

**Supplemental Figure 1. Characteristics of the non-diabetic and diabetic rats.** Box-and-whisker plots (min, max, 25th–75th percentile, median) comparing blood glucose, HbA1c and body weights of the diabetic rats with those of the non-diabetic controls. Data information: \*\*\*\* $P < 0.0001$  based on Mann–Whitney U-test;  $N = 69\text{--}96$  animals per group for weights,  $N = 72\text{--}74$  animals per group for blood glucose and  $N = 12\text{--}13$  animals per group for HbA1c.

## A Wildtype rat *Trpv2* genomic DNA sequence

|      |   |
|------|---|
| 8401 | GAGAGGAGGG GAGGCTCTGGT TGGCTGCTTC TTAATCTTTC TGATGTACCT CAGGGAGAGC TGGCTTCTG CCTGAGGAGC AGGAAGAGTA GTGAGSTAGA                           |
|      | CTCTGCTCCC CTCAGAGCCA ACCGACGGAG AATAAGAAAG ACTACATGGA GTCCCTCTCG ACCGAAAGAC GGACTCCTCG TCCTTCTCAT CACTCCATCT                           |
|      | Gly Glu Leu Pro Leu Ser Leu Ala Ala Cys Thr Lys Gln Trp Asp Val Val Thr Trp Leu Leu Glu Asn   |
| 8501 | GGTAGAGGCT CAAGCTGCC TCITGGTCCA CAGGAGAGCT ACCTCTTTCT CTGGCTGCGT GCACCAAGCA GTGGGATGTG GTGACCTACC TCCTGGAGAA                            |
|      | CCATCTCCGA GTTCGACGGG AGAACCAGGT GTCTCTCGA TGGAGAAAGA GACCGACGCA CGTGGTTCGT CACCTACAC CACTGGATGG AGGACCTCTT                             |
|      | Asn Pro His Gln Pro Ala Ser Leu Glu Ala Thr Asp Ser Leu Gly Asn Thr Val Leu His Ala Leu Val Met Ile Ala Asp Asn Ser Pro Glu Asn Ser Ala |
| 8601 | CCCACACCAG CCGGCCAGCC TGGAGGCCAC CGACTCCCTG GSCAACACAG TCCTGCAATG TCTGGTAATG ATTGCAGATA ACTCGCCTGA GAACAGTGCC                           |
|      | GGGTGTGTC GGCCTGTCGG ACCTCGGCTG GCTGAGGGAC CCGTGTGTG AGGACGTACG AGACCAATAC TAACGTCTAT TGAGCGGACT CTGTGACGG                              |
|      | Leu Val Ile His Met Tyr Asp Gly Leu Leu Gln Met Gly Ala Arg Leu Cys Pro Thr Val Gln Leu Glu Glu Ile Ser Asn His Gln Gly Leu Thr Pro Leu |
| 8701 | CTGGTGATCC ACATGTACGA CCGGCTTCTA CAATGGGGG CCGCCTCTG CCCCCTGTG CAGCTTGAGG AAATCTCCAA CCACCAAGGC CTCACACCCC                              |
|      | GACCACTAGG TGTACATGCT GCGCGAAGAT GTTACCCCC GCGCGGAGAC GGGGTGACAC GTGGAATCC TTAGAGGTT GGTGGTTCG GAGTGTGGG                                |
|      | Leu Lys Leu Ala Ala Lys Glu Gly Lys Ile Glu   |
| 8801 | TGAAACTAGC CGCCAAGGAA GSCAAATCG AGGTGAGTAC CATCCCTATC CTGCTCTCT TGGTGTCAAT GGGACTCAGG TACACACATA ATGCAAACAC                             |
|      | ACTTGTATCG GCGGTTCCTT CCGTITTAGC TCACCTCATG GTAGGATAG GACGGAGAGA ACCGACGTTA CCTGTGATCC ATGTGTAT TACGTTTGTG                              |

## B Founder: Genomic DNA sequence with 115bp deletion at 8584-8698 highlighted

|      |   |
|------|---|
| 8401 | GAGAGGAGGG GAGGCTCTGGT TGGCTGCTTC TTAATCTTTC TGATGTACCT CAGGGAGAGC TGGCTTCTG CCTGAGGAGC AGGAAGAGTA GTGAGSTAGA                           |
|      | CTCTGCTCCC CTCAGAGCCA ACCGACGGAG AATAAGAAAG ACTACATGGA GTCCCTCTCG ACCGAAAGAC GGACTCCTCG TCCTTCTCAT CACTCCATCT                           |
|      | Gly Glu Leu Pro Leu Ser Leu Ala Ala Cys Thr Lys Gln Trp Asp Val Val Thr Trp Leu Leu Glu Asn   |
| 8501 | GGTAGAGGCT CAAGCTGCC TCITGGTCCA CAGGAGAGCT ACCTCTTTCT CTGGCTGCGT GCACCAAGCA GTGGGATGTG GTGACCTACC TCCTGGAGAA                            |
|      | CCATCTCCGA GTTCGACGGG AGAACCAGGT GTCTCTCGA TGGAGAAAGA GACCGACGCA CGTGGTTCGT CACCTACAC CACTGGATGG AGGACCTCTT                             |
|      | Asn Pro His Gln Pro Ala Ser Leu Glu Ala Thr Asp Ser Leu Gly Asn Thr Val Leu His Ala Leu Val Met Ile Ala Asp Asn Ser Pro Glu Asn Ser Ala |
| 8601 | CCCACACCAG CCGGCCAGCC TGGAGGCCAC CGACTCCCTG GSCAACACAG TCCTGCAATG TCTGGTAATG ATTGCAGATA ACTCGCCTGA GAACAGTGCC                           |
|      | GGGTGTGTC GGCCTGTCGG ACCTCGGCTG GCTGAGGGAC CCGTGTGTG AGGACGTACG AGACCAATAC TAACGTCTAT TGAGCGGACT CTGTGACGG                              |
|      | Leu Val Ile His Met Tyr Asp Gly Leu Leu Gln Met Gly Ala Arg Leu Cys Pro Thr Val Gln Leu Glu Glu Ile Ser Asn His Gln Gly Leu Thr Pro Leu |
| 8701 | CTGGTGATCC ACATGTACGA CCGGCTTCTA CAATGGGGG CCGCCTCTG CCCCCTGTG CAGCTTGAGG AAATCTCCAA CCACCAAGGC CTCACACCCC                              |
|      | GACCACTAGG TGTACATGCT GCGCGAAGAT GTTACCCCC GCGCGGAGAC GGGGTGACAC GTGGAATCC TTAGAGGTT GGTGGTTCG GAGTGTGGG                                |
|      | Leu Lys Leu Ala Ala Lys Glu Gly Lys Ile Glu   |
| 8801 | TGAAACTAGC CGCCAAGGAA GSCAAATCG AGGTGAGTAC CATCCCTATC CTGCTCTCT TGGTGTCAAT GGGACTCAGG TACACACATA ATGCAAACAC                             |
|      | ACTTGTATCG GCGGTTCCTT CCGTITTAGC TCACCTCATG GTAGGATAG GACGGAGAGA ACCGACGTTA CCTGTGATCC ATGTGTAT TACGTTTGTG                              |

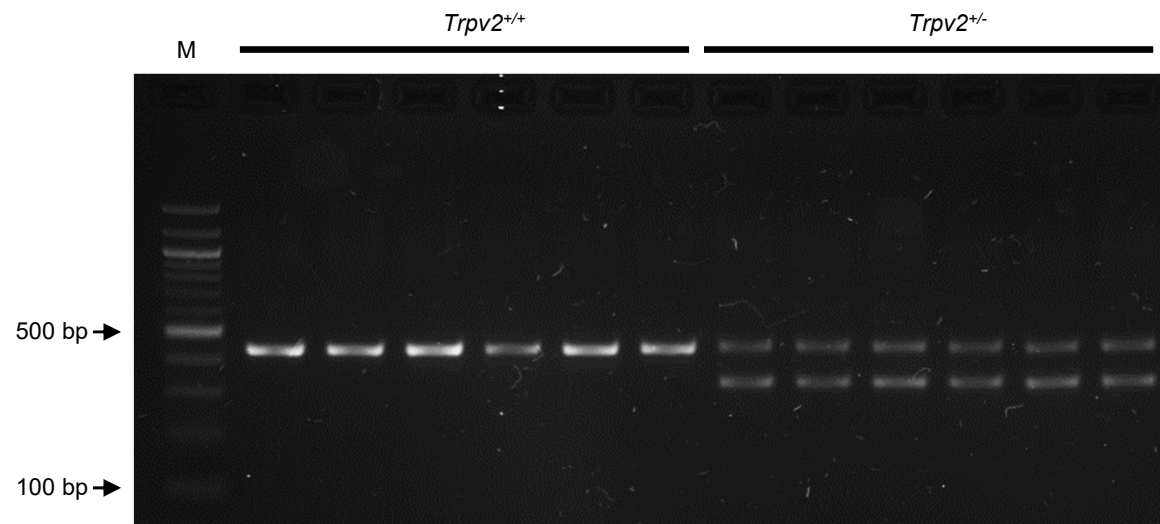
## C Founder: mRNA with 115bp deletion highlighted in blue

|      |   |
|------|---|
| 1001 | CTTCTCCAA AAGCACAAG GAACCTGTTT CTAATTTGA GAGCTACCTC TTCTCTGGC TGGGTGACAC AAGCAGTGG ATGTGGTGAC CTACCTCTG                                 |
|      | GAAGAAGGTT TCTGTGGTTC CTGACACAAA GATAAAACCT CTCGATGGAG AAGAGACCGC ACGCAGCTGG TTCGTACAC TACACCAAGG GATGGAGGAC                            |
|      | Glu Asn Pro His Gln Pro Ala Ser Leu Glu Ala Thr Asp Ser Leu Gly Asn Thr Val Leu His Ala Leu Val Met Ile Ala Asp Asn Ser Pro Glu Asn Ser |
| 1101 | GAGAACCCAC ACCACCGCGC CAGCTCTGAG GCCACCGACT CCGTGGSCAA CACAGTCTGT CATGCTCTGG TAATGATTGC AGATAATCGC CCGTGAACAA                           |
|      | CTCTTGGGTG TGGTGGCGCG GTGCGACCTC CGTGGCTGA GGGACCCGTT GTGTCAAGAC GTACGAGACC ATTACTAAGC TCTATTGAGC GGACTCTTGT                            |
|      | Ser Ala Leu Val Ile His Met Tyr Asp Gly Leu Leu Gln Met Gly Ala Arg Leu Cys Pro Thr Val Gln Leu Glu Glu Ile Ser Asn His Gln Gly Leu Thr |
| 1201 | GTGCCCTGGT GATCCACATG TACGCGGGC TTCTACAAAT GGGGGGCGCG CTCTGCCCA CTGTGACGT TGAGGAAATC TCCAAACACC AAGGCTTCAC                              |
|      | CACGGACCA CTAGGTGTAC ATGCTGCCCG AAGAATTGA CCCCCGCGCG GAGACGGGT GACACGTGCA ACTCTTTAG AGGTGTGGG TTCCGGAGTG                                |
|      | Thr Pro Leu Lys Leu Ala Lys Glu Gly Lys Ile Glu Ile Phe Arg His Ile Leu Gln Arg Glu Phe Ser Gly Pro Tyr Gln Pro Leu Ser Arg Lys Phe     |
| 1301 | ACCCCTGAAA CTAGCGGCCA AGGAAGCAA AATCGAGATT TTCAGGCACA TTCTGACGCG GGAATTTCTA GGAAGTACC AGCCCTTTC CCGAAAGTTT                              |
|      | TGGGACCTTT GATCGCGGTG TCTTCCGTTT TTAGCTCAA AAGTCCGTGT AAGACGTGCG CTTTAAAGAT CTTGGCATGG TGGGGGAAAG GGTCTTCAA                             |
|      | Thr Glu Trp Cys Tyr Gly Pro Val Arg Val Ser Leu Tyr Asp Ser Val Asp Ser Trp Glu Lys Asn Ser Val Leu Glu Ile Ile Ala Phe His Cys         |
| 1401 | ACTGATGGT GTTACGGTCC TGTGCGGCTA TCGTGTACG ACTGTCTCTC TGTGGACAGC TGGGAAAGA ACTCGGTGCT GGAATCATC GCTTTTCATT                               |
|      | TGACTCACCA CAATGCCAAG ACACGCCCAT AGCGACATGC TGGACAGGAG ACACCTGTG ACCCTTTTCT TGAGCCACGA CTTCTAGTAG CGAAAAGTAA                            |
|      | Cys Lys Ser Pro Asn Arg His Arg Met Val Val Leu Glu Pro Leu Asn Lys Leu Leu Gln Glu Lys Trp Asp Arg Leu Val Ser Arg Phe Phe Asn Phe     |
| 1501 | SCAGAGCCC GAACGGCAC CGCATGGTGG TTTTGAACCC ACTGAACAG CTCTGCGAG AGAAATGGGA TCGGCTCGTC TCAAGATTCT TCTTCAACTT                               |
|      | GTCTCTCGG GTTGGCGTG GGTACACCC AAAATCTTGG TGAATTTTTC GAAGACGTCC TCTTACCT AGCGGACGAG AGTTCTAAGA AGAAGTTGAA                                |

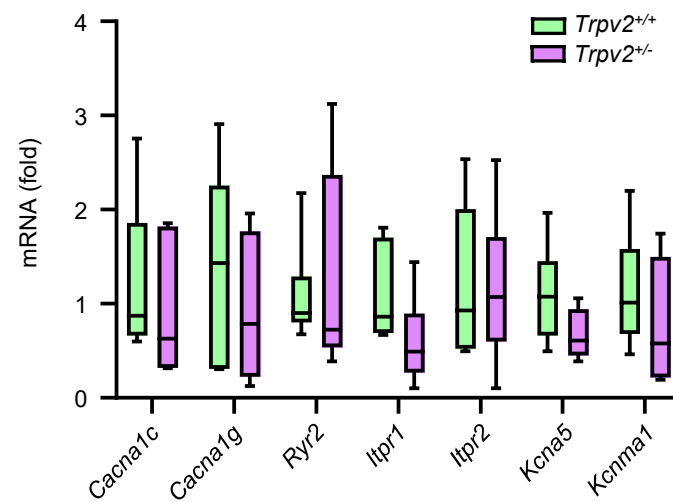
## D Founder: mRNA with 115bp deletion

|      |   |
|------|---|
| 1001 | CTTCTCCAA AAGCACAAG GAACCTGTTT CTAATTTGA GAGCTACCTC TTCTCTGGC TGGGTGACAC AAGCAGTGG ATGTGGTGAC CTACCTCTG                                 |
|      | GAAGAAGGTT TCTGTGGTTC CTGACACAAA GATAAAACCT CTCGATGGAG AAGAGACCGC ACGCAGCTGG TTCGTACAC TACACCAAGG GATGGAGGAC                            |
|      | Thr Cys Thr Thr Gly Phe Tyr Lys Trp Gly Arg Ala Ser Ala Pro Leu Cys Ser Leu Arg Lys Ser Pro Thr Thr Lys Ala Ser His Pro Asn Pro         |
| 1101 | ACATGTACGA CCGGCTTCTA CAATGGGGG CCGCCTCTG CCCCCTGTG CAGCTTGAGG AAATCTCCAA CCACCAAGGC CTCACACCCC TGAACATG                                |
|      | TGTACATGCT CCGCGAAGAT GTTACCCCC GCGCGGAGAC GGGGTGACAC GTGGAATCC TTAGAGGTT GGTGGTTCG GAGTGTGGG ACTTGTATCG                                |
|      | Pro Pro Arg Lys Ala Lys Ser Arg Phe Ser Gly Thr Phe Cys Ser Gly Asn Ser Gln Asp Arg Thr Ser Pro Phe Pro Glu Ser Leu Leu Ser Gly Val Thr |
| 1201 | CGCCAAGGAA GSCAAATCG AGATTTTCA GCAATTTCTG CAGCGGGAAT TCTCAGGACC GTACCAACCC CTTTCCCGAA AGTTTACTGA GTGGTGTAC                              |
|      | GCGGTTCCTT CCGTITTAGC TCTAAAGTTC CCGTGAAGAC GTGCGCTTGA AGATCTCTGG CATGGTCTGG GAAGGGGCTT TCAATGACT CACCAATATG                            |
|      | Thr Val Leu Cys Gly Tyr Arg Cys Thr Thr Cys Pro Leu Trp Thr Ala Gly Lys Arg Thr Arg Cys Trp Arg Ser Ser Leu Phe Ile Ala Arg Ala Arg Thr |
| 1301 | GTCTCTGTC GGTATGCTGT GTACGACTTG TCTCTGTGG ACAGTGGGA AAGAACTCG GTGCTGGAGA TCAATGCTTT TCAATGCAAG AGCCCAACCC                               |
|      | TCAGACACG CCAATAGGCA CATGCTGGAC AGGAGACACC GTGCGACCTT TTTCTTGGC CACGACCTCT AGTAGCGAAA AGTAACGTTC TCGGCTTGG                              |

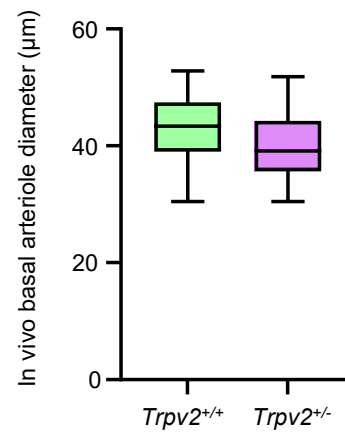
**Supplemental Figure 2. Generation of TRPV2 heterozygous knockout rats using CRISPR/Cas9 genome editing.** A. Part of the genomic DNA sequence of the wildtype rat *Trpv2* gene. Exon 5 is shown in yellow; the guide RNA (gRNA) site selected to target Exon 5 is coloured pink and the primer positions used for genotyping analysis are shown in cyan. B. The founder animal had a 115bp deletion at 8584-8698 of the *Trpv2* genomic DNA sequence (highlighted in blue). C. Wildtype mRNA sequence (top strand) with the deletion mutation highlighted in blue. Grey is exon 4, yellow is exon 5 and green is exon 6. D. mRNA sequence (top strand) after the deletion of the sequence highlighted in C. The 115bp deletion resulted in several early stop codons highlighted by the red boxes, the first of which was 57 nucleotides downstream of the start of exon 5.



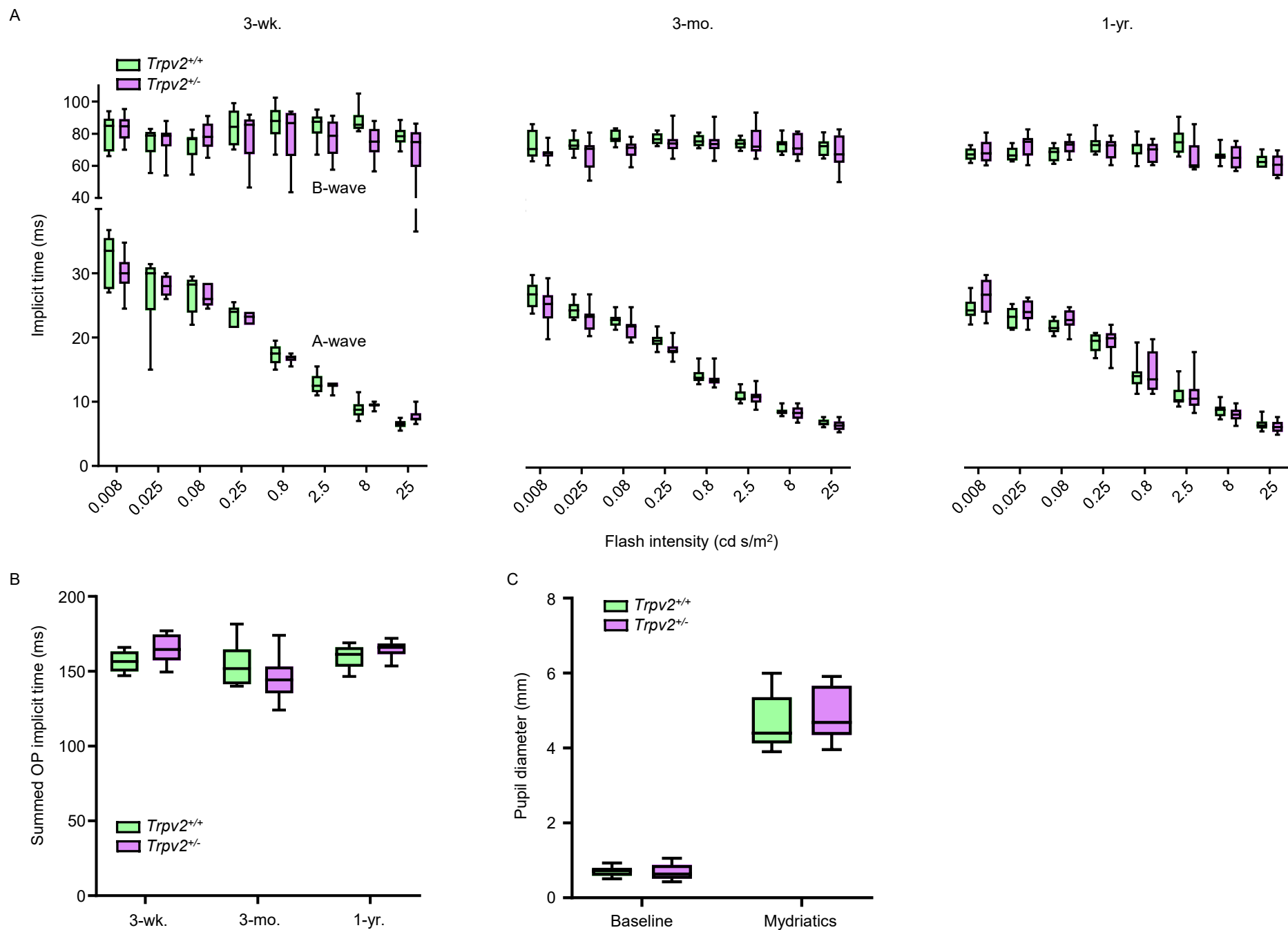
**Supplemental Figure 3. Genotyping of TRPV2 heterozygous knockout rats.** Representative genotyping gel of DNA from ear biopsies of TRPV2 WT and heterozygous knockout rats. Each lane represents an individual animal. TRPV2 WT rats showed a single band at 444bp, whereas the TRPV2 heterozygous knockout rats had an additional band at 329bp. The lengths of the PCR products were as expected based on the primer sets used (see Methods). “M” refers to the molecular weight marker lane.



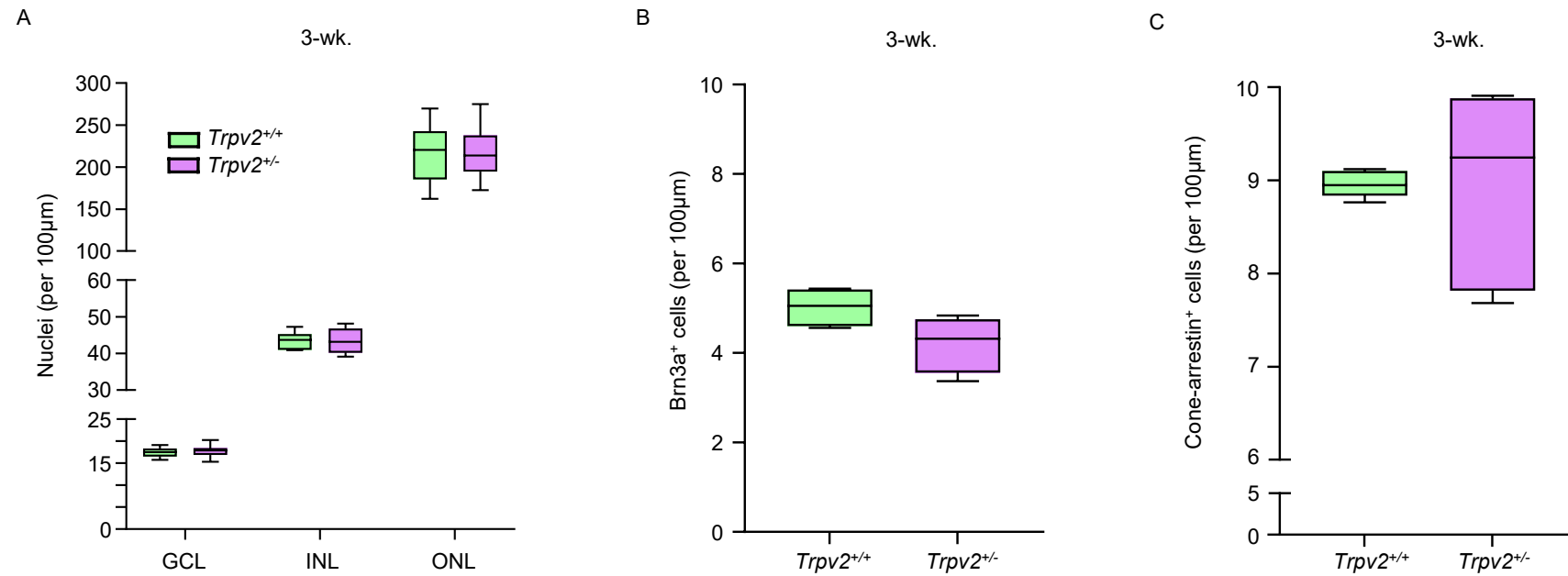
**Supplemental Figure 4. Relative transcript expression for other ion channels involved in the retinal myogenic response.** Box-and-whisker plots (min, max, 25th–75th percentile, median) showing that the mRNA expression levels of Ca<sup>2+</sup> (*Cacna1c*, *Cacna1g*, *Ryr2*, *Itpr1*, *Itpr2*) and K<sup>+</sup> (*Kcna5*, *Kcnma1*) channels previously implicated in retinal myogenic function were similar in isolated retinal arterioles from TRPV2 WT and heterozygous rats. Data information: NS for each gene based on Mann–Whitney U-tests; N=6 animals per group.



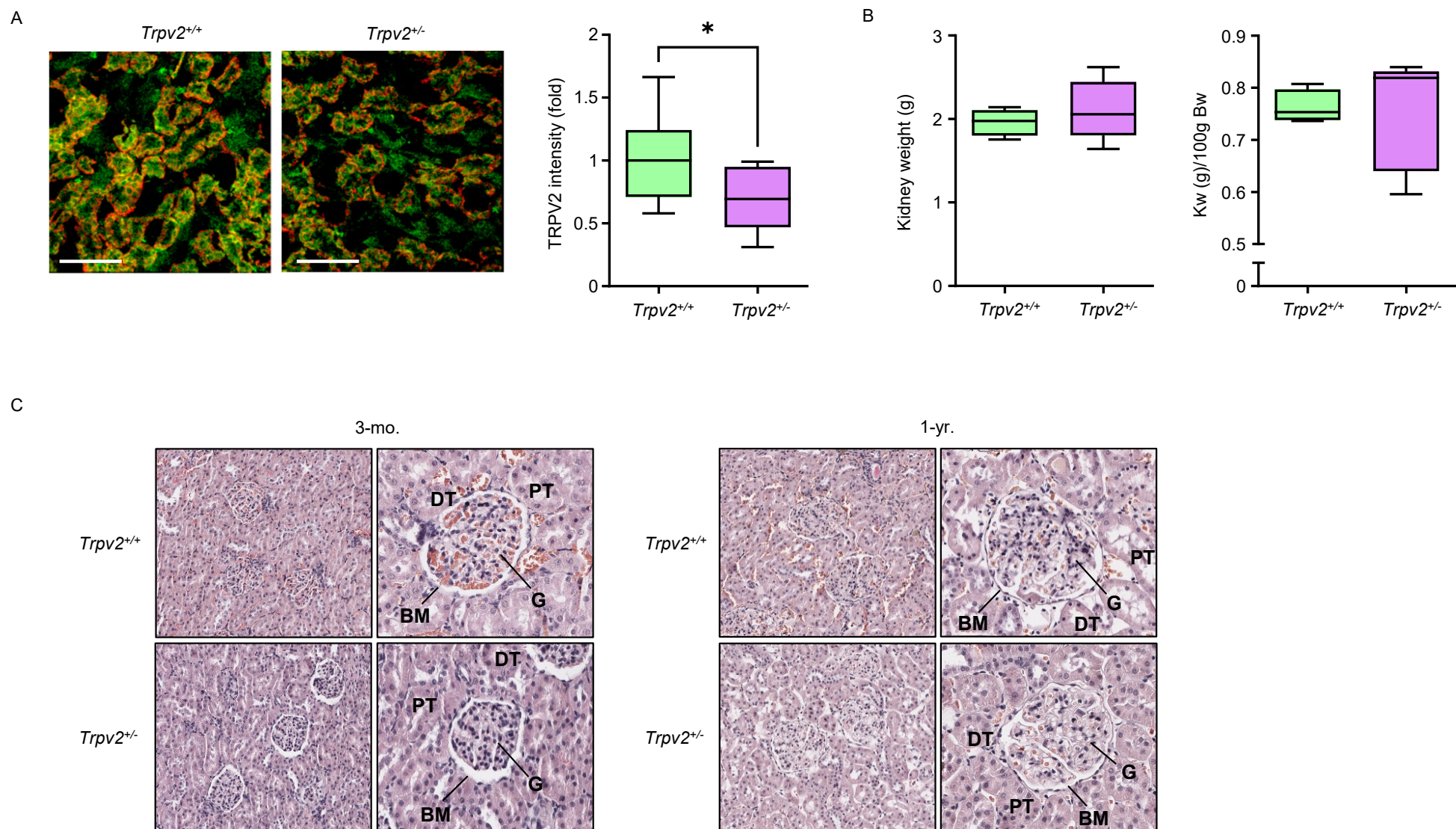
**Supplemental Figure 5. In vivo basal retinal arteriole diameters in TRPV2 WT and heterozygous rats.** Box-and-whisker plots (min, max, 25th–75th percentile, median) showing that in vivo retinal arteriole diameters were similar for both groups of animals under basal conditions. Data information: NS based on Mann–Whitney U-test; N=6 animals,  $n$ =19-23 arterioles per group.



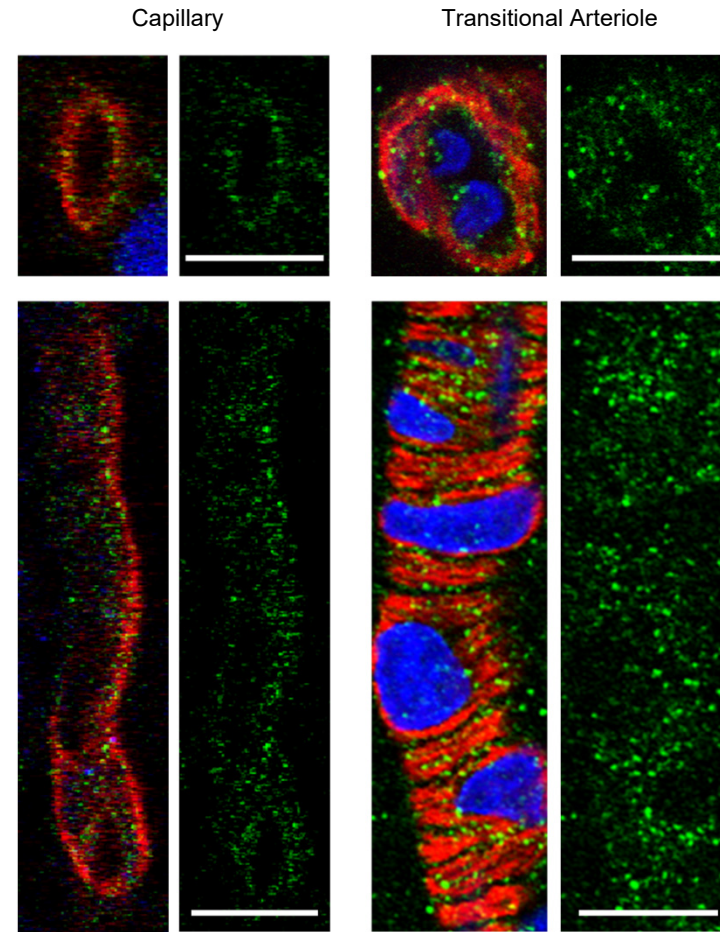
**Supplemental Figure 6. ERG implicit times and pupil diameters in TRPV2 WT and heterozygous rats.** A. Box-and-whisker plots (min, max, 25th–75th percentile, median) comparing ERG A- and B-wave implicit times for TRPV2 WT and heterozygous rats at 3-weeks, 3-months and 1-year of age. Data information: NS based on two-way ANOVA; N=6-7 animals per group. B. Summary data showing that summed oscillatory potential implicit times were similar between TRPV2 WT and heterozygous rats at all timepoints examined. Data information: NS based on two-way ANOVA; N=6-7 animals per group. C. Pupil diameters in TRPV2 WT and heterozygous rats (3-6 months of age) in the absence or presence of mydriatics (1% atropine and 2.5% phenylephrine). Data information: NS based on Mann–Whitney U-tests; N=7-8 animals per group.



**Supplemental Figure 7. Analysis of cell nuclei, ganglion cell and cone cell numbers in retinal sections from 3-week-old TRPV2 WT and heterozygous rats.** A. Box-and-whisker plots (min, max, 25th–75th percentile, median) showing the numbers of cell nuclei in the ganglion cell layer (GCL), inner nuclear layer (INL) and outer nuclear layer (ONL) of 3-week-old TRPV2 WT and heterozygous rats. Data information: NS based on Mann–Whitney U-tests; N=12 animals, n=12 retinas per group. B. Summary data showing the numbers of Brn3a positive retinal ganglion cells in TRPV2 WT and heterozygous rats at 3-weeks of age. Data information: NS based on Mann–Whitney U-test; N=4 animals, n=4 retinas per group. C. Pooled data showing that cone cell numbers were similar in TRPV2 WT and heterozygous rats at 3-weeks of age. Data information: NS based on Mann–Whitney U-test; N=5 animals, n=5 retinas per group.



**Supplemental Figure 8. Kidney structure is normal in TRPV2 heterozygous rats.** A. Left, representative confocal images showing that TRPV2 protein levels (green) were reduced in the kidneys of TRPV2 heterozygous rats at 3-months of age. Kidney sections were co-labelled with anti-pan-cadherin antibodies (red) to mark the renal tubular epithelial cells. Scale bars = 100µm. Right, TRPV2 fluorescence intensity in kidney sections from TRPV2 heterozygous rats expressed relative to TRPV2 WT controls. Data information: \* $P < 0.05$  based on Mann–Whitney U-test;  $N = 3$  animals,  $n = 9$  renal sections per group. B. Box-and-whisker plots (min, max, 25th–75th percentile, median) comparing kidney weights and kidney weights (Kw) adjusted for body weight (Bw) between TRPV2 WT and heterozygous rats at 3-months of age. Data information: NS based on Mann–Whitney U-test;  $N = 5$  animals per group. C. Representative photomicrographs of H&E stained kidney sections from TRPV2 WT and heterozygous rats at 3-months and 1-year of age. Renal morphology appeared normal in both groups of animals. G – glomerulus, BM – basement membrane, DT – distal tubule. PT – proximal tubule.



**Supplemental Figure 9. TRPV2 protein expression in a retinal capillary pericyte and VSMCs of a transitional retinal arteriole.** Left, confocal cross-sectional (top) and en face images (bottom) from a rat retinal wholemount preparation showing TRPV2 protein expression (green) in an NG2-labelled retinal capillary pericyte (red). Blue staining in the cross-sectional image represents a BRN3a-positive RGC. Right, Equivalent confocal images to those on the left, but showing TRPV2 protein expression (green) in  $\alpha$ -SMA-labelled VSMCs (red) of a transitional retinal arteriole. Cell nuclei are labelled using TO-PRO-3 (pseudo-colored blue). Scale bars in all images = 15 $\mu$ m.

| Inflammatory factor | Fold change<br><i>Trpv2<sup>+/-</sup></i> vs <i>Trpv2<sup>+/+</sup></i> | Adjusted P |
|---------------------|---|------------|
| Activin A           | 1.33  | P>0.05     |
| Agrin               | 1.56  | P>0.05     |
| B7-2/CD86           | 0.94  | P>0.05     |
| B-NGF               | 0.95  | P>0.05     |
| CINC-1              | 1.17  | P>0.05     |
| CINC-2a             | 1.29  | P>0.05     |
| CINC-3              | 1.66  | P>0.05     |
| CNTF                | 1.86  | P>0.05     |
| Fas-Ligand          | 1.77  | P>0.05     |
| Fractalkine         | 2.58  | P>0.05     |
| GM-CSF              | 4.39  | P<0.05     |
| ICAM-1              | 5.31  | P<0.0001   |
| IFN- $\gamma$       | 3.28  | P>0.05     |
| IL-1a               | 2.66  | P>0.05     |
| IL-1B               | 2.12  | P>0.05     |
| IL-1R6              | 2.57  | P>0.05     |
| IL-2                | 2.04  | P>0.05     |
| IL-4                | 1.90  | P>0.05     |
| IL-6                | 1.87  | P>0.05     |
| IL-10               | 1.69  | P>0.05     |
| IL-13               | 3.69  | P<0.05     |
| Leptin              | 4.63  | P>0.05     |
| LIX                 | 4.27  | P>0.05     |
| L-Selectin          | 4.70  | P>0.05     |
| MCP-1               | 3.29  | P>0.05     |
| MIP-3a              | 3.31  | P>0.05     |
| MMP-8               | 2.34  | P>0.05     |
| PDGF-AA             | 3.17  | P>0.05     |
| Prolactin R         | 3.07  | P>0.05     |
| RAGE                | 1.28  | P>0.05     |
| CXCL7               | 2.13  | P<0.05     |
| TIMP-1              | 1.70  | P>0.05     |
| TNF-a               | 3.40  | P<0.05     |
| VEGF                | 2.65  | P>0.05     |

**Supplemental Table 1. Summary of rat cytokine array results.** The Abcam Rat Cytokine Antibody Array was used to simultaneously detect the levels of 34 cytokines in retinal samples from TRPV2 WT and heterozygous rats. Relative quantification of spot intensities between the two groups was performed using Image J. Statistical comparisons are based on two-way ANOVA; blots were performed in triplicate with three different biological pools of retinas for each genotype; N=18 animals per group in total, N=6 animals per replicate.

| Gene           | Forward Primer          | Reverse Primer        |
|----------------|-------------------------|-----------------------|
| <i>Actb</i>    | TGCCCTAGACTTCGAGCAAG    | GGCAGCTCATAGCTCTTCTCC |
| <i>Trpv2</i>   | GACCTCCTAAAACACTTCTGCTC | AGAGTCGGTCACGGTCAAAC  |
| <i>Cacna1c</i> | GGAGGCAGAATGCAAGGGTA    | TGTTCTCCCAACTTCGAGGC  |
| <i>Cacna1g</i> | CTTCCAGGACAGGTGGAACC    | GGAGCACCCCTCATGATACGG |
| <i>Ryr2</i>    | ATCCCAACGCAGCAAGGAAA    | TTCACCTTTGCTGGCACTGA  |
| <i>Itpr1</i>   | GCTGGCTGCTGTGGGTTGAC    | CCCAAAGAAGAGCTGCTCCC  |
| <i>Itpr2</i>   | CAGTGCGGTGGCATGTGATG    | CAGAACTCCAGTCACAGG    |
| <i>Kcna5</i>   | CAGGACCAGCCAAGGATCG     | TTCCCACACCCCCAACTCA   |
| <i>Kcnma1</i>  | GGCGGCTGATCTATTCCAAGAT  | CTCAGAACGTCCGCAATCAA  |

**Supplemental Table 2. Primer sequences used for RT-qPCR.** All primers were purchased from Integrated DNA Technologies (Coralville, IA, USA), with the exception of those used in Fig 2A, which were from Roche (Roche, Basel, Switzerland).

| Target                             | Antibody                        | Company – Cat No.     | Dilution |
|------------------------------------|---------------------------------|-----------------------|----------|
| TRPV2                              | Rabbit polyclonal               | Merck (PC421)         | 1:100    |
| $\alpha$ -SMA                      | Mouse monoclonal Cy3 conjugated | Sigma (C6198)         | 1:200    |
| Albumin                            | Goat polyclonal                 | Bethyl (A90-134A)     | 1:1000   |
| Collagen IV                        | Rabbit polyclonal               | Bio-Rad (2150-1470)   | 1:200    |
| RUNX1                              | Sheep polyclonal                | Lifespan (LS-C94757)  | 1:100    |
| GFAP                               | Rabbit polyclonal               | Dako (N1506)          | 1:200    |
| Vimentin                           | Mouse monoclonal                | Sigma (V6630)         | 1:200    |
| Iba1                               | Rabbit polyclonal               | Wako (019-19741)      | 1:500    |
| Brn3a                              | Goat polyclonal                 | Santa Cruz (sc-31984) | 1:200    |
| Cone arrestin                      | Rabbit polyclonal               | Merck (AB15282)       | 1:500    |
| GABA                               | Rabbit polyclonal               | Sigma (A2052)         | 1:500    |
| Secondary Antibody                 |                                 | Company – Cat No.     | Dilution |
| Donkey anti-rabbit Alexa Fluor-488 |                                 | ThermoFisher (A21206) | 1:200    |
| Donkey anti-goat Alexa Fluor-488   |                                 | ThermoFisher (A11055) | 1:200    |
| Donkey anti-sheep Alexa Fluor-405  |                                 | Abcam (ab175676)      | 1:200    |
| Donkey anti-mouse Alexa Fluor-568  |                                 | ThermoFisher (A10037) | 1:200    |

**Supplemental Table 3. Primary and secondary antibodies used for the immunolabelling of rat retinal wholemount preparations and cryosections.**

| Donor           | Sex    | Age      |
|-----------------|--------|----------|
| Non-diabetic    | Male   | 44 years |
| Non-diabetic    | Male   | 87 years |
| Non-diabetic    | Male   | 68 years |
| Non-diabetic    | Female | 72 years |
| Type 2 diabetes | Male   | 56 years |
| Type 2 diabetes | Female | 59 years |
| Type 2 diabetes | Male   | 64 years |
| Type 2 diabetes | Female | 70 years |

**Supplemental Table 4. Demographics of the non-diabetic and diabetic human sample donors.** The mean age ( $\pm$  standard deviation) of the non-diabetic and diabetic donors was 67.8 ( $\pm$  17.8) and 62.3 ( $\pm$  6.1) years, respectively. Data information: NS based on Student' t test.