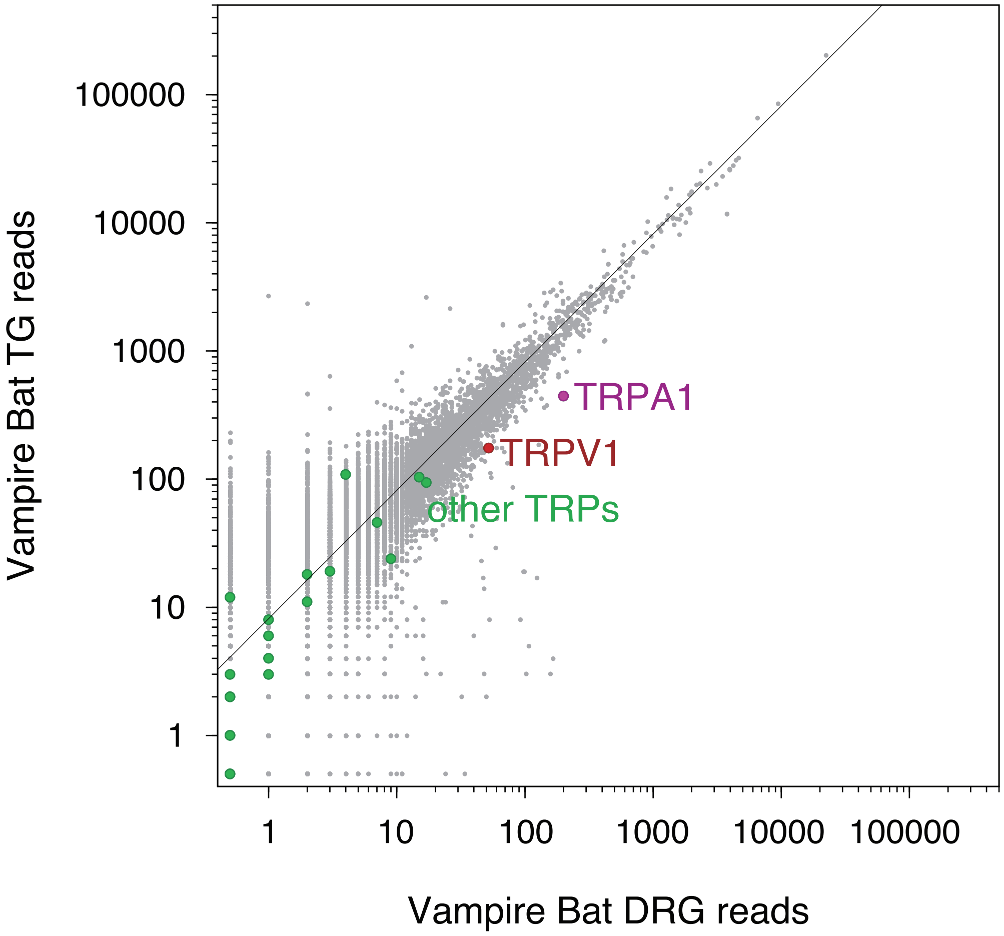
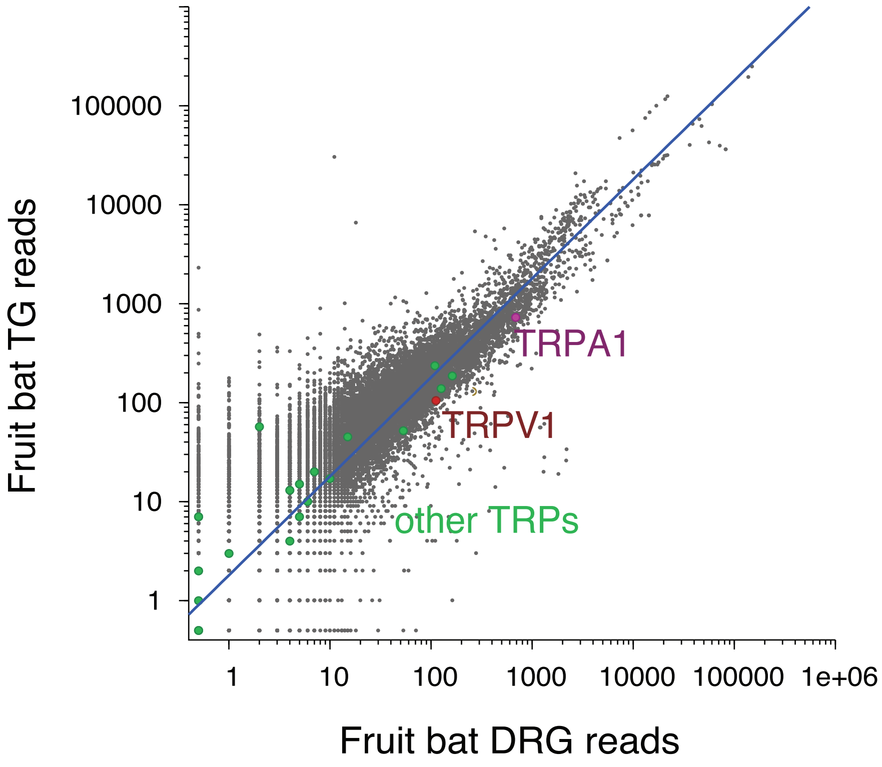

Vampire Bat TG reads
100000
10000
1000
100
10
1
TRPA1
TRPV1
other TRPs
1
10
100
1000
10000
100000
Vampire Bat DRG reads


Fruit bat TG reads
100000
10000
1000
100
10
1
TRPA1
TRPV1
other TRPs
1
10
100
1000
10000
100000
1e+06
Fruit bat DRG reads

Supplementary Figure 1

Transcriptome profiling of vampire bat and fruit bat sensory ganglia

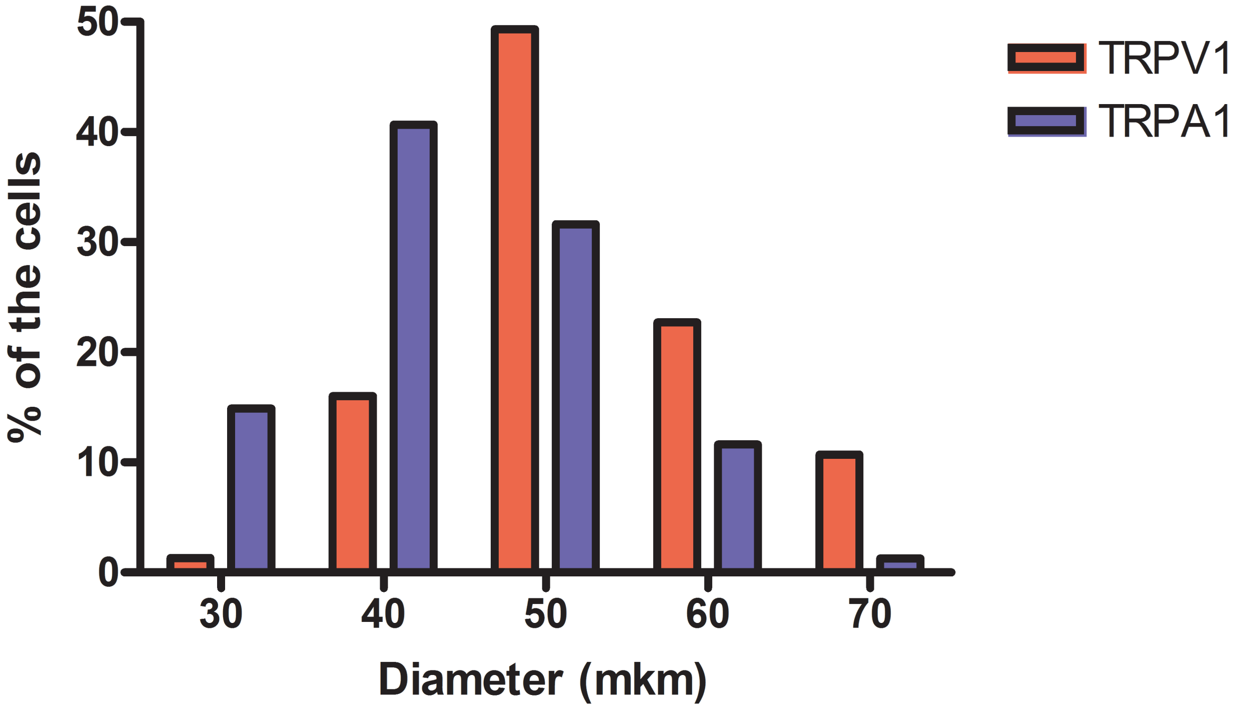
Number of mRNA-seq reads from sensory ganglia of vampire bat (*Desmodus rotundus*, top) and fruit bat (*Carollia brevicauda*, bottom) ganglia that align to the cow proteome. Blue line indicates expected number of sequencing reads for genes with similar expression levels in the two samples based on the total number of aligned reads from each.

```
  1 mkkrgssdsgesedlpqedslpdpldgnphsrpapaksnilmakrrrrlfgkgdseeaspqdcsykeghpascpaitvspvltvqktedgptctwqlcqdsvpagtkkclklydrrkifeavaqnnceel
  1 mkkrgssdsgesedlpqedplpdpldgdphsrpapakpniptaksrsrlfgkgdseeassldcsykeggpascpaitvspvlmvqktedgptctwqlcqdsvpagtkkslklydrrkifeavaqnnceel

131 eslllflqkskkhlmdrefkdpetgktcllkamlnlhngqnntipllleiarqtdslkelvnasytdsyykgqtalhiaierrnmalvtllvengadvqaaangdffkktkgrpgfyfgelplslaactn
131 eslllflqrskkhlmdsefkdpetgktcllkamlnlhngqnntipllleiarqtdslkelvnasyidsyykgqtalhiaierrnmalvtllvengadvqaaangdffkktkgrpgfyfgelplslaactn

261 qlgivkfllqnswqpadisardsvgntvlhalvevadntadntkfvtsmyneililgaklhptlkleelinkkgltplalaassgkigvlayilqreihepecrylsrkftewaygpvhsslydlscidt
261 qlgivkfllqnswqpadisardsvgntvlhalvevadntadntkfvtsmyneililgaklhptlkleelinkkgltplalaassgkigvlayilqreihepecrhlsrkftewaygpvhsslydlscidt

391 ceknsvleviayssnetpnrhdmllveplnrllqdkwdrfvkrifyfnffvyclymiifttvayyrpveglppykvkhtvgdyfrvigeilsvlggvyfffrgiqyflqrrpslkslfvdsyseilffvq
391 ceknsvleviayssnetpnrhdmllveplnrllqdkwdrfvkrifyfnffvyclymiifttvayyrpveglppykvkhtvgdyfrvtgeilsvlggvyfffrgiqyflqrqpslkslfvdsysetlffvq

521 slfmlgtvvlyfcqckeyvasmvfslamgwtnmlyytrgfqqmgiyavmiekmilrdlcrfmfvylvflfgfstavvtliedgkndsvstettphrwrgpcyrspdssynslystclelfkftigmgdle
521 slfmlgtvvlyfcqckeyvasmvfslamgwtnmlyytrgfqqmgiyavmiekmilrdlcrfmfvyliflfgfstavvtliedgkndsvstettphrwrgpcyrspdssynslystclelfkftigmgdle

651 ftenydfkavfiilllayviltyilllnmlialmgetvnkiaqeskniwklqraitildteksflkcmrkafrsgkllqvgytpdgkddyrwcfrvdevnwttwntnvgiinedpgncegikrtlsfslr
651 ftenydfkavfiilllayviltyilllnmlialmgetvnkiaqeskniwklqraitildteksflkcmrkafrsgkllqvgytpdgkddyrwcfrvdevnwttwntnvgiinedpgncegikrtlsfslr

781 ssrvagrnwknfalvpllrdastrerqpaqpeevhlkhfsgslkpedaxvfkdsaalgesekgestv
781 ssrvagrnwknfalvpllrdastrerqpaqpeevhlkhfsgslkpedaevfkdpaalg---------
```

Top: Vampire bat (*Desmodus rotundus*) TRPV1-L
Bottom: Fruit bat (*Carollia brevicauda*) TRPV1-L

Supplementary Figure 2

Protein sequence alignment for vampire bat (*Desmodus rotundus*, top) and fruit bat (*Carollia brevicauda*, bottom) TRPV1-L isoforms.


TRPV1
TRPA1
% of the cells
50
40
30
20
10
0
30
40
50
60
70
Diameter (mkm)

Supplementary Figure 3

Neuronal size distribution of TRPV1-positive and TRPA1-positive neurons in trigeminal ganglia of vampire bats detected by *in situ* hybridization histochemistry of frozen tissue sections.

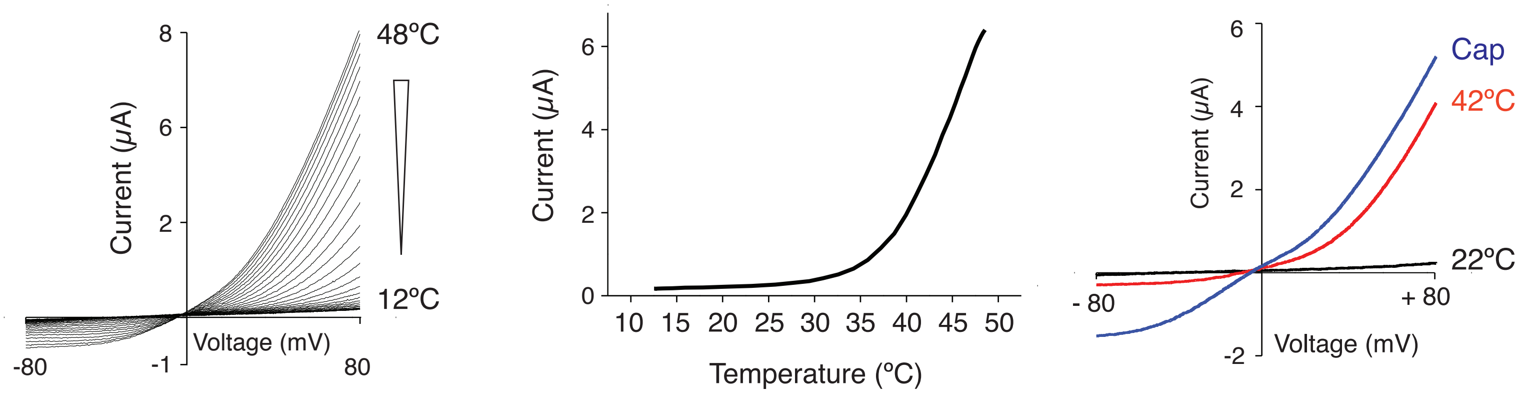
TRPV1	**Q_{10}**	**Q_{10}**	**Temperature threshold (°C)**
Vampire bat (Short)	5.1 ± 0.8	1.4 ± 0.1	31.2 ± 1.5
Vampire bat (Long)	11.5 ± 1.2	1.6 ± 0.1	40.2 ± 0.7
Short:Long (1:1)	5.7 ± 1.3	1.4 ± 0.1	33.9 ± 1.2
Zebrafish	4.6 ± 0.5	1.4 ± 0.1	32.9 ± 1.2
Fruit bat (Short)	5.1 ± 1.2	1.4 ± 0.3	30.8 ± 2
Fruit bat (Long)	9.9 ± 1.4	1.5 ± 0.2	40 ± 0.5
Cow (Long)	16 ± 1.7	1.6 ± 0.3	40.5 ± 0.6
Mole (Short)	4.4 ± 0.5	1.5 ± 0.3	31.3 ± 1.1
Mole (Long)	7.5 ± 0.6	1.7 ± 0.2	38.3 ± 0.9
Rat	21.7 ± 1.1	1.3 ± 0.1	42.3 ± 1.2

Supplementary Figure 4

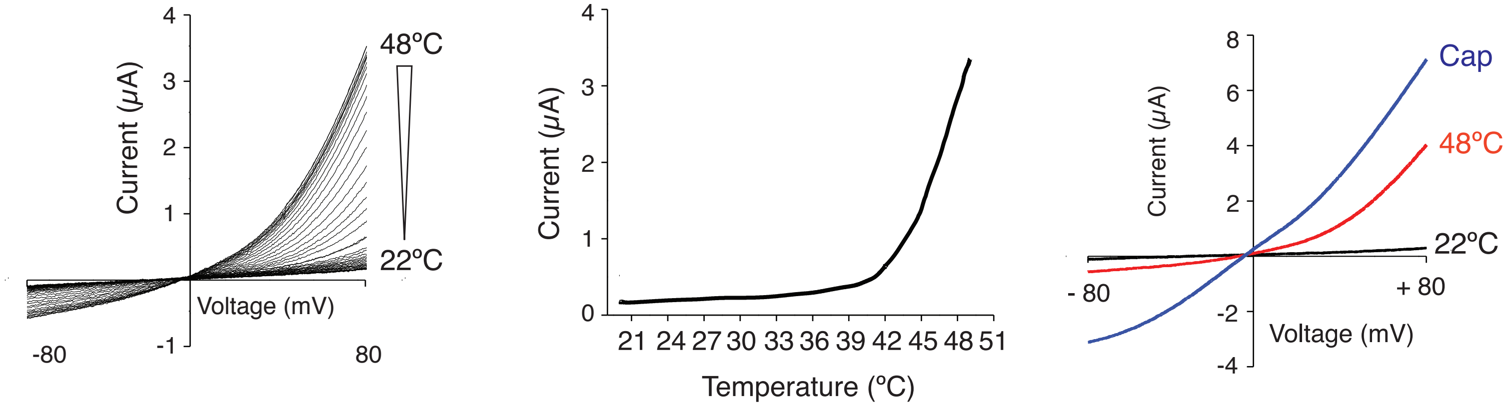
Thermal properties of cloned TRPV1 channels

TRPV1 cDNAs expressing short or long channel isoforms from various organisms (as indicated) were expressed in oocytes and subjected to temperature ramps while recording membrane currents in two-electrode voltage-clamp mode (V_h = -80 mV). Temperature coefficient (Q_{10}) for baseline and steepest component of the heat-evoked current and activation thresholds were derived from Arrhenius plots, as described in Methods.

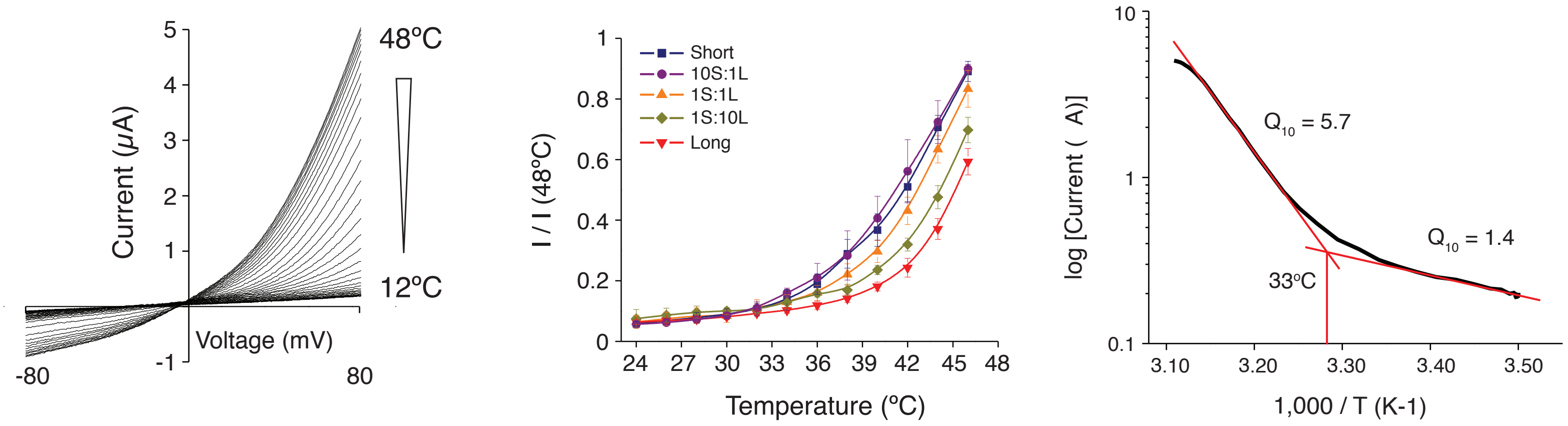
Vampire bat TRPV1-S isoform



Vampire bat TRPV1-L isoform



Vampire bat TRPV1-S:TRPV1-L = 1:1

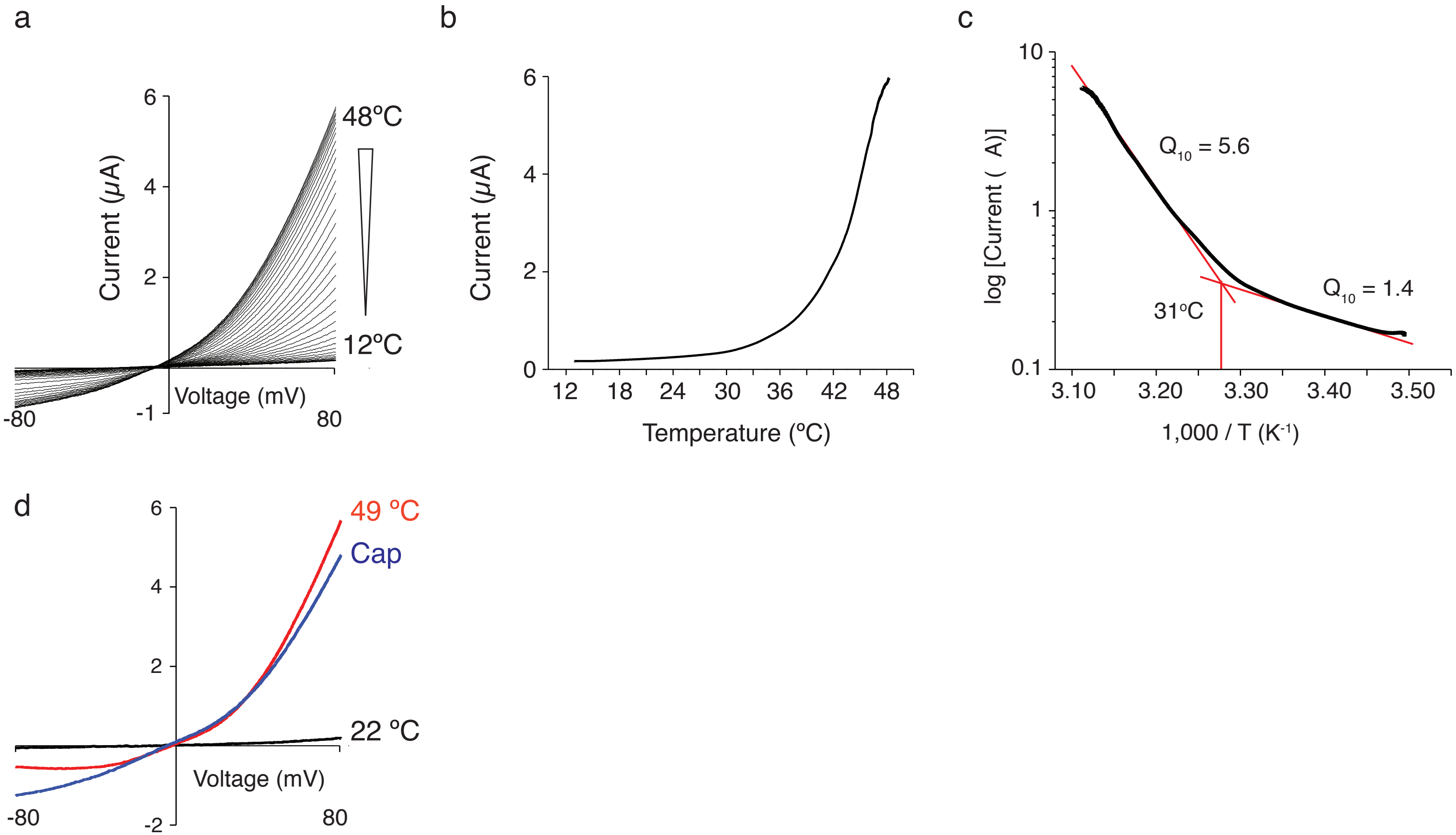


Supplementary Figure 5

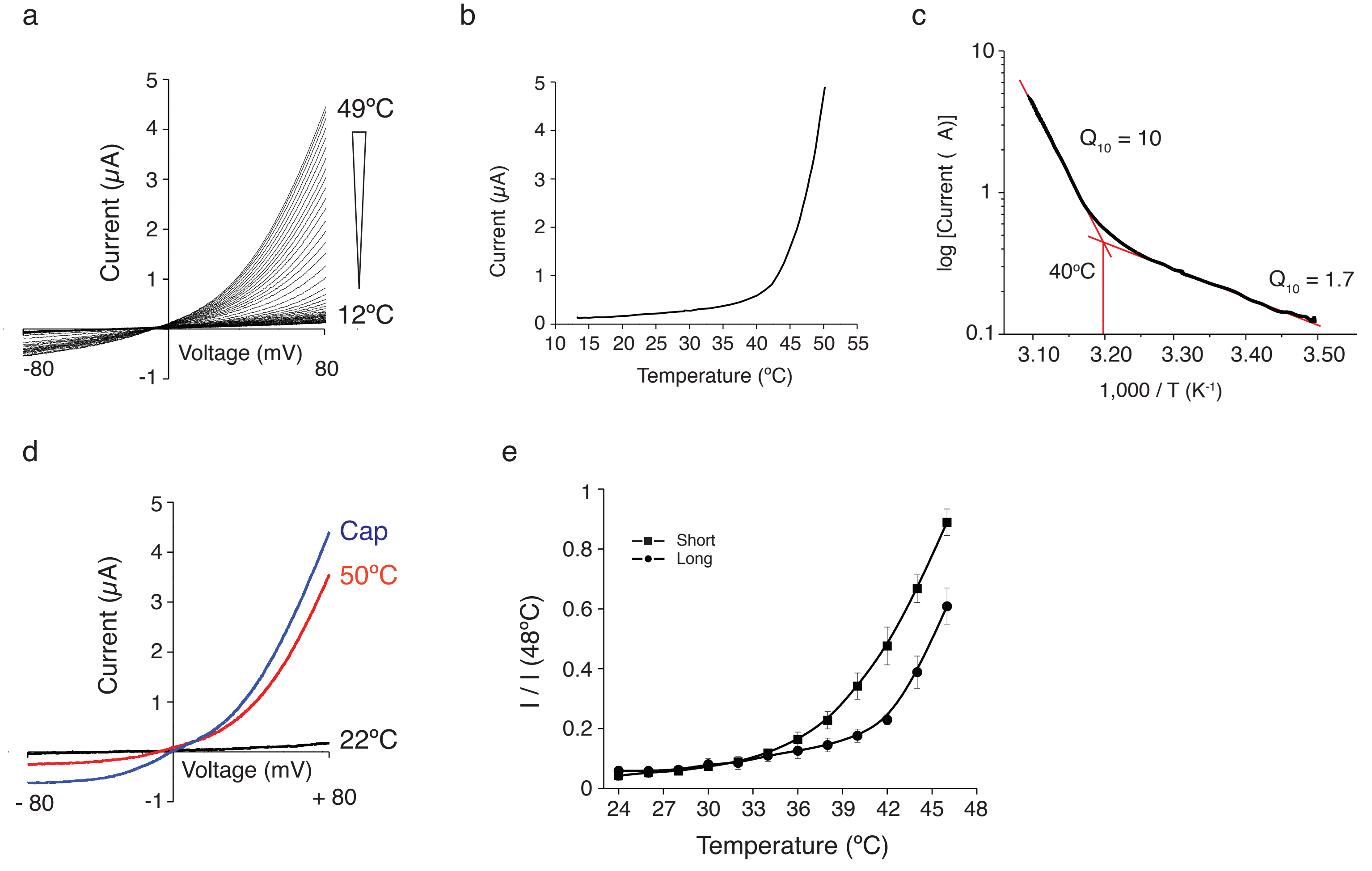
Functional analysis of vampire bat TRPV1 channel isoforms

Data are shown for oocytes expressing vampire bat (*D. rotundus*) TRPV1-S, TRPV1-L, or both, as indicated. In each case, left panel shows representative current-voltage relationships for heat-evoked responses during temperature ramp; middle panel shows temperature-response relationship; right panel shows representative current-voltage relationships for heat and capsaicin (10 μM)-evoked responses, or Arrhenius plot showing thermal threshold and Q_{10} values for baseline and evoked responses. All data were collected in two-electrode voltage-clamp mode (V_h = -80 mV).

Fruit bat TRPV1-S isoform



Fruit bat TRPV1-L isoform

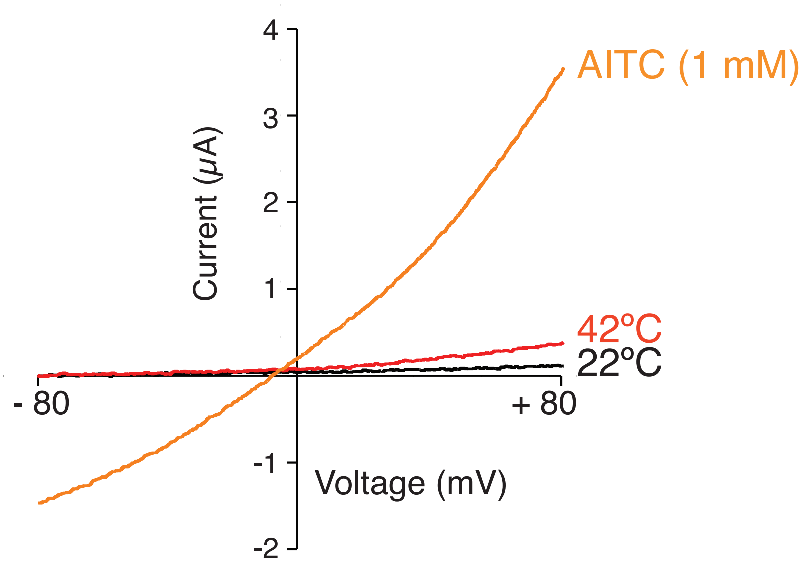


Supplementary Figure 6

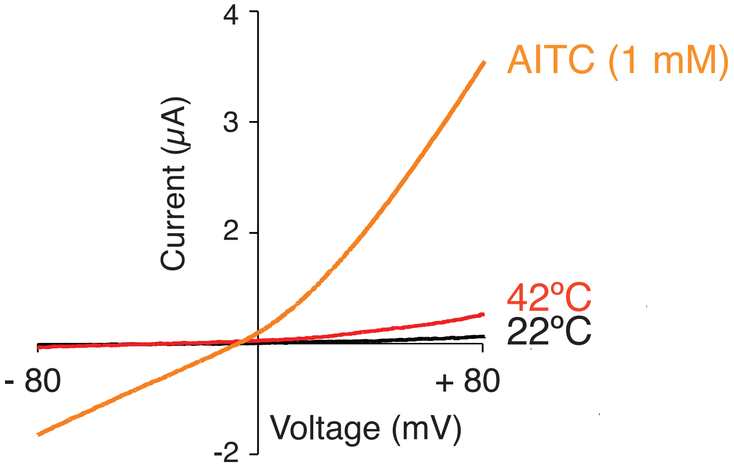
Functional analysis of fruit bat TRPV1 channel isoforms

Data are shown for oocytes expressing fruit bat (*C. brevicauda*) TRPV1-S, TRPV1-L, or both, as indicated. In each case, panel **a** shows representative current-voltage relationships for heat-evoked responses during temperature ramp; panel **b** shows temperature-response relationship; panel **c** shows Arrhenius plot showing thermal threshold and Q_{10} values for baseline and evoked responses; panel **d** shows representative current-voltage relationships for heat and capsaicin (10 μM)-evoked responses; panel **e** compares average temperature-response relationships for short and long TRPV1 isoforms.

All data were collected in two-electrode voltage-clamp mode (V_h = -80 mV).



Vampire bat TRPA1



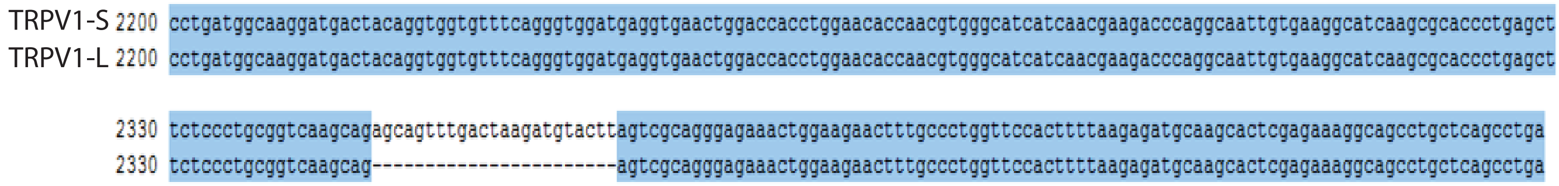
Fruit bat TRPA1

Supplementary Figure 7

Functional analysis of vampire and fruit bat TRPA1 channels

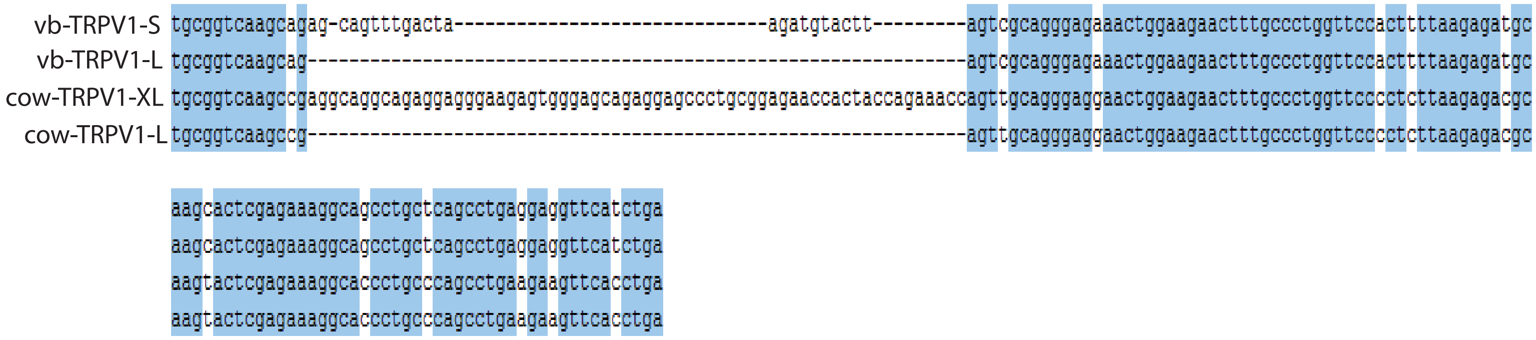
Thermal and chemical sensitivities of cloned vampire (*D. rotundus*) and fruit (*C. brevicauda*) bat TRPA1 channels, as indicated. Current-voltage relationships were determined by two-electrode voltage clamp recording of TRPA1-expressing oocytes challenged with heat (42°C) or AITC (1 mM).

a



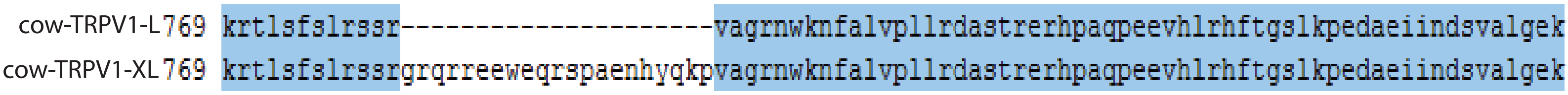
```
TRPV1-S 2200 cctgatggcaaggatgactacaggtggtgtttcagggtggatgaggtgaactggaccacctggaacaccaacgtgggcatcatcaacgaagacccaggcaattgtgaaggcatcaagcgcaccctgagct
TRPV1-L 2200 cctgatggcaaggatgactacaggtggtgtttcagggtggatgaggtgaactggaccacctggaacaccaacgtgggcatcatcaacgaagacccaggcaattgtgaaggcatcaagcgcaccctgagct

        2330 tctccctgcggtcaagcagagcagtttgactaagatgtacttagtcgcagggagaaactggaagaactttgccctggttccacttttaagagatgcaagcactcgagaaaggcagcctgctcagcctga
        2330 tctccctgcggtcaagcag-----------------------agtcgcagggagaaactggaagaactttgccctggttccacttttaagagatgcaagcactcgagaaaggcagcctgctcagcctga
```

b



```
vb-TRPV1-S   tgcggtcaagcagag-cagtttgacta------------------------------agatgtactt---------agtcgcagggagaaactggaagaactttgccctggttccacttttaagagatgc
vb-TRPV1-L   tgcggtcaagcag---------------------------------------------------------------agtcgcagggagaaactggaagaactttgccctggttccacttttaagagatgc
cow-TRPV1-XL tgcggtcaagccgaggcaggcagaggagggaagagtgggagcagaggagccctgcggagaaccactaccagaaaccagttgcagggaggaactggaagaactttgccctggttcccctcttaagagacgc
cow-TRPV1-L  tgcggtcaagccg---------------------------------------------------------------agttgcagggaggaactggaagaactttgccctggttcccctcttaagagacgc

             aagcactcgagaaaggcagcctgctcagcctgaggaggttcatctga
             aagcactcgagaaaggcagcctgctcagcctgaggaggttcatctga
             aagtactcgagaaaggcaccctgcccagcctgaagaagttcacctga
             aagtactcgagaaaggcaccctgcccagcctgaagaagttcacctga
```

c

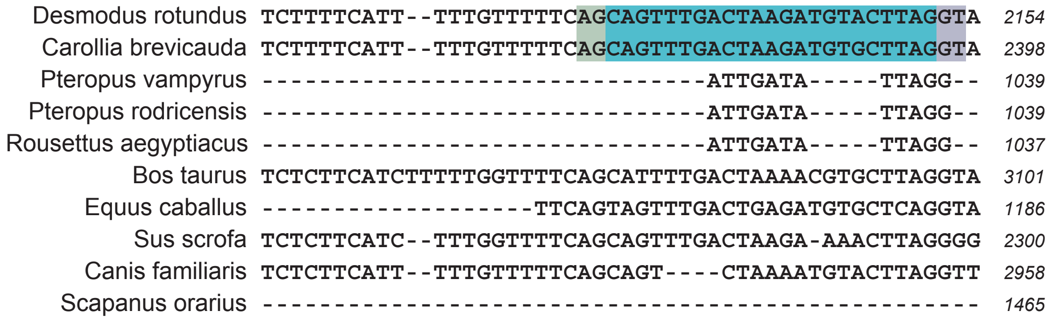


```
cow-TRPV1-L  769 krtlsfslrssr---------------------vagrnwknfalvpllrdastrerhpaqpeevhlrhftgslkpedaeiindsvalgek
cow-TRPV1-XL 769 krtlsfslrssrgrqrreeweqrspaenhyqkpvagrnwknfalvpllrdastrerhpaqpeevhlrhftgslkpedaeiindsvalgek
```

Supplementary Figure 8

Genomic organization of TRPV1 gene locus in bats and cows

a, Partial cDNA sequence alignment of short (TRPV1-S) and long (TRPV1-L) vampire bat isoforms showing the presence of exon 14a-derived insert in the former. **b**, Partial sequence alignment between cow and bat TRPV1 cDNAs corresponding to regions encoded by exons14 and 15, demonstrating conserved splice junctions in these species. **c**, Alignment of deduced amino acid sequences for large (TRPV1-L) and extra large (TRPV1-XL) TRPV1 isoforms from cow.



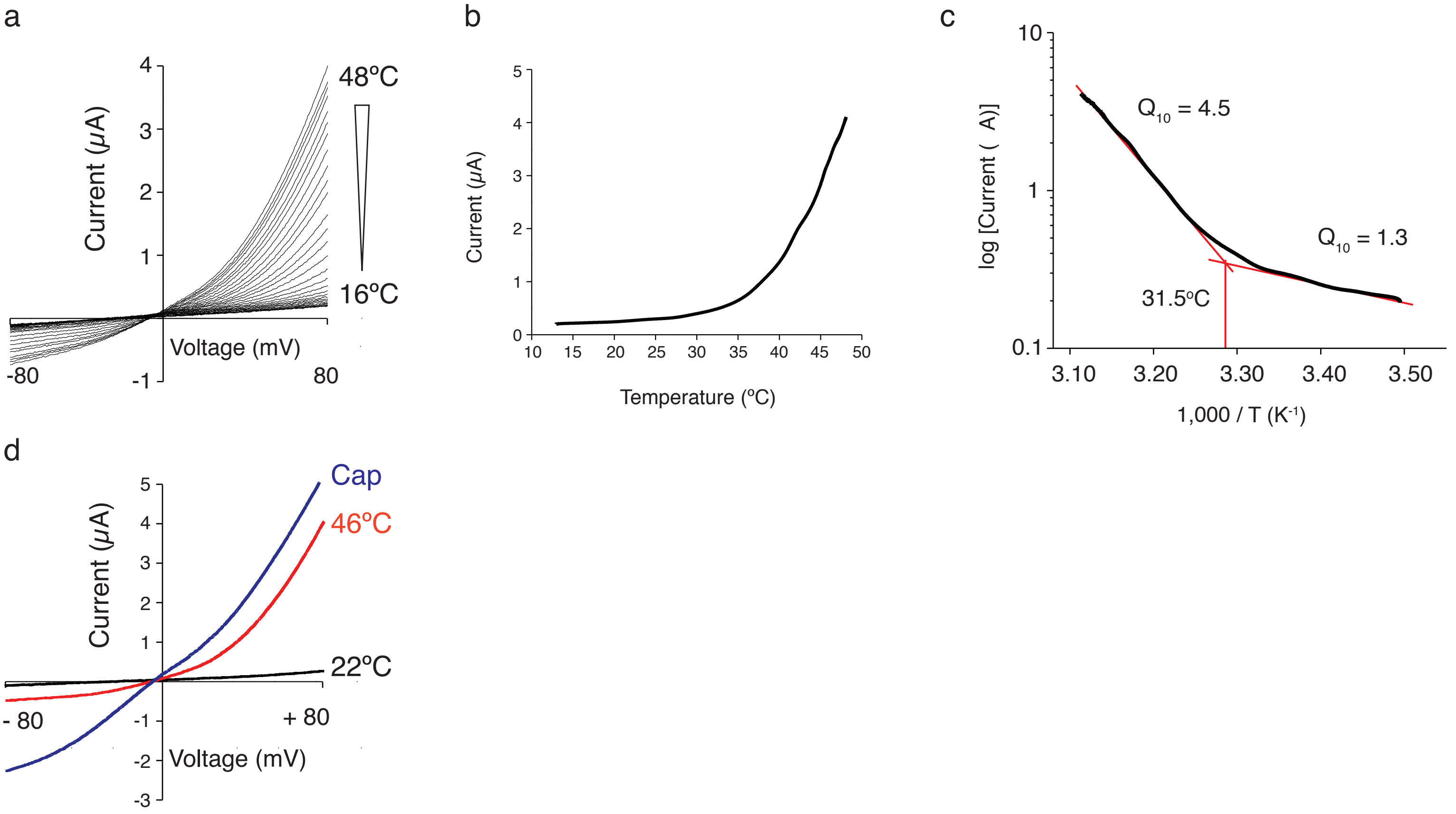
```
Desmodus rotundus      TCTTTTCATT--TTTGTTTTTCAGCAGTTTGACTAAGATGTACTTAGGTA  2154
Carollia brevicauda    TCTTTTCATT--TTTGTTTTTCAGCAGTTTGACTAAGATGTGCTTAGGTA  2398
Pteropus vampyrus      -------------------------------ATTGATA-----TTAGG--  1039
Pteropus rodricensis   -------------------------------ATTGATA-----TTAGG--  1039
Rousettus aegyptiacus  -------------------------------ATTGATA-----TTAGG--  1037
Bos taurus             TCTCTTCATCTTTTTGGTTTTCAGCATTTTGACTAAAACGTGCTTAGGTA  3101
Equus caballus         -------------------TTCAGTAGTTTGACTGAGATGTGCTCAGGTA  1186
Sus scrofa             TCTCTTCATC--TTTGGTTTTCAGCAGTTTGACTAAGA-AAACTTAGGGG  2300
Canis familiaris       TCTCTTCATT--TTTGTTTTTCAGCAGT----CTAAAATGTACTTAGGTT  2958
Scapanus orarius       --------------------------------------------------  1465
```

Supplementary Figure 9

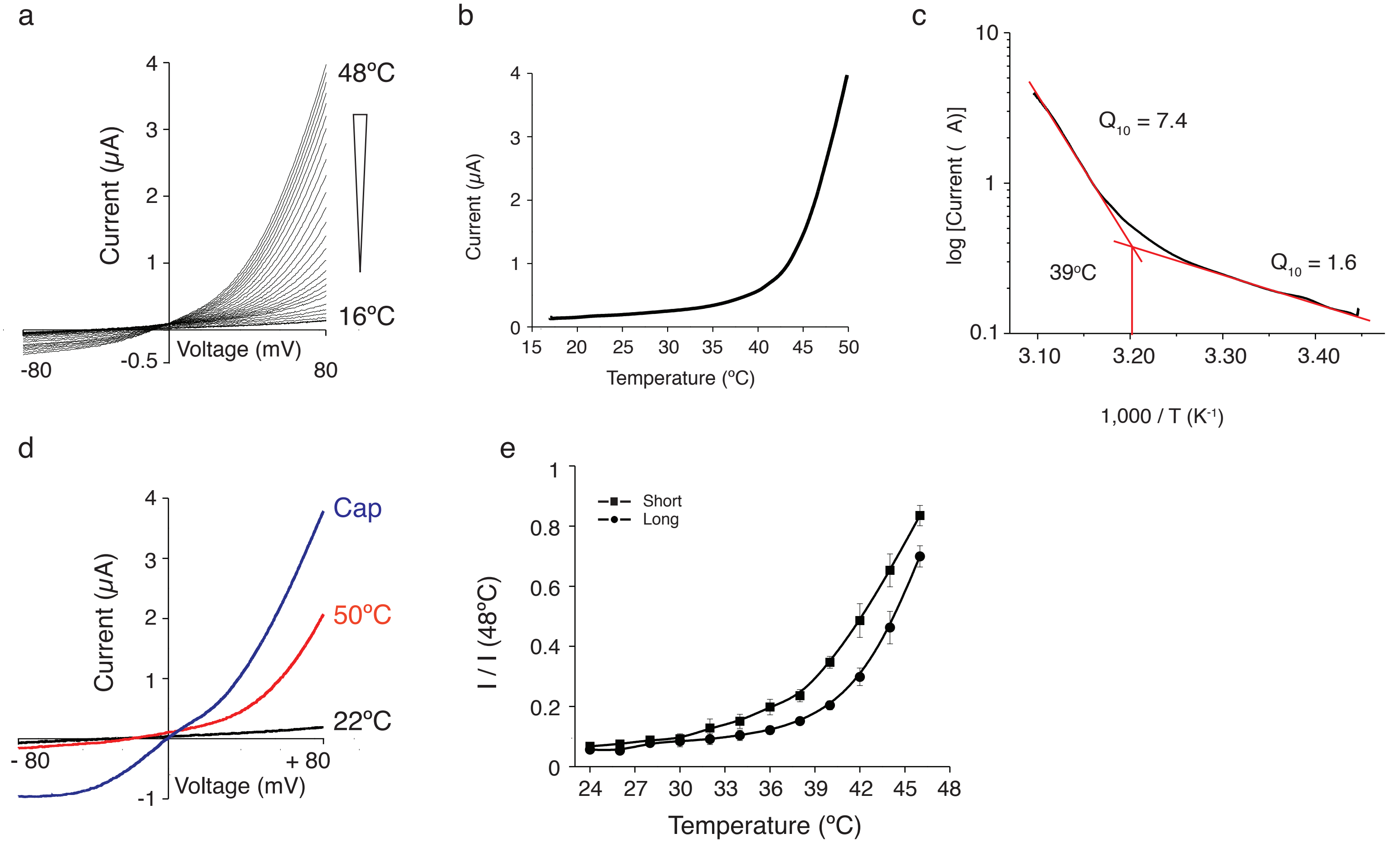
Alignment of exon 14a from microbats with intronic region of other mammals

The region encoding exon 14a in vampire (*D. rotundus*) and fruit (*C. brevicauda*) bats is highlighted. Splice acceptor (-AG-) and donor (-GT-) sites are highlighted in green and grey, respectively. Numbers at right indicate relative distance from exon 14 (position 1 corresponds to 12 nucleotides from the end of exon 14 in all species shown). Dashes indicate regions of non-identity.

Coast mole TRPV1-S isoform



Coast mole TRPV1-L isoform

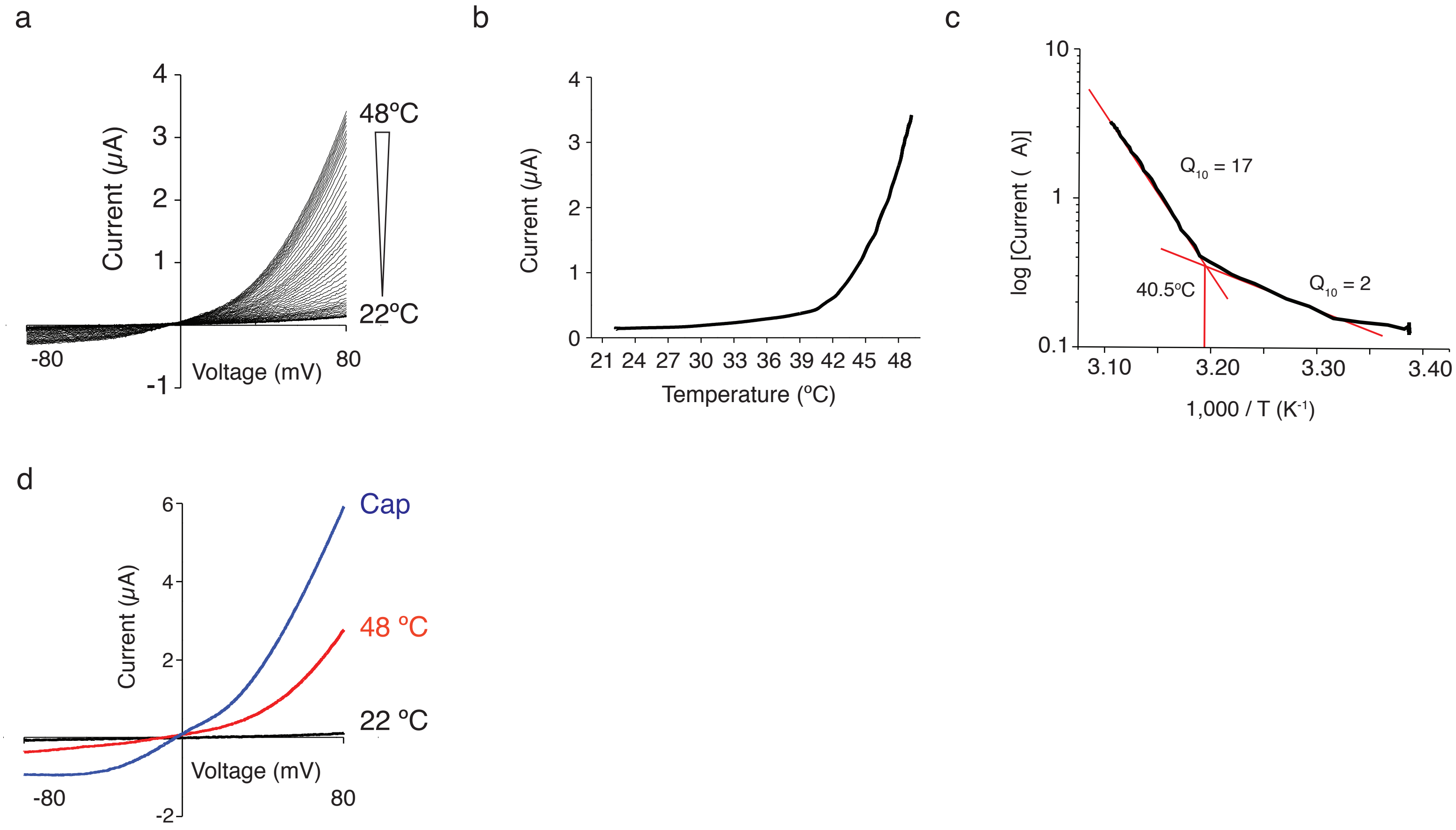


Supplementary Figure 10

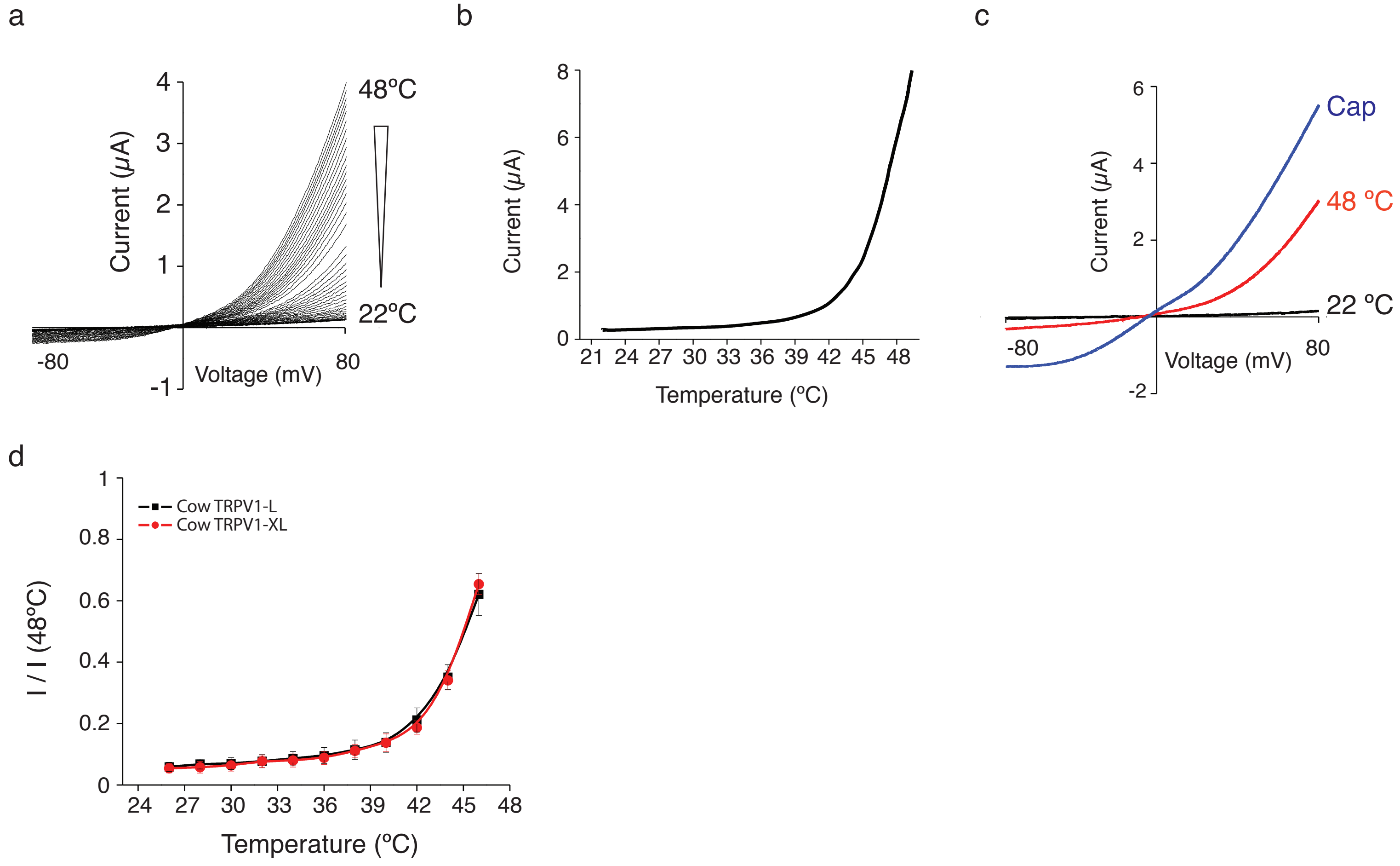
Functional analysis of Coast mole TRPV1 channel isoforms

Data are shown for oocytes expressing Coast mole (*Scapanus orarius*) TRPV1-S or TRPV1-L isoforms, as indicated. In each case, panel **a** shows representative current-voltage relationships for heat-evoked responses during temperature ramp; panel **b** shows temperature-response relationship; panel **c** shows Arrhenius plot showing thermal threshold and Q_{10} values for baseline and evoked responses; panel **d** shows representative current-voltage relationships for heat and capsaicin (10 μM)-evoked responses. Panel e in bottom group compares average temperature-response relationships for short and long TRPV1 isoforms. All data were collected in two-electrode voltage-clamp mode (V_h = -80 mV).

Cow TRPV1-L isoform



Cow TRPV1-XL isoform



Supplementary Figure 11

Functional analysis of bovine TRPV1 channel isoforms

Data are shown for oocytes expressing cow (*Bos taurus*) TRPV1-L or TRPV1-XL isoforms, as indicated. For TRPV1-L, panel **a** shows representative current-voltage relationships for heat-evoked responses during temperature ramp; panel **b** shows temperature-response relationship; panel **c** shows Arrhenius plot showing thermal threshold and Q_{10} values for baseline and evoked responses; panel **d** shows representative current-voltage relationships for heat and capsaicin (10 μM)-evoked responses. For TRPV1-XL panel panel **a** shows representative current-voltage relationships for heat-evoked responses during temperature ramp; panel **b** shows temperature-response relationship; panel **c** shows representative current-voltage relationships for heat and capsaicin (10 μM)-evoked responses; panel d compares average temperature-response relationships for short and long TRPV1 isoforms. All data were collected in two-electrode voltage-clamp mode (V_h = -80 mV).

a

```
    Desmodus rotundus  -----GGCAGGCACAGGAGGGAAGGACAGGAAGAGTGAAGGGTACACCTT  452
   Carollia brevicauda  -----GGCAGGTACAGGAGGTAAGAACGAGAAGAGTAAAGGGTACACCTT  454
     Pteropus vampyrus  --CCAGGTAGGCAGAGGAGGGAGGAATGGGA-CAGTAAAGGGTACACCTT  466
   Pteropus rodricensis  --CCAGGTAGGCAGAGGAGGGAGGAATGGGA-CAGTAAAGGGTAAACCTT  466
 Rousettus aegyptiacus  --CCAGGTAGGCAGAAGAGGGAGCAATGGGA-GAGTAAAGGGTGCACCTT  465
            Bos taurus  ---------TTCACACGCAGGCAGGC--AGAGGAGGGAAGAGT-----GG  354
        Equus caballus  AGCCAGGCAGGCAGAGGAGGGAAGAATGGGACGAGTAAAGGGTACATCTT  477
            Sus scrofa  --------GTGCAGAGGAGGGAAGGGTGGGAGGGGCCAAGGGTACACCTT  374
      Canis familiaris  ----ATCCAGCTGGCAGA-GGAAGAATGGGAAGAGTAACGAGTATATCAT  473
      Scapanus orarius  -GTCTGGTAGGGAGAGGAGGGAAGAGTGGGAGGAGGAGAGGGTACATCTG  469

    Desmodus rotundus  -GAGCAGAAAAGCCCTGCAGAAAATCACTACCAGAAAA-AAGTCCTTTAA  500
   Carollia brevicauda  -GAGCAGAAAAGCCCTGCAGGAAGTCACTACCAGAAAA-AAGTTGTTTAA  502
     Pteropus vampyrus  -GAGTGGAAAAGTCCTGCGGAAAATCACTACCAGAAAAAAAGTCCTTTAC  515
   Pteropus rodricensis  -GAGTGGAAAAGTCCTGCGGAAAATCACTACCAGAAAAAAAGTCCTTTAC  515
  Rousettus aegyptians  -GAGTGGAAAAGTCCTGCAGAAAATCACTACCAGAAAAAAAGTCCTTTAC  514
            Bos taurus  -GAGCAGAGGAGCCCTGCGGAGAACCACTACCAGAAACCAGGTCTTTAAA  403
        Equus caballus  -GGACAGAACAGCCCTGCGGAAAGTCACTGCCAGAAACAAAAGCCTTGT-  525
            Sus scrofa  -GAACCGAGAAGCCCTGCGGAAAATCACTACCAGAAA--A-GTCCTTTAA  420
      Canis familiaris  AAAGCAGAAATGCTCTGCAGAAAATCACTACCAGAAAAAAGGTCCTTTAT  523
      Scapanus orarius  -GAGCAGAAACAGTCTGAGGAAAATCATTAGTGGAAAG-AAGTCCTTGAA  517
```

b

```
    Desmodus_rotundus  TTTTAAG-CTT-TATT-----------ATGGTAGATCTG-TGGACACTCC  3015
   Carollia_brevicauda  TTTTAAG-CTT---TT-----------ATGGTAGATCTG-TGGACACTCC  3257
     Pteropus_vampyrus  TTTTAAC-CTT-TATT-----------ATGGTAGATCTG-TAGACACTAC  1745
   Pteropus_rodricensis  TTTTAAC-CTT-TATT-----------ATGGTAGATCTG-TAGACACTAC  1745
 Rousettus_aegyptiacus  TTTTAAG-CTT-TATT-----------ATTGTAGATCTG-TGGACACTAC  1747
            Bos_taurus  CTTTAGC-ATTTAATT-----------ATGGTAGATCTGT-GGAAATGTC  3918
        Equus_caballus  TTTTAAA-CTT-TATT-----------ATGATAGATCTGT-GGAAATGCC  1921
            Sus_scrofa  TTTTAAA-GTT-TATT-----------TTAGTAGATATGT-GGAAATGCC  3008
      Canis_familiaris  TTTTAAA-CTT-TATT-----------ATGGTAGATATG-TG-AAATGCC  3887
      Scapanus_orarius  TTTTTATATTT-CATCAACTTGATTTTATTTTTATTTTTTTG-AGAACAG  2137

    Desmodus_rotundus  AAGGT----ATTTGCTAATCCCATAAAACTTGT--GGGACTCAGCC----  3055
   Carollia_brevicauda  AAGGT----ATTTGCTGATCCCATAAAACTTTT--GGGACTCAGCC----  3297
     Pteropus_vampyrus  AAGAT----ATTTGTCAATCTCATCAAACTTGT--GGGATTCAGCC----  1785
   Pteropus_rodricensis  AAGAT----ATTTGTCAATCTCATCAAACTTGT--GGGATTCAGCC----  1785
 Rousettus_aegyptiacus  AAGAT----ATTTGTCAATCTCATCAAGCTTGT--GGGATTCAGCC----  1787
            Bos_taurus  AAGAT----GTTTACCAATCCCATCAAACTTGT--GGGACTCAACC----  3958
        Equus_caballus  GAGGT----GTTTGCCAGTCCCATCAAGCTGGT--GGGATTCAACC----  1961
            Sus_scrofa  AAGGT----ATTAGCCAATCCCATCAAAC-----------TCAACC----  3039
      Canis_familiaris  AAAGT----ATTTGCCAATTCCATAAAACTTTT--GGGACTCAACC----  3927
      Scapanus_orarius  AAAAGGCGGATTTAT---TGAAATACACTGCTAAGAGAAGCAGCGGGCG  2183
```

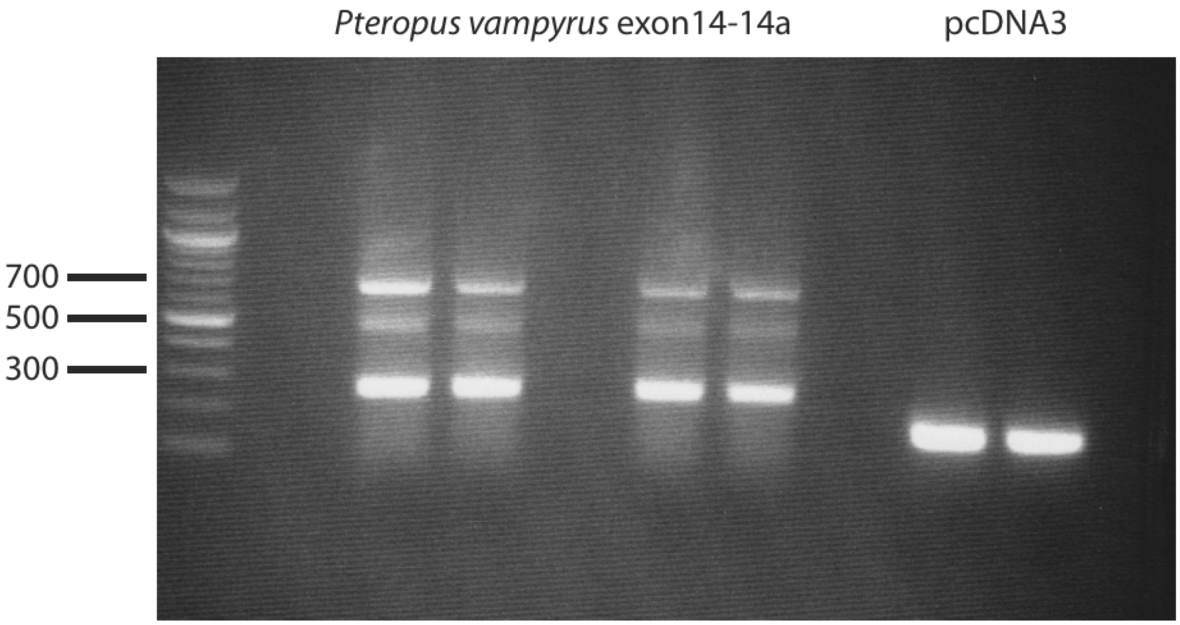
⋮

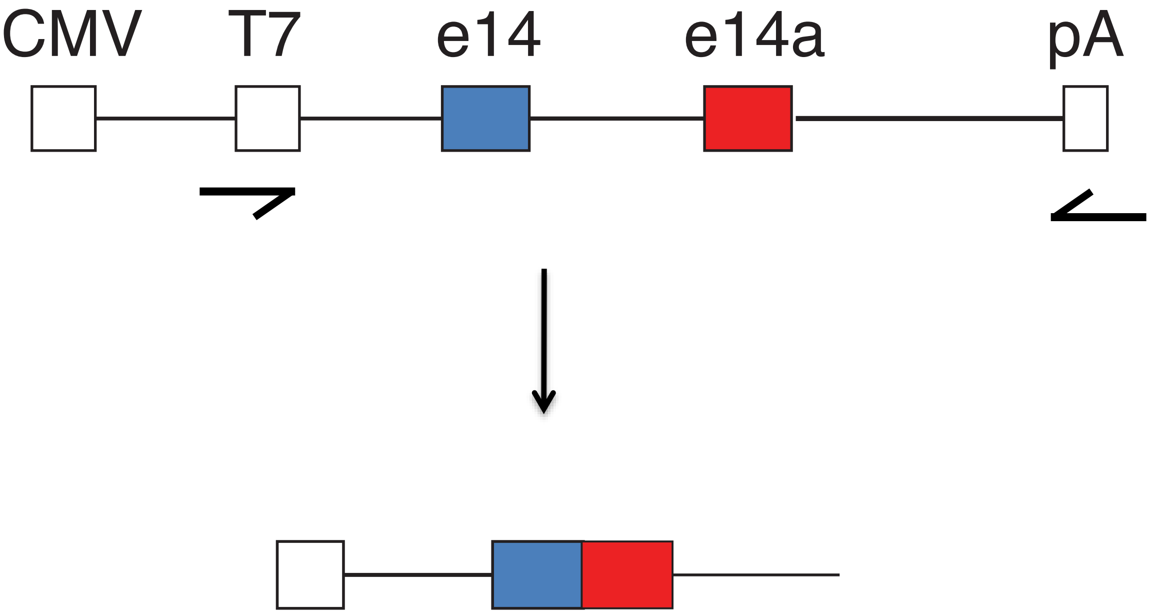
```
    Desmodus_rotundus  GTGAGTCTTGAG-T-AGTGCTTACTCTA-GG-----TTATGTAGAGTA--  3147
   Carollia_brevicauda  GTGAGTCTTGAG-T-AGCCCTTACTCTA-GG-----TTATGTAGAGTA--  3389
     Pteropus_vampyrus  GTGGGTCTTAAG-TTAAACCTTACCCTA-GG-----GCATGCAAAGTA--  1878
   Pteropus_rodricensis  GTGGGTCTTAAG-TTAAACCTTACCCTA-GG-----GCATGCAAAGTA--  1878
 Rousettus_aegyptiacus  GTGGGTATTAAG-TTAAACCTTACCCTA-GG-----GCATGTAAAGTA--  1880
            Bos_taurus  GTGGGTCTTGAG-T-AGACCTTATTCTAG-T-----GTGTATAGAGTA--  4189
        Equus_caballus  GTGGGTCTTGAG-T-AGAACTTACTCTAG-G-----GC-TGTAGAGTA--  2055
            Sus_scrofa  GTGGATCTTGAG-T-AGCTCTTGCTCTAG-T-----GCTTATAGAGTA--  3134
      Canis_familiaris  GTGGGTCCCTCA-T-AGACCTTACTATA-GG------TACATAGAGTA--  4021
      Scapanus_orarius  AACTTTATTAAGAT-ATAACTTACTACAAAATACACACATTTAAAATGTA  2293

    Desmodus_rotundus  -CGTGGGGGC-ATTTCTGGTAT-T-TTA----------GCTTAAT-----  3178
   Carollia_brevicauda  -CGTGG-GGC-ATTTCTGGTAT-T-TTA----------GCTTAAT-----  3419
     Pteropus_vampyrus  -AGTAG-GGC-ATTTTTAGTAT-T-TTG----------TCTAGATCC---  1910
   Pteropus_rodricensis  -AGTAG-GGC-ATTTTTAGTAT-T-TTG----------TCTAGATCC---  1910
 Rousettus_aegyptiacus  -AGTAG-GGC-ATTTTTAGTAT-T-TTA----------GCTAGATCC---  1912
            Bos_taurus  -AGCAG-GGC-ATTTCTGGTAT-T-TTA----------GCTTGATCC---  4221
        Equus_caballus  -AGGAG-GGC-ATTTCTGGCGT-C-TCA----------GTTTGATCC---  2087
            Sus_scrofa  -AGTAG-TG--ATTTCTGATGT-TTTTA----------ACTTGGTTC---  3166
      Canis_familiaris  -AGTAG-GGC-ATTTCTGGTAT-TTTTA----------GCCTGATC---C  4054
      Scapanus_orarius  TAGTTT-GGTAAGTTTCAGCAAATATACACTCAGGTAACCTCCATCTCAC  2342
```

Supplementary Figure 12

Alignment of exon 14a from cows and moles with intronic region of other mammals

The region encoding exon 14a in cow (*Bos tauru*; panel **a**) and Coast moles (*Scapanus orarius*; panel **b**) is highlighted. Splice acceptor (-AG-) and donor (-GT-) sites are highlighted in green and grey, respectively. Numbers at right indicate relative distance from exon 14 (position 1 corresponds to 12 nucleotides from the end of exon 14 in all species shown). Dashes indicate regions of non-identity.

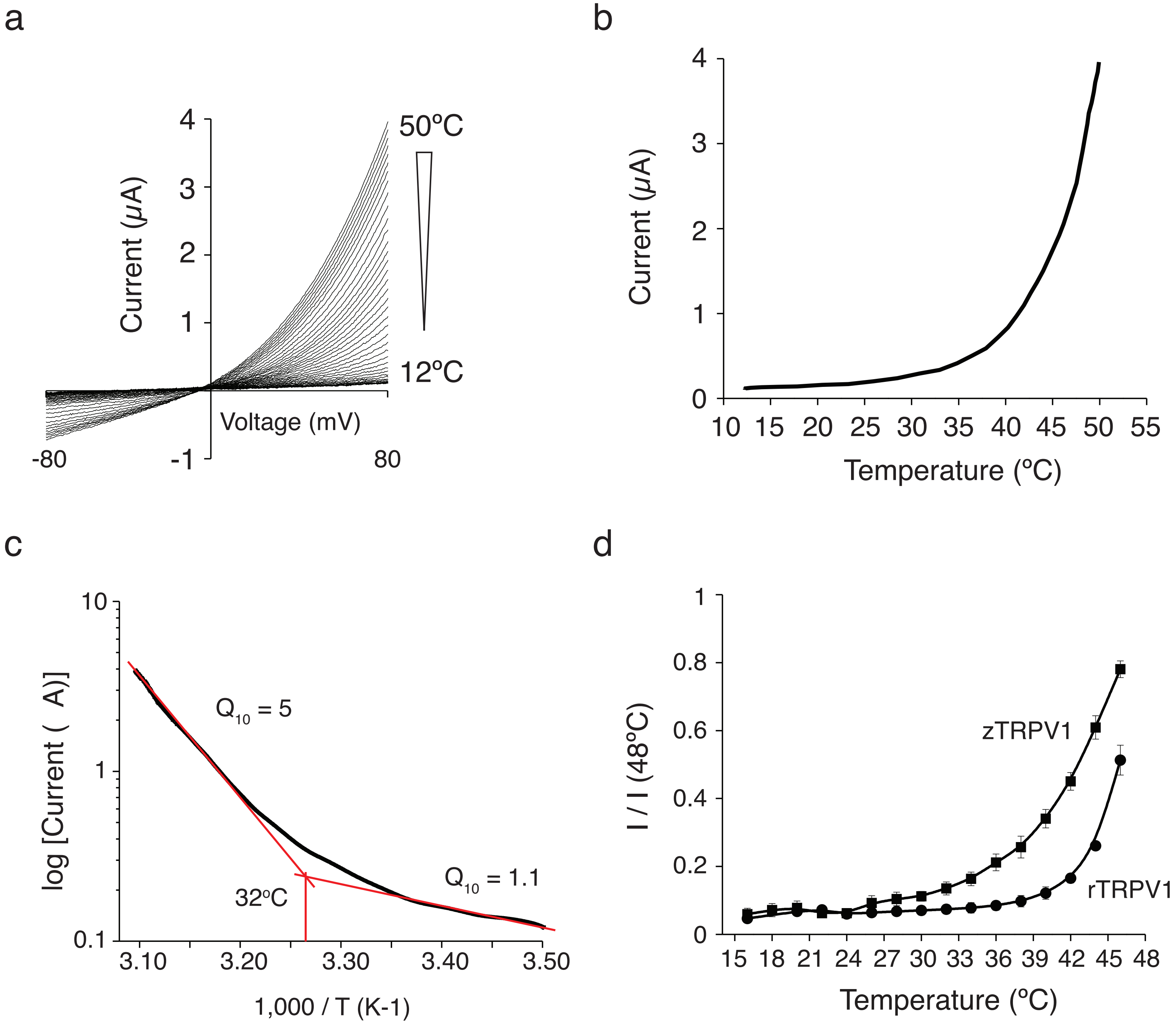

Pteropus vampyrus exon14-14a
pcDNA3
700
500
300


CMV
T7
e14
e14a
pA

Supplementary Figure 13

In vivo splicing assay suggests presence of TRPV1 exon 14a in megabats

Diagram shows structure of mini-gene used for in vivo splicing assay in HEK293 cells, indicating location of CMV promoter and polyadenylation site (pA), defining the start and end of the transcribed unit. Transcripts were reverse transcribed using oligo-dT in combination with a primer annealing to T7 promoter to amplify reverse transcripts. Reaction products were resolved on 1.5% agarose gel (shown above with samples run in quadruplicate), and major bands collected for sequencing. Control reaction with vector (pcDNA3) is shown at right. Schematic of major splice product (~300 bp) is shown at bottom.



e

rV1 TLSFSLRSGRVSGRNWKNFALVPLLRDASTRDRHATQQEEVQLKHYTGSLKPEDAEVFKDSMVPGEK
vbV1s TLSFSLRSGRAV
zV1 ANVQREPSR ——————— GVLQTFSRRRR—TQRAQTREGHELSPLAEASSSV

Supplementary Figure 14

Functional characterization and sequence analysis of zebrafish TRPV1

a-b, Representative current-voltage and temperature-response relationships for zebrafish TRPV1 channels expressed in oocytes. **c**, Arrhenius plot showing thermal threshold and Q_{10} values for baseline and evoked responses. **d,** Relative heat response profiles of zebrafish and rat TRPV1 channels expressed in oocytes (holding potential (Vh) = -80 mV; $n \geq 5$; mean ± s.d.). **e,** Alignment of deduced amino acid sequences for C-terminal domain of rat TRPV1, vampire bat TRPV1-S, and zebrafish TRPV1 channels.

Global coordinates for bat collection

Sampling Point	Latitude (N)	Longitude (E)	Meridian
1	987682	600729	19
2	990981	601590	19
3	989922	605086	19
4	986630	604268	19
5	983530	605045	19

Summary of species examined

Species	Transcriptome	Genomic (experimental)	Genomic (database)
Desmodus rotundus (vampire bat) (n = 4)	X	X	
Carollia brevicauda (microbat) (n = 6)	X	X	
Anoura cultrata (microbat) (n = 1)	X		
Uroderma bilobatum (microbat) (n = 1)	X		
Sturnira lilium (microbat) (n = 1)	X	X	
Pteropus vampyrus (megabat) (n = 1)		X	
Pteropus rodricensis (megabat) (n = 1)		X	
Rousettus aegyptiacus (megabat) (n = 1)		X	
Scapanus orarius (coast mole) (n = 1)	X	X	
Bos taurus (cow) (n = 1)	X		X
Canis lupus (dog)			X
Sus scrofa (pig)			X
Mus musculus (mouse) (n ≥ 6)	X		X
Rattus norvegicus (rat)			X
Oryctolagus cuniculus (rabbit)			X
Loxodonta africana (elephant)			X
Homo sapiens (human)			X
Macaca mulatta (macaque)			X

Supplementary Figure 15

Compendium of animals examined

Top table indicates global coordinates at which bat species were collected. Bottom table summarizes all species examined, either through analysis of tissue samples and/or bioinformatically. Where relevant, the number of individual animals examined for each species is indicated in parenthesis.