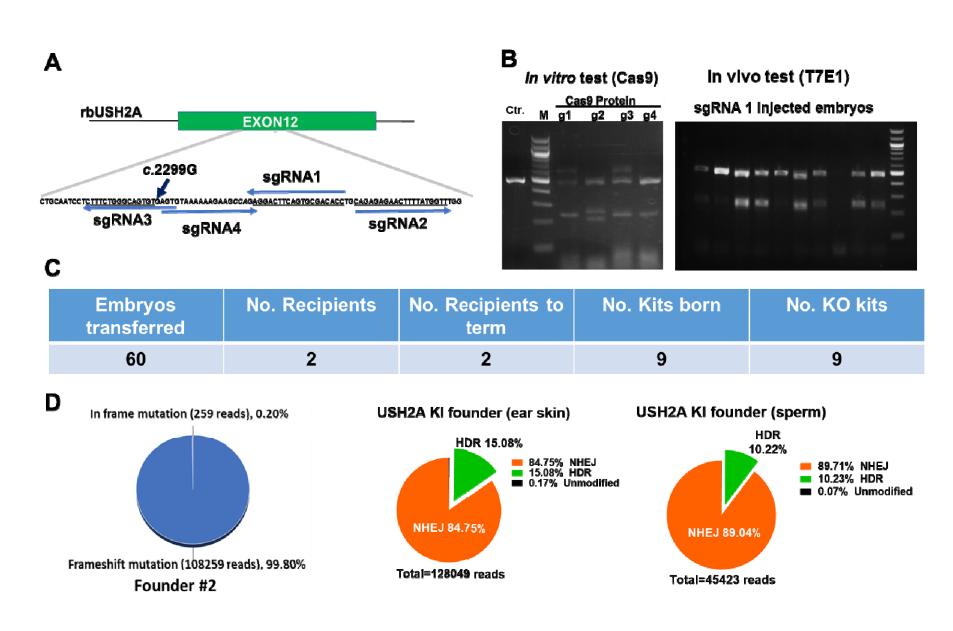


Figure 2. Production of USH2A mutant rabbits



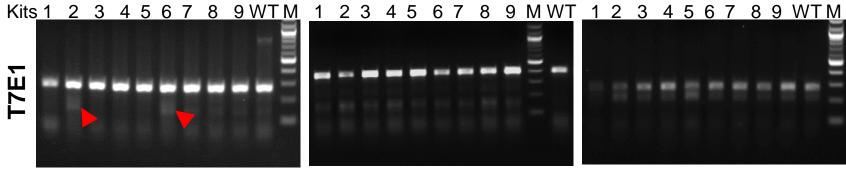
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Figure 3. USH2A KO line establishment and off-target analysis

Α

Male	Female	Kits	USH2A mutant	Germline transmission	
Founder #2	Wild-type	19	9	Yes	
B					
Genotype	DI	NA sequence		Predicted Protein sequence	
Wildtype	GAGTGTAAAAAAGAAGCCAGAGGACTTCAGTGCG			ECKKEARGLQCDTCRENFYGLDVTDX	
<i>c.</i> 2315_2325 <i>del</i> 11 GAGTGTAAAAAAGAAGCAGTGCG <i>p. R773Vfs</i> *17				ECKKEAVRHLQRELLWFGCHRLX	
c.2321_2334ins14 GAGTGTAAAAAAGAAGCCAGAGTAACCTTTGTTACTGACTTCAGTGCG p. G774Efs*106				ECKKEAR VTFVTDFSATPAERTFX	
c.2321insA GAGTGTAAAAAAGAAGCCAGAGAGACTTCAGTGCG p.G774Efs*20				ECKKEARETSVRHLQRELLWFGCHRLX	

С



OT1: intergenic:RELL1-PGM2 GGTGTCGCACTGAAGTCCTCTGG On Off GGGGTCGCACGGAAGTCCTCAGG OT2:intergenic:CD9-PLEKHG6 GGTGTCGCACTGAAGTCCTC*TGG* **GGTTTCGCACTGAAGTCCTT***TGA*

OT3:intergenic:LY86-RREB1 GGTGTCGCACTGAAGTCCTC TGG TG TCTCACACTGAAGTCCTC AGG

USH2A expression

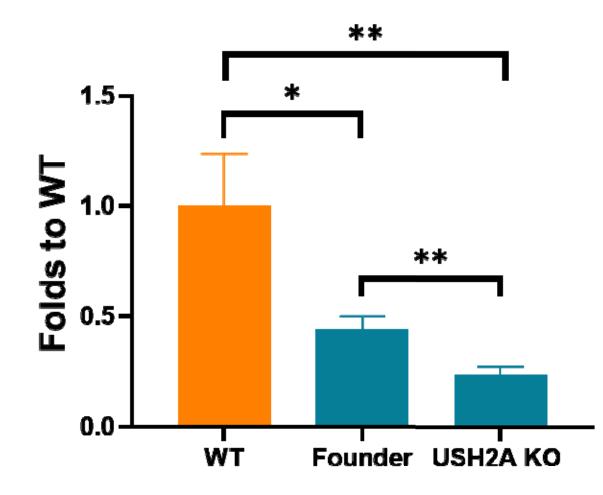


Figure 5. Retinal imaging in USH2A KO rabbit

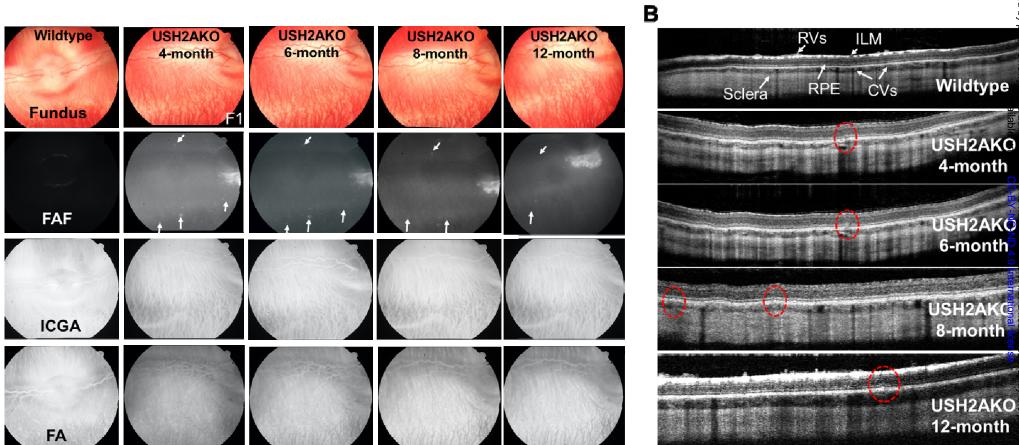
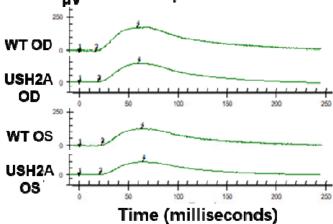


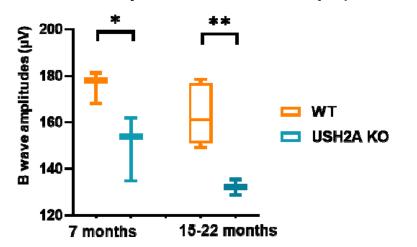


Figure 6. Progressive retina degeneration in USH2A KO rabbits





Scotopic ~24 dB Flash B wave (OD)



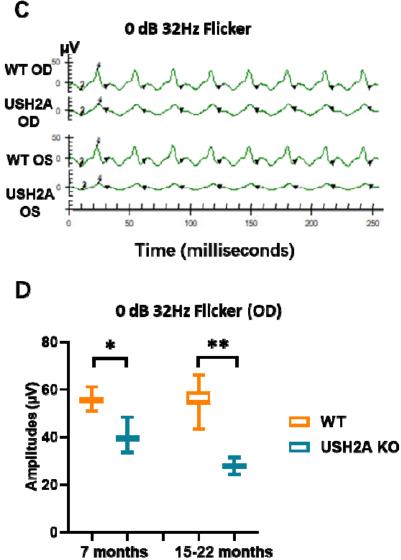
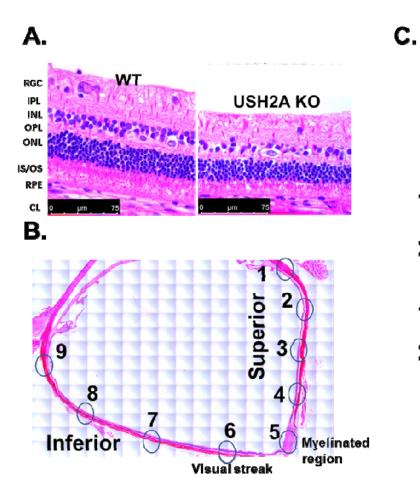
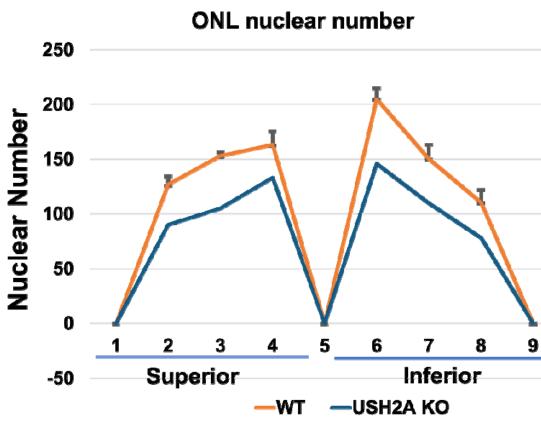


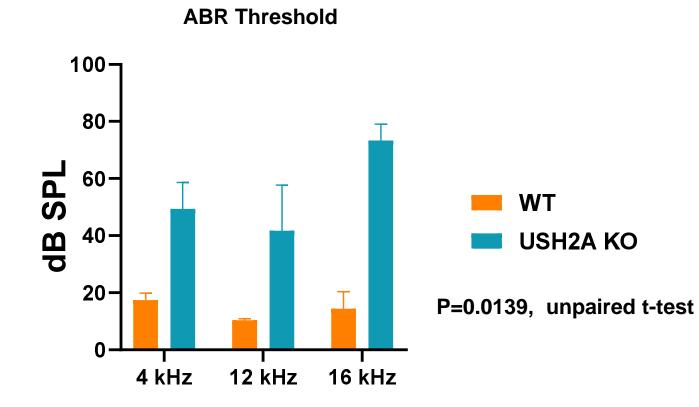
Figure 7. Photo receptor loss in USH2A KO rabbit



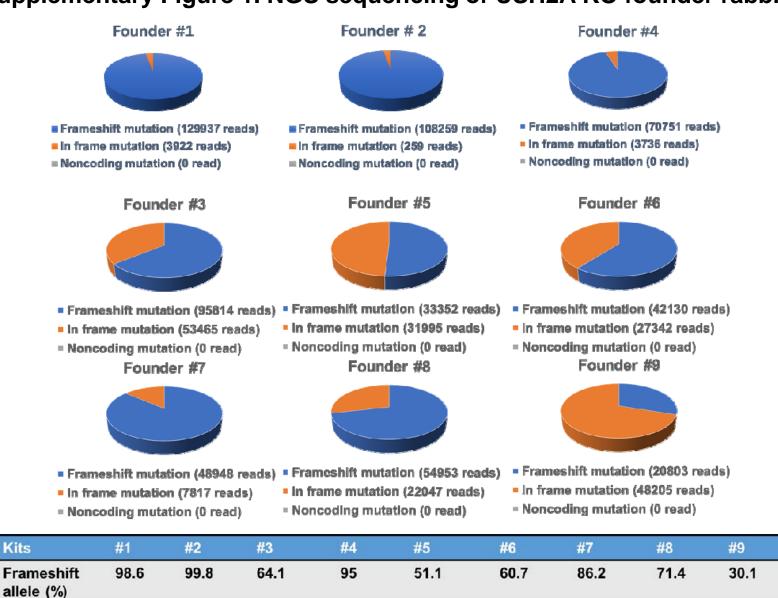


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Figure 8. Hearing loss in USH2A KO rabbits



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Inframe allele

Ki allel (%)

(%)

1.4

0.01

0.2

15.08

35.9

0

5

0

48.9

0

39.3

0

13.8

0

28.6

0

69.9

0.08

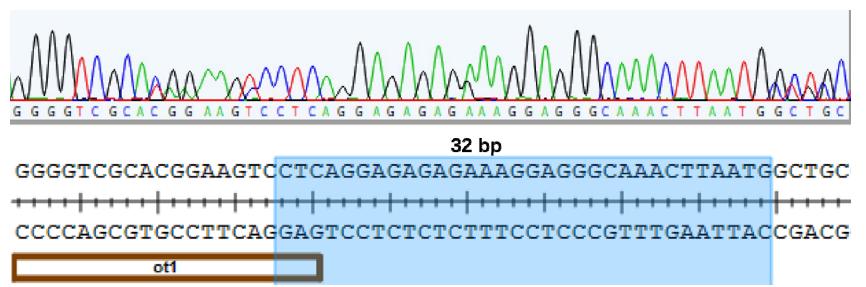
Supplementary Figure 1. NGS sequencing of USH2A KO founder rabbits

Supplementary Figure 2. Germline transmission of the mutant alleles in F1 generation rabbits (A) and Sanger sequencing of the OT1 off-target mutation (B). Ot1: the off-target binding sequence. The 32 bp shadow part indicated the distance from the indels mutation (double peaks) site to the Cas9 cleavage site (3 bp upstream of the AGG PAM sequence)

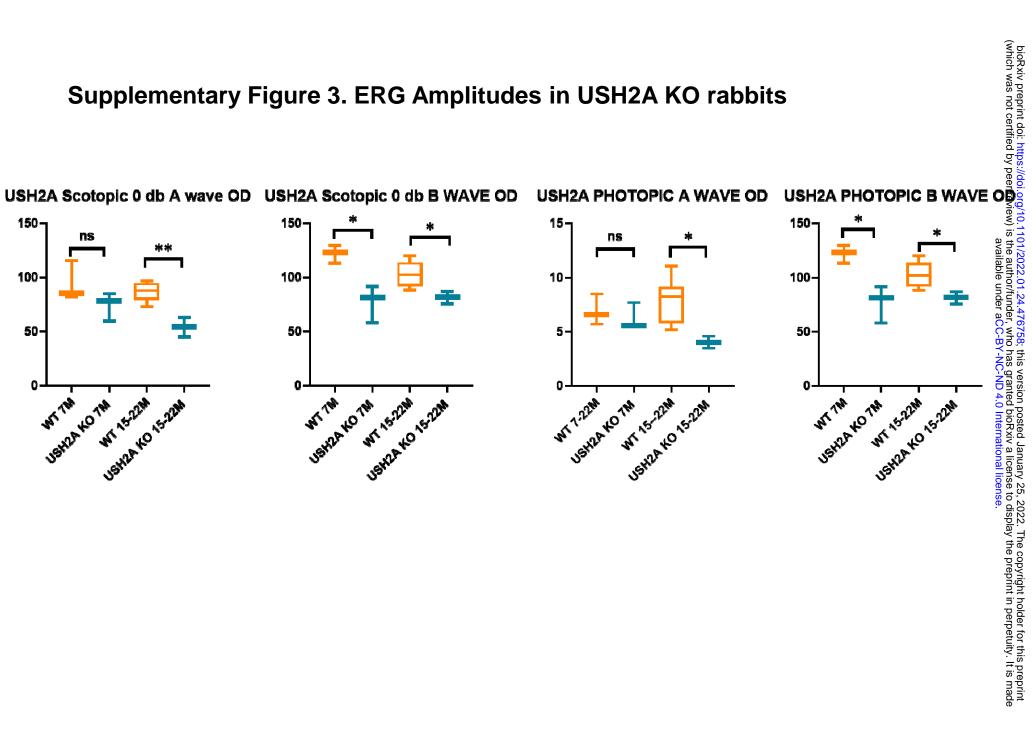
Α

- Wt GAAGC-----CAGAG-----GACTTCAGTGCGACACCTGCAGAGAGAACTTTT
- (+14bp) GAAGC-----CAGAGTAACCTTTGTTACTGACTTCAGTGCGACACCTGCAGAGAGAACTTTT (Kits #1,2,3,9)
- (+11bp) GAAGCCCAGAGGACTTCAGAG------GACTTCAGTGCGACACCTGCAGAGAGAACTTTT (kits # 4,5,6,7)
- (-26bp) GAAGC------AACTTTT (Kits #8)

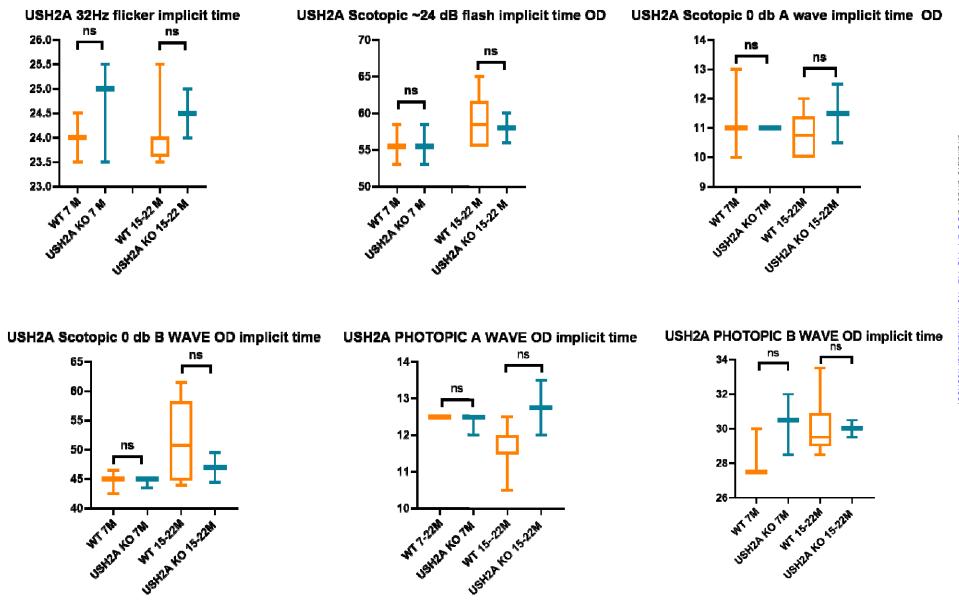
В



Supplementary Figure 3. ERG Amplitudes in USH2A KO rabbits



Supplementary Figure 4. ERG implicit time in USH2A KO rabbits



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upplementary table 1

sgRNA1	GGTGTCGCACTGAAGTCCTC <u>TGG</u>
sgRNA2	CAGAGAGAACTTTTATGGTT <u>TGG</u>
sgRNA3	CACTCACACTGCCCAGAAAG AGG
sgRNA4	GAGTGTAAAAAAGAAGCCAG <u>AGG</u>

Supplementary table 2

Primers	Sequence
F1	TCTGCAGTAGCATTGTTTGTGATT
R1	GTCCCAGTCTCATCACAGTTACAA
F2	ATTGCAATTTTGGATTTA
R2	ACGTTGGGTCTACAGAGGCACT
dsF	AGCCCTGCCAGTGTAACCTC
dsR	AGTGACTGAGCCTGCTGTGTTG
RTF1	AATTCAGGCCAGTGCAAGTG
RTR1	GCCCAGAAAGAGGATTGCAG
RTF2	GGAGAAGAAGAGGGTGTGCT
RTR2	GACTCTCCACTGGAAGCTGA