Supplementary Materials for

Rapid molecular evolution of pain insensitivity in multiple African rodents

Ole Eigenbrod*, Karlien Y. Debus*, Jane Reznick, Nigel C. Bennett, Oscar Sánchez-Carranza, Damir Omerbašić, Daniel W. Hart, Alison J. Barker, Wei Zhong, Heike Lutermann, Jestina V. Katandukila, Georgies Mgode, Thomas J. Park, Gary R. Lewin†

*These authors contributed equally to this work.
†Corresponding author. Email: glewin@mdc-berlin.de

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This PDF file includes:

Other Supplementary Material for this manuscript includes the following:
(available at science.sciencemag.org/content/364/6443/852/suppl/DC1)

Movie S1 (.mp4)

Materials and Methods

Animals

All animal protocols were approved by the University of Illinois at Chicago Institutional Animal Care and Use Committee, the German federal authorities (State of Berlin), or the Animal Use and Care Committee of the University of Pretoria, Republic of South Africa. Naked mole-rats used in this study were kept either at the Max-Delbrück Center for Molecular Medicine or at the University of Illinois at Chicago. All *Bathyergidae* species and East African root rats were housed at the University of Pretoria. Algogens in this study produce a very short duration pain behavior, as reflected in foot lifting or licking, that usually lasts less than 60 s in duration and was mostly over within the first 2-3 minutes following the injection. To avoid undue stress animals were normally confronted with only one algogen per day and most animals in this study were never confronted with more than two algogens in total. No long term adverse effects of algogen injections were ever observed in any of the animals used in this study.

Molecular Biology

The tissues analysed in this study were rapidly removed from euthanized animals and snap frozen in liquid nitrogen. Euthanasia was carried by first anesthetizing mole-rats with the inhalation anaesthetic halothane followed by cervical dislocation before the removal of tissues. Total RNA was isolated from the collected DRGs and spinal cord samples with TRIzol (Life Technologies) and dissolved in 30 µL RNase-free water. Paired-end, strand-specific (dUTP) libraries were prepared from RNA samples isolated from three biological replicates per species and sequenced on the Illumina HiSeq2500 platform. For cDNA cloning 1–3 µg total RNA was used to clone channel cDNAs amplified with specific primers from reverse transcribed material. The desired cDNA cloned into an IRES-dsRed or EGFP containing expression vector using the

SLIC reaction(*44*). Mutations were introduced by PCR and multiple-fragment SLIC cloning. In some cases, we obtained synthesized cDNAs constructs (GeneArt Invitrogen).

RNA sequencing and bioinformatic pipeline

Sequencing of cDNA libraries was done at the Scientific Genomics Platform at the Berlin Institute of Medical Systems Biology at the Max Delbrück Center. Sequencing yielded around 30 Mio read pairs per sample. Quality clipping of the raw reads was performed with Trimmomatic 0.32(*45*). Adapters were clipped off using 1 seed mismatch, a palindromic score threshold of 30 and a simple clip threshold of 15. Minimum quality for trailing bases was set to 20. Leading 10 bases were clipped to avoid bias introduced by random hexamer priming. Read pairs with at least one read shorter than 30 bases after quality clipping were discarded. Sequencing yielded 156 to 229 Mio quality clipped read pairs per species (see table 1). During quality clipping, between 1.6% and 2.1% of the read pairs were discarded per sample. RNAseq reads from *Bathyergidae* and the East African root rat were used for *de novo* transcriptome assembly. RNAseq reads were pooled per species to create the *de novo* transcriptome assembly. Transcriptomes from mouse (accession GCF 000001635.25, downloaded on 27/12/2016), naked mole-rat (accession GCF 000247695.1, downloaded on 29/12/2016) and Damaraland mole-rat (accession GCF 000743615.1, downloaded on 29/12/2016) were not assembled, as annotated sequence data were available from the RefSeq database(*46*). The Trinity tool (version 20140717)(*17*) and the Bridger software (version 2014-12-01)(*16*) were used with default parameters to assemble raw transcriptomes. Both assemblies were combined using the Contig Assembly Program version 3, CAP3(*47*) and all merged and non-merged sequences were used for downstream analyses. Sequencing library contamination in the assemblies were detected using BLASTn against mouse, naked mole-rat and human ribosomal and mitochondrial DNA sequences obtained from RefSeq

as well as sequences from bacterial genomes often found in laboratory samples(*48*). All assembled transcripts with a BLAST hit with an E-value < 1e-20 against ribosomal RNA, bacterial or mitochondrial DNA that covers at least 10% of the transcript were discarded. Transcripts putatively originating from human or mouse were discarded if they showed an E-value < 1e-20 and sequence identity of > 99% and covered at least 70% of the transcript.

Orthologous transcripts were identified by applying a reciprocal best hit strategy using a mouse protein data set derived from RefSeq(*46*) (accession number GCF 000001635.25, downloaded on 27/12/2016). Only the longest isoform per protein was considered for annotation. If available, protein sequences with experimental evidence (RefSeq-ID NP) were preferred over predicted sequences (RefSeq-ID XP). Cleaned transcript sequences were aligned against the mouse RefSeq protein data sets using BLASTx. All hits with an E-value < 1e-20 in forward direction and a sequence similarity of ≥ 75% were considered for further analyses. The same stringency level was used for the alignment of protein sequences against the transcript sequences using tBLASTn. Putatively chimeric transcripts were discarded if multiple co-linear hits were identified using tBLASTn or BLASTx. Additionally, transcripts were excluded from downstream analysis if there was more than one protein with a best hit to that transcript ("collapse factor" > 1(*49*)). Reciprocal best hits were computed and a full-length protein annotation was assigned if the BLASTx hit covered at least 80% of the protein sequence. Protein-coding transcripts identified by the reciprocal best hit strategy were extracted from the assembly as a reference transcriptome and further tested for assembly or annotation errors. TransRate was applied on each reference transcriptome, and sequences with more than 40% of the bases covered with mapped reads (s(Ccov) > 0.4) were kept for further analysis(*50*).

Transcriptome completeness is a measure that reflects what fraction of transcripts was recovered in the assembly and annotation process in comparison to a reference transcriptome. The completeness score was calculated using BUSCO (Benchmarking Universal Single-Copy Orthologs, version 1.22)(*51*) with the vertebrate data set as background in transcriptome mode. The E-value cutoff was set to 1e-20.

Orthologous transcripts in African mole-rats and other rodents were identified based on identical gene name. *De novo* assembled and annotated full-length transcripts from *Bathyergidae* species and the East African root rat were used as well as RefSeq mRNA sequences of other rodents, in which the longest gene isoform or, if available, an isoform with experimental support was selected. The transcriptome of *Fukomys darlingi* was generated based on published RNAseq reads from brain samples using the same assembly pipeline presented in this study(*28*).

Multiple sequence alignments were performed for all sets of orthologous sequences using Multiple Alignment using Fast Fourier Transform MAFFT (version 7.299b) in accurate mode (mafft-linsi)(*52*). The longest consecutive intersecting region per orthologous transcript was used for downstream analyses to focus on comparable regions of the assembled transcripts for phylogenetic tree reconstruction and transcript quantification. Only the region in the alignment between the first and the last base that could be aligned in all investigated species was used further. Additionally, any alignment regions with gaps longer than 100 nucleotides were removed as they might represent assembly errors. GUIDANCE2 (version 2.02)(*53*) was used to identify intersected alignments with falsely assigned sequences, and alignments with an average column score < 0.5 were excluded from further analysis.

The 6,427 orthologous protein-coding transcripts present in all 10 rodent species were used to reconstruct a phylogenetic tree, while *Mus musculus* and *Tachyoryctes splendens* were set as

outgroup species. A phylogenetic tree was calculated with a maximum likelihood (ML) approach implemented in the RAxML tool (version 8.2.3)(*54*). The general time reversible model was used to account for variable base frequencies and symmetrical substitution rates. A gamma distribution was assumed to underlie the rate heterogeneity over the sites. One hundred rapid bootstrap searches were performed in addition to 20 ML searches and the best ML tree was reported. Divergence times of rodent species were estimated using the mcmctree software of the PAML package(*55*). Fossil calibration for the divergence of *Muroidea* and *Ctenohystrica* was set to 47.6 to 59.2 Myr. Approximate likelihood calculations were performed due to the size of the alignment. The general time reversible model was chosen as a nucleotide substitution model. The MCMC (Markov chain Monte Carlo) search was run for 53,000 generations, while the first 3,000 generations were discarded as a burn-in and every fifth generation was sampled. Divergence times were stable across multiple repetitions of the calculations. The resulting phylogenetic tree was visualized using FigTree (version 1.4.2)(*56*).

Annotated transcriptomes of six *Bathyergidae* species, East African root rat and mouse were used as reference sequences for read count-based transcript quantification. *Heliophobius emini* and samples were excluded from quantitative analyses. The *Heliophobius emini* samples were excluded because of insufficient biological replicates as many library preparations failed from this species. We used single-linkage clustering of pairwise sample correlation based on logarithmized TPM (transcripts per million) values to cluster data from each tissue and species. When the *Cryptomys hottentotus mahali* samples were included, the data from dorsal root ganglia and spinal cord did not cluster cleanly, but rather with more distantly related species. Such an inaccurate clustering suggested to us that some of the sensory tissues were contaminated with non-sensory tissue during collection making expression data from these tissues unreliable.

Comparing transcript abundances between different species is a challenging task, as the quantification can be biased by the number of reference transcripts, transcript length, base composition and sequencing depth(*57*). The reference transcriptomes were prepared to create references with the same number of transcripts, approximately equal transcript lengths and base compositions to minimize the possible biases in transcript quantification. In total, the expression levels of 6,878 transcripts were compared between the East African root rat, mouse, naked mole-rat and five *Bathyergidae* species. Quality clipped reads were mapped to the curated transcriptomes. Bowtie2 (version 2.0.5)(*58*)was used to map the reads to the references. The second read of each pair had to map upstream of the reverse complement of the first paired read. Only paired alignments with the second read mapping to the reverse complement strand of the first read were allowed (parameters: --fr --nofw --no-discordant). After the alignment step, reads with a mapping quality lower than 30 were discarded using samtools (version 1.3)(*59*). Reads per transcript were quantified using eXpress (version 1.5.1)(*60*). Only read pairs from alignments with the first read on the reverse complement sequence and the second read on the forward strand were counted (parameter: --rf-stranded). Log-transformed transcripts per million values were used for data visualization, a pseudocount was added to the TPM values prior to applying the logarithm to avoid negative expression values. Estimated raw counts were normalized for library size with the TMM (trimmed mean of M values) method implemented in the edgeR tool for differential expression analysis(*61*, *62*).

Multi-dimensional data like high-throughput transcript expression levels can be embedded in a two-dimensional space by t-SNE (t-distributed stochastic neighbor embedding) for quality control or clustering purposes(*63*). A quantitative comparison of transcriptomes was performed using spinal cord and dorsal root ganglion samples from eight rodent species. Transcript read

counts (log2(TPM+1)) were visualized using t-SNE implemented in the Rtsne package for R (Krijthe, J. Rtsne: T-distributed stochastic neighbor embedding using Barnes-Hut implementation. R package version 0.10, URL http://CRAN. R-project.org/package=Rtsne (2015).). Default parameters were used to embed the samples in two-dimensional space.

A neighbor joining tree based on euclidean distances of sample expression values per tissue was generated with the "visTreeBootstrap" function of the "supraHex" R package with 1000 bootstraps. Counts were transformed to logCPM (counts per million) and fed into a phylogenetic generalized least squares model (pGLS, "pgls" function from the "caper" R package(*64*)). A pGLS model was built per tissue and insensitivity type for each gene with the neighbor joining tree representing the sample distances. The algogen insensitivity of each sample was represented by a binary classifier in the pGLS model. Statistical significance of the model fit was evaluated by performing an ANOVA (analysis of variance), p-values of the F-test were adjusted for multiple testing afterwards using the Benjamini and Hochberg method. Genes were considered as differentially expressed if they showed an absolute mean log fold change larger than 1 and an adjusted p-value less than 0.05.

Multiple alignments of amino acid sequences of orthologous transcripts of 17 species were aligned and intersected to infer differences in selection pressure during evolutionary history (see Extended Data Table 4). Protein sequences were derived from the intersected transcripts using TransDecoder (version 2.0.1)(*65*) while only protein sequences in forward direction of the transcripts were considered. The longest predicted open reading frame per transcript was chosen as the representative protein-coding amino acid sequence. Peptide sequences were aligned using MAFFT (version 7.299b)(*52*), and codon alignments were generated with PAL2NAL (version 14)(*66*). Intersected coding sequences were then further processed with GUIDANCE2 (version

2.02)(*53*). Alignment columns with a score < 0.93 and whole alignments with an average column score < 0.9 were removed from the data set to focus on high quality annotated sequences and alignments.

We used CodeML from the PAML package (version 4.8)(*55*) to infer differences in selection pressures acting on specific branches of the phylogeny. Differences in selection pressure were inferred using a model that was designed to identify specific residues under divergent selection. Clade model C(*67*) tests for divergent selection by comparing the ratio of non-synonymous (dN) to synonymous substitutions (dS) in foreground versus background branches of the phylogenetic tree. Clade model C assumes three classes of sites within the codon alignment, while the model M2a_rel(*68*) serves as null model. Log-likelihood values of the two models were compared using a likelihood-ratio-test with one degree of freedom. Genes with a median distance between significant Bayes Empirical Bayes sites (BEB) (probability > 0.9) of 15 or lower were filtered out to correct for alignment errors. If only two BEB sites were detected, the filtering distance threshold was reduced to five. The false discovery rate was controlled for using the Benjamini and Hochberg method, and only genes with an adjusted p value < 0.05 and at least one significant BEB site were assumed to be under divergent selection.

Due to assembly errors like family collapse, where gene sequences from highly conserved gene families cannot be distinguished from each other on the basis of short reads, we were not able to assemble reliable transcripts for the SCN9A gene in most species. A guided assembly approach was used to retrieve the SCN9A sequences of *Bathyergidae* species and *Tachyoryctes splendens*. The SCN9A sequence of *Heterocephalus glaber* from RefSeq (XM_013076951.1) was used as a reference and DRG sample reads from *Tachyoryctes splendens, Heliophobius emini, Georychus capensis, Cryptomys hottentotus hottentotus, Cryptomys hottentotus mahali, Cryptomys*

hottentotus natalensis and *Cryptomys hottentotus pretoriae*, respectively, were mapped against it. Sensitive mapping setting for bowtie2 (version 2.0.5)(*58*) were chosen to account for sequence differences between the species (parameters --fr --nofw –nodiscordant --no-mixed --very-sensitive --score-min L,0,-1). Consensus sequences were created with samtools (version 1.3, mpileup and bcftools commands)(Li et al., 2009). Final coding sequences were derived with TransDecoder (version 2.0.1)(*65*) and then aligned with MAFFT (version 7.299b)(*52*). Jalview (version 2.9.0b2)(*69*) was used to visualize protein alignments.

Data from single-cell RNASeq sequencing experiments of DRG neurons was downloaded from http://linnarssonlab.org/drg/(*19*). A transcript was considered as expressed if the expression was >1 TPM in a cell. Cells were assigned to cell types according to Level 1 annotation of the scRNASeq study.

Cell culture and calcium imaging

HEK293 cells (used for electrophysiology) as well as AD293 cells (Agilent, used for calcium imaging) were cultured in DMEM/glutamax medium (Gibco) supplemented with 10% fetal calf serum and 1% penicillin and streptomycin. For single cell calcium imaging and electrophysiology, the cells were plated on PLL coated round glass coverslips (Roth) (10mm) and transfected after 24h with FUGENE (Promega). Imaging was performed typically one day after transfection, electrophysiology 48h after. Only EGFP and/or dsRed expressing cells were selected for electrophysiological recordings.

The calcium dye (CAL520® AM, AAT Bioquest, Inc.), a single wavelength calcium indicator, was dissolved in DMSO and 0.02% pluronic acid and loaded onto the cells one hour before the experiment. The coverslip was transferred to a custom made chamber, and perfused with extracellular buffer at room temperature for 10 – 20 minutes. Calcium imaging was carried out

with an Olympus BX51WI microscope equipped with the MetaFluor imaging system, including DG4 wavelength switcher (Sutter Instruments) and a CoolSNAP ES camera (Visitron). The settings were as follows: 20x water immersion objective, 14 bit resolution, sampling rate 3 seconds. The cells were excited with a 520 nm wavelength to see the red fluorescence from dsRed and a 480 nm for the Ca2+ indicator CAL520® AM. AITC was applied after 30 seconds of imaging for a period of 90 seconds. To normalize the signals, 1µM ionomycin was applied at the end.

High throughput Calcium imaging (FLIPR tetra)

Two days before measuring cells were plated in a black 384 well microplates with transparent bottom (Corning, 3683). 24h later they were in plate transfected using FuGENE (Promega). Per transfection mixture 64 wells were transfected, subjected to 8 different concentrations of AITC. Per TRPA1 species, at least 5 transfection mixtures were made in order to have minimum 40 wells measured per concentration. The transfection efficiency was tested one day later on a TECAN plate reader exciting with 556 nm and collecting the 586 nm wavelength. The values were used to calculate transfection outliers using the quartal method, which were excluded from further analysis. Fluo-4 (Thermofischer) was added one hour before the measurement and washed off with extracellular buffer (in mM: 140 NaCl, 4 glucose, 10 HEPES, 4 KCl, 2 CaCl2, 1 mgCl2, NaOH 5N until pH 7.4) right before placing the 384 well plates in the FLIPR device. Sampling rate was 1 second and AITC was added after 5 seconds. 180 seconds later ionomycin was added (final concentration 1µM).

qPCR

Total RNA was collected from tissues using ReliaPrep^{TM} RNA Tissue Miniprep system (Promega), according to manufacturer's instructions. For reverse transcription with the

Superscript III reverse polymerase (Invitrogen) 0.5 µg of total RNA was taken and cDNA was analysed using the Universal Probe library (Roche) in a CFX384 Real Time PCR detection system. Primers to quantify Highveld and Natal mole-rat *NALCN* were F: 5'-TTCCAACAAATGTGGGGGTCA-3' R: 5'-TGCATCTTCGTGAAACATCTG-3' designed using the transcript sequences found doing RNAseq. The standard curve method with known doses of a plasmid containing the cDNA amplicon from the primer pair, was used to quantitate mRNA transcripts by extrapolating a value by comparing unknowns to the standard curve of known transcript amounts.

Electrophysiology

Whole cell patch clamp recordings were conducted on dsRed and/or EGFP-positive HEK293 cells 48 hours post transfection at room temperature. Patch pipettes were pulled from borosilicate glass capillaries and had a tip resistance of 3-6 MΩ. Pipette solution contained (in mM): 150 CsCl, 10 NaCl, 10 EGTA, 2 Mg_2ATP and 10 HEPES (pH 7.4. Osm ~320mOsm/L). Bath solution contained (in mM): 150 NaCl, 3.5 KCl, 2 $MgCl_2$, 1.2 $CaCl_2$, 10 HEPES, and 20 glucose (pH 7.4, Osm ~350mOsm/L). Recordings were made using EPC-9 amplifier (HEKA) and Patchmaster software (HEKA). A standard voltage-step protocol was used whereby cells were held at 0mV for 50 ms before stepping to the test potential -60mV – +60 mV (in 20mV increments) for 300ms, returning to the holding potential (0mV for 50 ms) between sweeps.

Performing current clamp, current pulses from -60pA to +20pA (20pA increments) were injected in the cell. The steady-state voltage responses were plotted against the amplitude of the current injection. The slope of the linear fit of this relationship was determined to calculate the input resistance.

Additional statistical analyses were performed using the GraphPad Prism software. Unless otherwise stated, a two-tailed unpaired t-test or Mann-Whitney test was employed, where * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$. All data are shown as mean ± SEM.

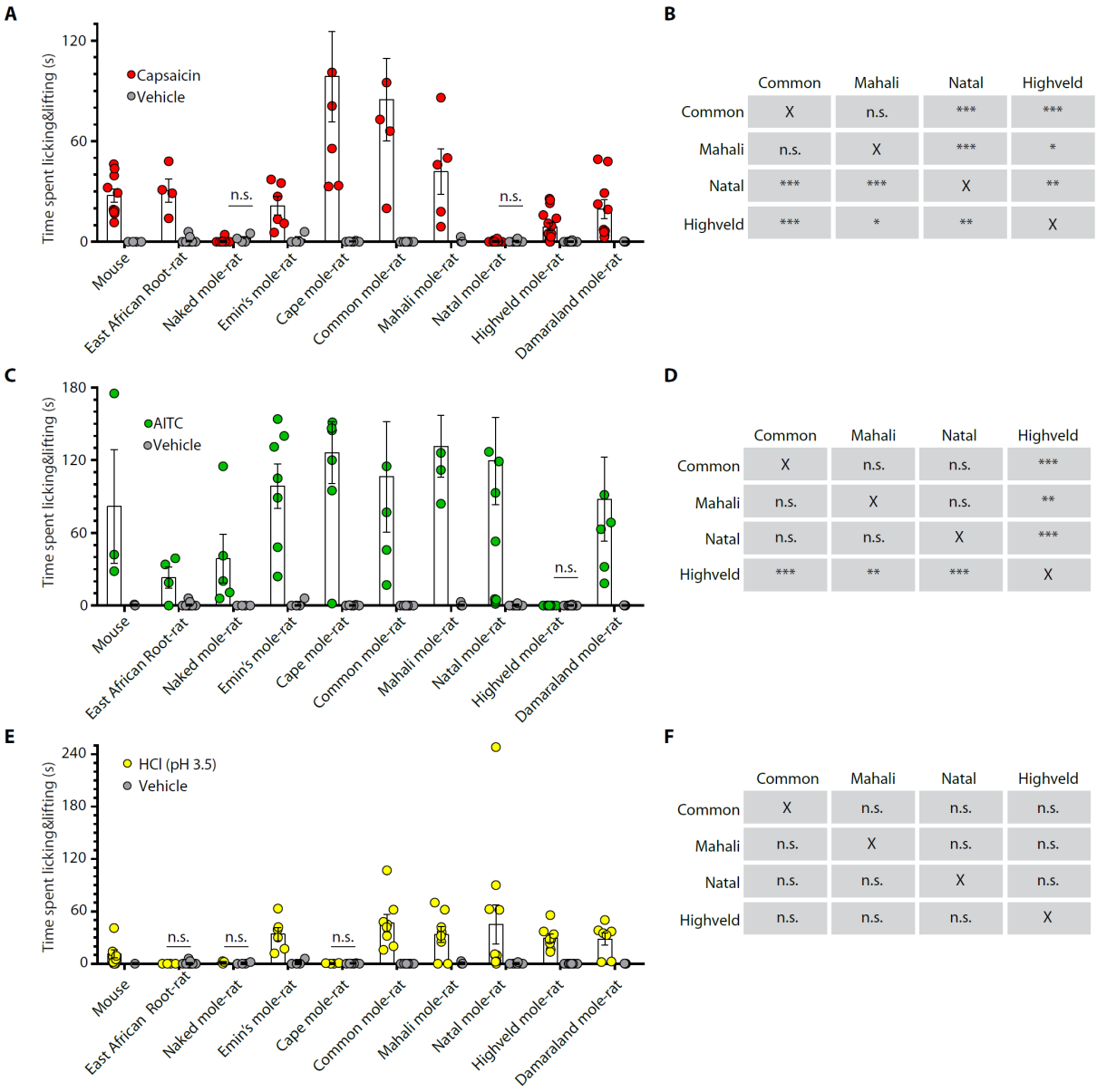

Fig. S1

Vehicle data and interspecies comparisons A) Summed response times for all species of rodents after capsaicin injection into the paw versus a vehicle injection (error bars indicate SEM; ns: P>0.05; *Mann–Whitney U* test). B) Statistical comparisons within the genus. Note that Highveld mole-rats have a significantly blunted pain response to capsaicin compared to other *Cryptomys* species with the exception of the capsaicin insensitive Natal mole-rat. C) Summed response time of rodents upon injection of AITC to the paw plotted versus vehicle controls. D) Statistical comparisons within the genus. Note that all *Cryptomys* species with the exception of Highveld mole-rat have similar magnitudes of pain response to AITC. E) Cumulative response time of rodents upon injection of acid into the paw versus a vehicle injection (ns: P>0.05; *Mann–Whitney U* test). F) Statistical comparisons within the genus. Note that all *Cryptomys* species showed a robust behavioral response to acid and there was no statistically significant differences within the genus *Cryptomys* (error bars indicate SEM; for all tests: ns: P>0.05; *P ≤ 0.05, **P ≤ 0.01, ***P ≤ 0.001; *Mann–Whitney U* test)

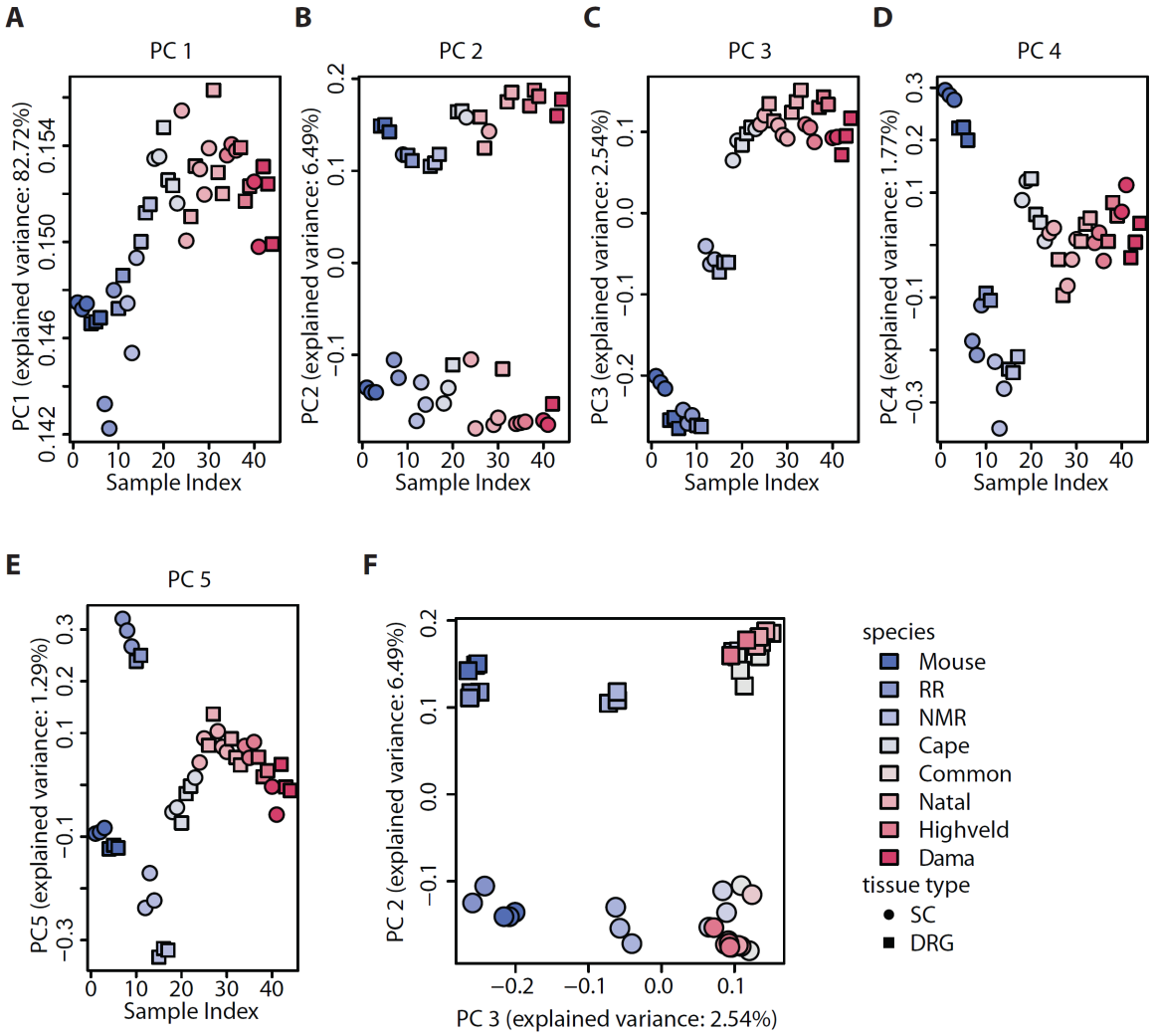

Fig S2

Principal component analysis (PCA) of transcript expression data. PCA values for the first five PCs. **A)** PC1 shows mostly biological variation across all samples with a slight phylogenetic component. **B)** PC2 clearly separates spinal cord from dorsal root ganglion samples. **C)** PC3 shows a phylogenetic signal, separating mice, root rats, naked mole-rats and the Bathyergidae species. **D)** PC4 seems to separate root rat and mouse spinal cord samples, while PC5 has the most extreme values for root rat and naked mole-rat. **E)** By plotting PC2 against PC3 a good separation of both tissues and species was achieved

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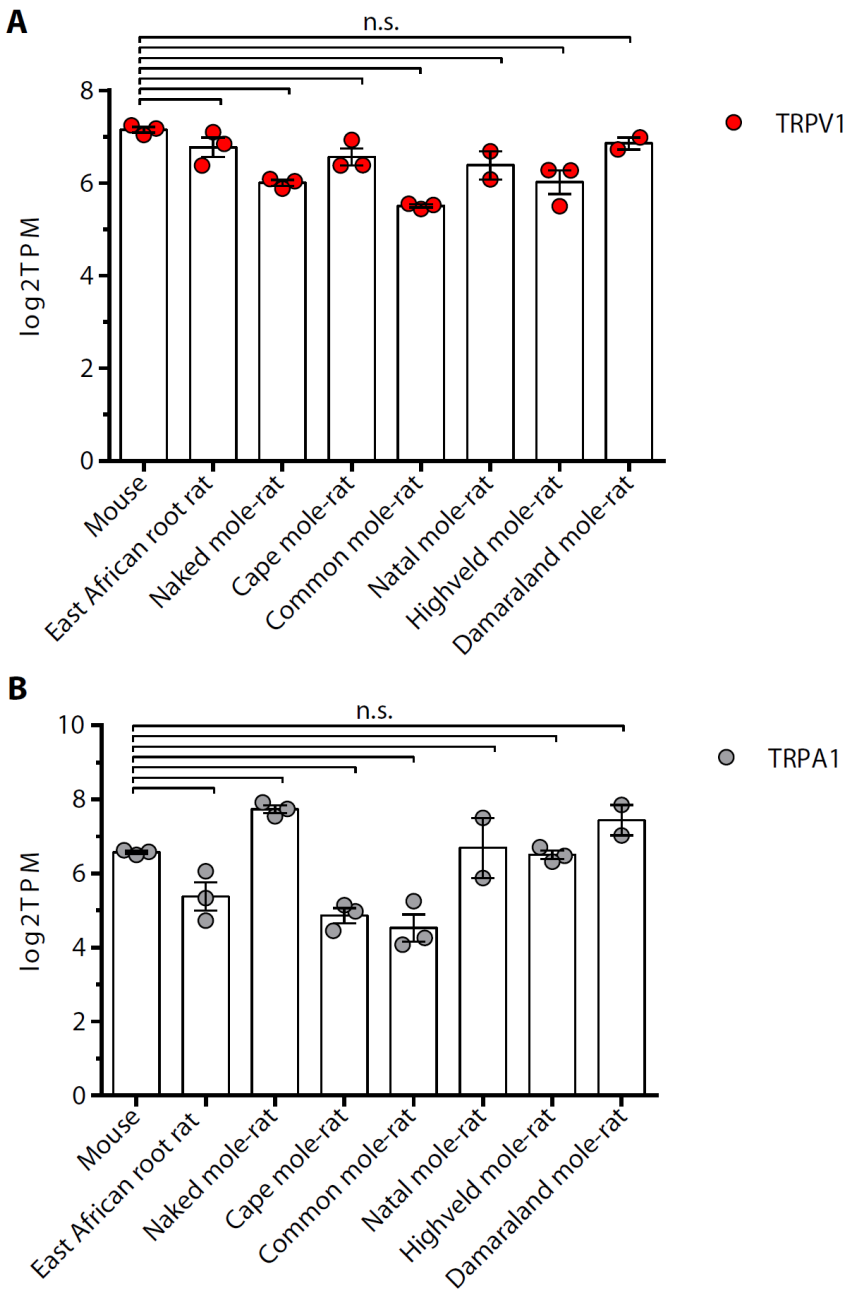

Fig. S3

TRPA1 and TRPV1 expression level in dorsal root ganglia. A) Log2TPM values for TRPV1 in dorsal root ganglia from mouse, root rat and six *Bathyergidae* species show no significant difference between them. The same is shown for TRPA1 in B). There was no indication that TRPA1 or TRPV1 was differentially expressed in the DRG based on the pGLS model (see Figure 2), this was also the case when using a simple *Mann–Whitney U* test on the raw TPM values. Error bars indicate SEM;

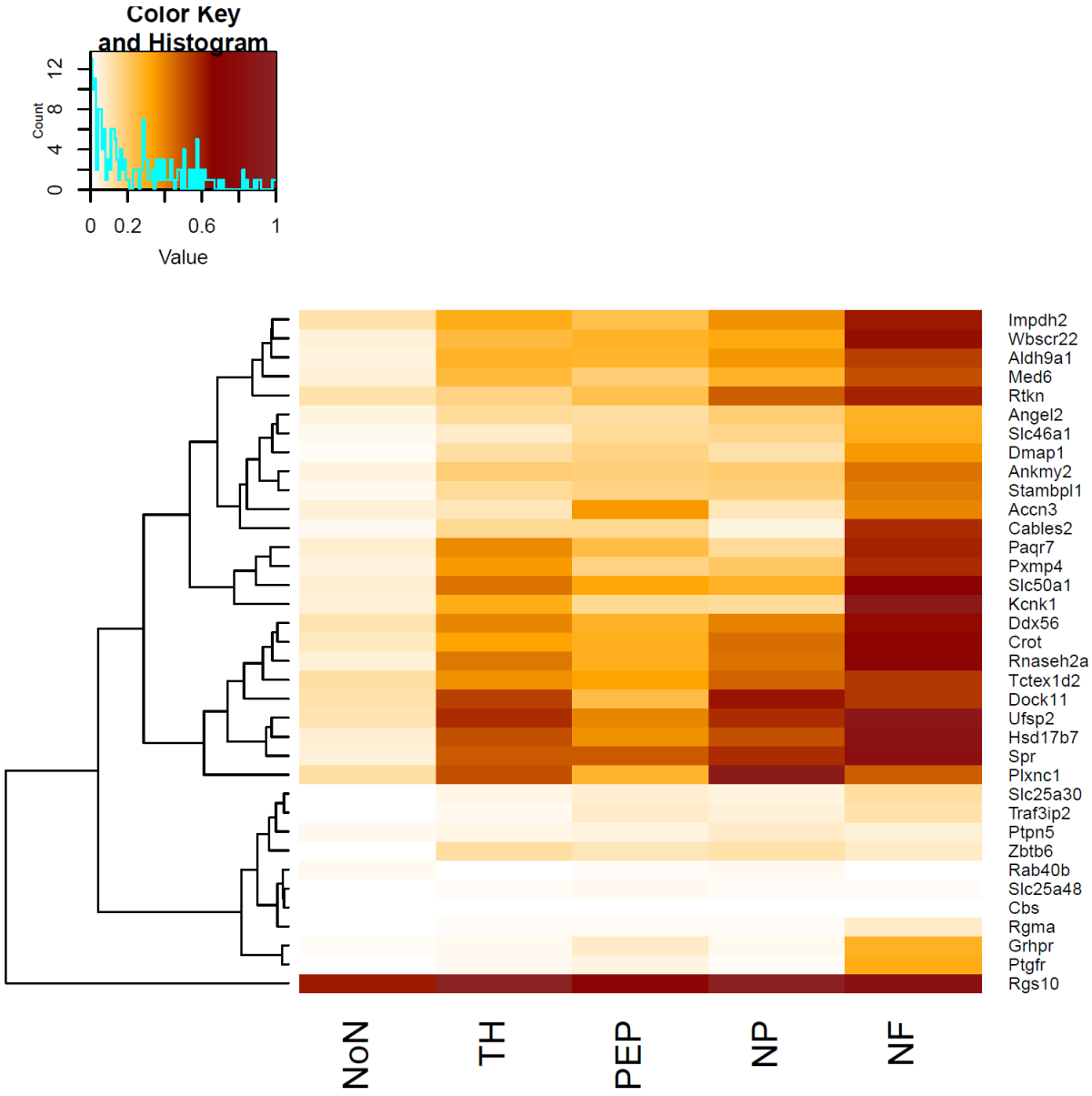

Fig. S4.

Cell-specific expression of differentially expressed genes in acid-insensitive species. Heatmap of the fraction of dorsal root ganglia cells that express transcripts identified as differentially expressed in the DRG of acid-insensitive species grouped by neuron type. Single-cell gene expression data was downloaded from (Usoskin et al., 2015).

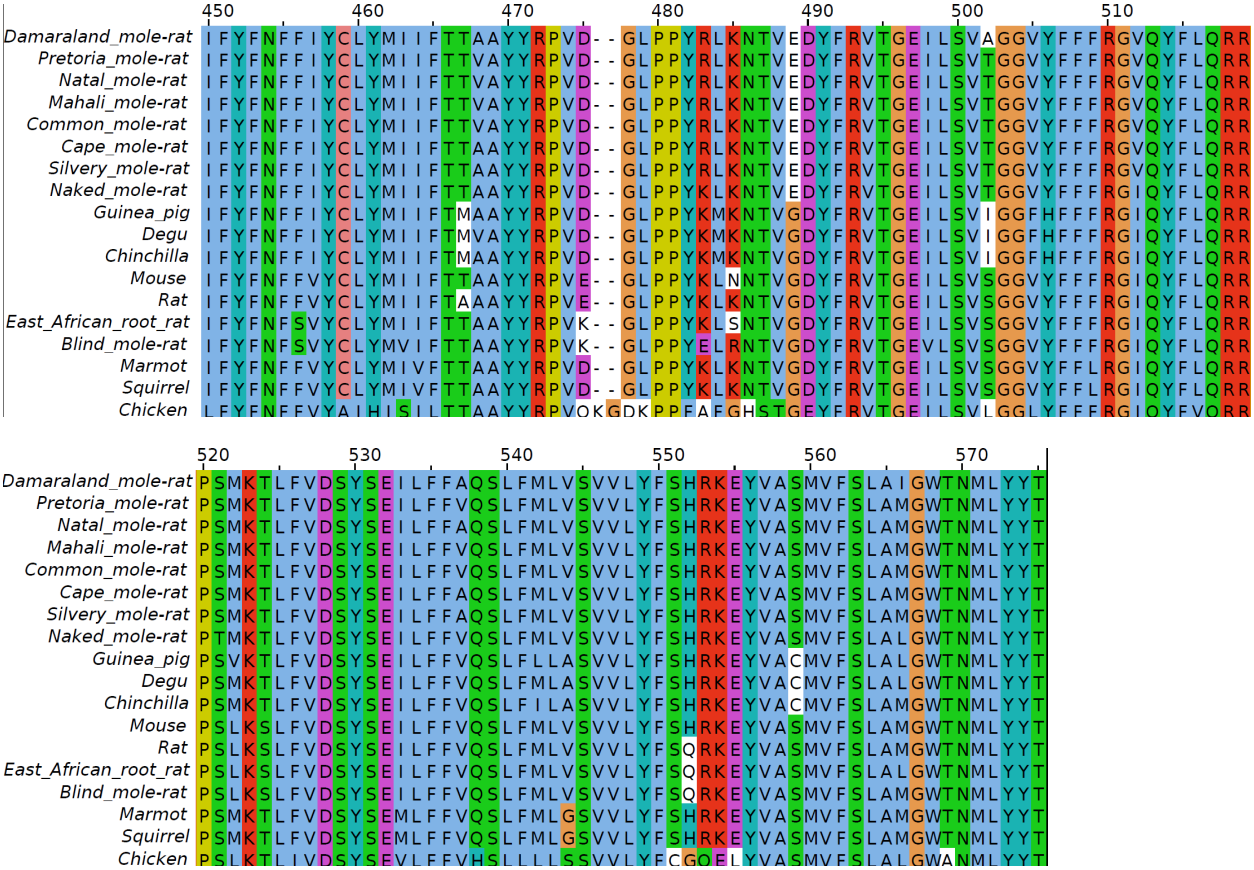

Fig. S5.

TRPV1 alignment S2-S4. Multiple protein sequence alignment of the TRPV1 ion channel in the putative capsaicin-binding region between the second and fourth transmembrane domain (S2-S4). Numbers on top of the alignment depict amino acid positions.

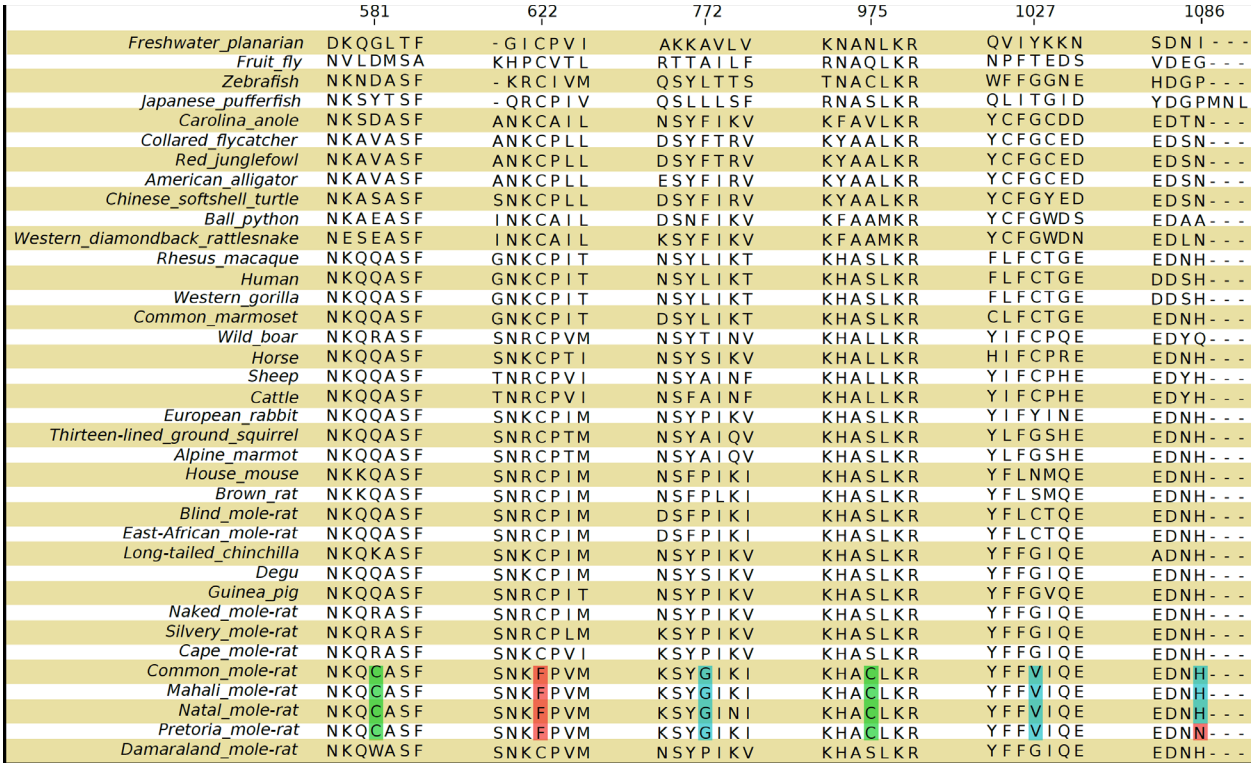

Fig. S6. Cryptomys-specific variants in TRPA1. Multiple protein sequence alignment of the TRPA1 ion channel. Regions were selected based on *Cryptomys*-specific variants in the protein. Numbers on top of the alignment depict amino acid positions.

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Danio_rerio                     MCSAGAISALLFPLIHSLYSTASPSMLKRKQSSRVEAQPMTDFGPDETLTDSADILWINK    60
Marmota_marmota                       ------------------------MLKRKQSSRVEAQPVTDFGPDESLSDNADILWINK    35
Tachyoryctes_splendens                ------------------------MLKRKQSSRVEAQPVTDFGPDESLSDNADILWINK    35
Rattus_norvegicus                     ------------------------MLKRKQSSRVEAQPVTDFGPDESLSDNADILWINK    35
Mus_musculus                          ------------------------MLKRKQSSRVEAQPVTDFGPDESLSDNADILWINK    35
Nannospalax_galili                    ------------------------MLKRKQSSRVEAQPVTDFGPDESLSDNADILWINK    35
Homo_sapiens                          ------------------------MLKRKQSSRVEAQPVTDFGPDESLSDNADILWINK    35
Pan_troglodytes                       ------------------------MLKRKQSSRVEAQPVTDFGPDESLSDNADILWINK    35
Cavia_porcellus                       ------------------------MLKRKQSSRVEAQPVTDFGPDESLSDNADILWINK    35
Heterocephalus_glaber                 ------------------------MLKRKQSSRVEAQPVTDFGPDESLSDNADILWINK    35
Georychus_capensis                    ------------------------MLKRKQSSRVEAQPVTDFGPDESLSDNADILWINK    35
Heliophobius_emini                    ------------------------MLKRKQSSRVEAQPVTDFGPDESLSDNADILWINK    35
Fukomys_damarensis                    ------------------------MLKRKQSSRVEAQPVTDFGPDESLSDNADILWINK    35
Cryptomys_hottentotus_hottentotus     ------------------------MLKRKQSSRVEAQPVTDFGPDESLSDNADILWINK    35
Cryptomys_hottentotus_mahali          ------------------------MLKRKQSSRVEAQPVTDFGPDESLSDNADILWINK    35
Cryptomys_hottentotus_pretoriae       ------------------------MLKRKQSSRVEAQPVTDFGPDESLSDNADILWINK    35
Cryptomys_hottentotus_natalensis      ------------------------MLKRKQSSRVEAQPVTDFGPDESLSDNADILWINK    35
                                                **************:********:*:*:********

Danio_rerio                     PWVHSLLRACAIISVISVCMNTPKTFEHYPPLQYVTFALDTLLMFLYTAEMIAKMHIRGI    120
Marmota_marmota                       PWVHSLLRICAIISVISVCMNTPMTFEHYPPLQYVTFTLDTLLMFLYTAEMIAKMHIRGI     95
Tachyoryctes_splendens                PWVHSLLRICAIMSVISVCMNTPMTFEHYPPLQYVTFTLDTLLMFLYTAEMIAKMHIRGI     95
Rattus_norvegicus                     PWVHSLLRICAIISVISVCMNTPMTFEHYPPLQYVTFTLDTLLMFLYTAEMIAKMHIRGI     95
Mus_musculus                          PWVHSLLRICAIISVISVCMNTPMTFEHYPPLQYVTFTLDTLLMFLYTAEMIAKMHIRGI     95
Nannospalax_galili                    PWVHSLLRICAIISVISVCMNTPMTFEHYPPLQYVTFTLDTLLMFLYTAEMIAKMHIRGI     95
Homo_sapiens                          PWVHSLLRICAIISVISVCMNTPMTFEHYPPLQYVTFTLDTLLMFLYTAEMIAKMHIRGI     95
Pan_troglodytes                       PWVHSLLRICAIISVISVCMNTPMTFEHYPPLQYVTFTLDTLLMFLYTAEMIAKMHIRGI     95
Cavia_porcellus                       PWVHSLLRICAIISVISVCMNTPMTFEHYPPLQYVTFTLDTLLMFLYTAEMIAKMHIRGI     95
Heterocephalus_glaber                 PWVHSLLRICAIISVISVCMNTPMTFEHYPPLQYVTFTLDTLLMFLYTAEMIAKMHIRGI     95
Georychus_capensis                    PWVHSLLRICAIISVISVCMNTPVTFEHYPPLQYVAFALDTLLMFLYTAEMIAKMHIRGI     95
Heliophobius_emini                    PWVHSLLRICAIISVISVCMNTPVTFEHYPPLQYVAFALDTLLMFLYTAEMIAKMHIRGI     95
Fukomys_damarensis                    PWVHSLLRICAIISVISVCMNTPVTFEHYPPLQYVAFALDTLLMFLYTAEMIAKMHIRGI     95
Cryptomys_hottentotus_hottentotus     PWVHSLLRICAIISVISVCMNTPVTFEHYPPLQYVAFALDTLLMFLYTAEMIAKMHIRGI     95
Cryptomys_hottentotus_mahali          PWVHSLLRICAIISVISVCMNTPVTFEHYPPLQYVAFALDTLLMFLYTAEMIAKMHIRGI     95
Cryptomys_hottentotus_pretoriae       PWVHSLLRICAIISVISVCMNTPVTFEHYPPLQYVAFALDTLLMFLYTAEMIAKMHIRGI     95
Cryptomys_hottentotus_natalensis      PWVHSLLRICAIISVISVCMNTPVTFEHYPPLQYVAFALDTLLMFLYTAEMIAKMHIRGI     95
                        ******** ***.********** **********:*:**********************

Danio_rerio                     IKGENSYVKDRWCMFDGFMVVFLWVSLVLQVFEIAELVDQMSPWGMLRIPRALIMIRVFR    180
Marmota_marmota                       VKGDNSYVKDRWCVFDGFMVFCLWVSLVLQVFEIADIVDQMSPWGMLRIPRPLIMIRAFR    155
Tachyoryctes_splendens                VKGDSSYVKDRWCVFDGFMVFCLWVSLVLQVFEIADIVDQMSPWGMLRIPRPLIMIRAFR    155
Rattus_norvegicus                     VKGDSSYVKDRWCVFDGFMVFCLWVSLVLQVFEIADIVDQMSPWGMLRIPRPLIMIRAFR    155
Mus_musculus                          VKGDSSYVKDRWCVFDGFMVFCLWVSLVLQVFEIADIVDQMSPWGMLRIPRPLIMIRAFR    155
Nannospalax_galili                    VKGDSSYVKDRWCVFDGFMVFCLWVSLVLQVFEIADIVDQMSPWGMLRIPRPLIMIRAFR    155
Homo_sapiens                          VKGDSSYVKDRWCVFDGFMVFCLWVSLVLQVFEIADIVDQMSPWGMLRIPRPLIMIRAFR    155
Pan_troglodytes                       VKGDSSYVKDRWCVFDGFMVFCLWVSLVLQVFEIADIVDQMSPWGMLRIPRPLIMIRAFR    155
Cavia_porcellus                       VKGDSSYVKDRWCVFDGFMVFCLWVSLVLQVFEIADIVDQMSPWGMLRIPRPLIMIRAFR    155
Heterocephalus_glaber                 VKGDSSYVKDRWCVFDGFMVFCLWVSLVLQVFEIADIVDQMSPWGMLRIPRPLIMIRAFR    155
Georychus_capensis                    VKGDNSYVKDRWCVFDGFMVFCLWVSLVLQVFEIADIVDQMSPWGMLRIPRPLIMIRAFR    155
Heliophobius_emini                    VKGDSSYVKDRWCVFDGFMVFCLWVSLVLQVFEIADIVDQMSPWGMLRIPRPLIMIRAFR    155
Fukomys_damarensis                    VKGDSSYVKDRWCVFDGFMVFCLWVSLVLQVFEIADIVDQMSPWGMLRIPRPLIMIRAFR    155
Cryptomys_hottentotus_hottentotus     VKGDSSYVKDRWCVFDGFMVFCLWVSLVLQVFEIADIVDQMSPWGMLRIPRPLIMIRAFR    155
Cryptomys_hottentotus_mahali          VKGDSSYVKDRWCVFDGFMVFCLWVSLVLQVFEIADIVDQMSPWGMLRIPRPLIMIRAFR    155
Cryptomys_hottentotus_pretoriae       VKGDSSYVKDRWCVFDGFMVFCLWVSLVLQVFEIADIVDQMSPWGMLRIPRPLIMIRAFR    155
Cryptomys_hottentotus_natalensis      VKGDSSYVKDRWCVFDGFMVFCLWVSLVLQVFEIADIVDQMSPWGMLRIPRPLIMIRAFR    155
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Danio_rerio                     IYFRFELPRSRITNILKRSGEQIWSVTIFLLFFLLLYGILGVQMFGTFNHHCVTNETEKE    240
Marmota_marmota                       IYFRFELPRTRITNILKRSGEQIWSVSIFLLFFLLLYGILGVQMFGTFTYHCVVNDTKPG    215
Tachyoryctes_splendens                IYFRFELPRTRITNILKRSGEQIWSVSIFLLFFLLLYGILGVQMFGTFTYHCVVNDTKPG    215
Rattus_norvegicus                     IYFRFELPRTRITNILKRSGEQIWSVSIFLLFFLLLYGILGVQMFGTFTYHCVVNDTKPG    215
Mus_musculus                          IYFRFELPRTRITNILKRSGEQIWSVSIFLLFFLLLYGILGVQMFGTFTYHCVVNDTKPG    215
Nannospalax_galili                    IYFRFELPRTRITNILKRSGEQIWSVSIFLLFFLLLYGILGVQMFGTFTYHCVVNDTKPG    215
Homo_sapiens                          IYFRFELPRTRITNILKRSGEQIWSVSIFLLFFLLLYGILGVQMFGTFTYHCVVNDTKPG    215
Pan_troglodytes                       IYFRFELPRTRITNILKRSGEQIWSVSIFLLFFLLLYGILGVQMFGTFTYHCVVNDTKPG    215
Cavia_porcellus                       IYFRFELPRTRITNILKRSGEQIWSVSIFLIFFLLLYGILGVQMFGTFTYHCVVNDTKPG    215
Heterocephalus_glaber                 IYFRFELPRTRITNILKRSGEQIWSVSIFLIFFLLLYGILGVQMFGTFTYHCVVNDTKPG    215
Georychus_capensis                    IYFRFELPRTRITNILKRSGEQIWSVSIFLIFFLLLYGILGVQMFGTFTYHCVVNDTKPG    215
Heliophobius_emini                    IYFRFELPRTRITNILKRSGEQIWSVSIFLIFFLLLYGILGVQMFGTFTYHCVVNDTKPG    215
Fukomys_damarensis                    IYFRFELPRTRITNILKRSGEQIWSVSIFLIFFLLLYGILGVQMFGTFTYHCVVNDTKPG    215
Cryptomys_hottentotus_hottentotus     IYFRFELPRTRITNILKRSGEQIWSVSIFLIFFLLLYGILGVQMFGTFTYHCVVNDTKPG    215
Cryptomys_hottentotus_mahali          IYFRFELPRTRITNILKRSGEQIWSVSIFLIFFLLLYGILGVQMFGTFTYHCVVNDTKPG    215
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Cryptomys_hottentotus_pretoriae      IYFRFELPRTRITNILKRSGEQIWSVSIFLIFFLLLYGILGVQMFGTFTYHCVVNDTKPG   215
Cryptomys_hottentotus_natalensis     IYFRFELPRTRITNILKRSGEQIWSVSIFLIFFLLLYGILGVQMFGTFTYHCVVNDTKPG   215
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Danio_rerio                    KVTWNSLAIPDTHCSPN-GEGYQCPVGFKCVDLEDYGLSRQELGYSGFNELGTSIFTVYE   299
Marmota_marmota                    NVTWNSLAIPDTHCSPELEEGYQCPPGFKCMDLEDLGLSRQELGYSGFNEIGTSIFTVYE   275
Tachyoryctes_splendens              NVTWNSLAIPDTHCSPELEEGYQCPPGFKCMDLEDLGLSRQELGYSGFNEIGTSIFTVYE   275
Rattus_norvegicus                 NVTWNSLAIPDTHCSPELEEGYQCPPGFKCMDLEDLGLSRQELGYSGFNEIGTSIFTVYE   275
Mus_musculus                      NVTWNSLAIPDTHCSPELEEGYQCPPGFKCMDLEDLGLSRQELGYSGFNEIGTSIFTVYE   275
Nannospalax_galili                NVTWNSLAIPDTHCSPELEEGYQCPPGFKCMDLEDLGLSRQELGYSGFNEIGTSIFTVYE   275
Homo_sapiens                      NVTWNSLAIPDTHCSPELEEGYQCPPGFKCMDLEDLGLSRQELGYSGFNEIGTSIFTVYE   275
Pan_troglodytes                   NVTWNSLAIPDTHCSPELEEGYQCPPGFKCMDLEDLGLSRQELGYSGFNEIGTSIFTVYE   275
Cavia_porcellus                   NVTWNSLAIPDTHCSPELEEGYQCPPGFKCMDLEDLGLSRQELGYSGFNEIGTSIFTVYE   275
Heterocephalus_glaber              NVTWNSLAIPDTHCSPELEEGYQCPAGFKCMDLEDLGLSRQELGYSGFNEIGTSIFTVYE   275
Georychus_capensis                NVTWNSLAIPDTHCSPELEEGYQCPPGFKCMDLEDLGLSRQELGYSGFNEIGTSIFTVYE   275
Heliophobius_emini                NVTWNSLAIPDTHCSPELEEGYQCPPGFKCMDLEDLGLSRQELGYSGFNEIGTSIFTVYE   275
Fukomys_damarensis                NVTWNSLAIPDTHCSPELEEGYQCPPGFKCMDLEDLGLSRQELGYSGFNEIGTSIFTVYE   275
Cryptomys_hottentotus_hottentotus     NVTWNSLAIPDTHCSPELEEGYQCPPGFKCMDLEDLGLSRQELGYSGFNEIGTSIFTVYE   275
Cryptomys_hottentotus_mahali          NVTWNSLAIPDTHCSPELEEGYQCPPGFKCMDLEDLGLSRQELGYSGFNEIGTSIFTVYE   275
Cryptomys_hottentotus_pretoriae       NVTWNSLAIPDTHCSPELEEGYQCPPGFKCMDLEDLGLSRQELGYSGFNEIGTSIFTVYE   275
Cryptomys_hottentotus_natalensis      NVTWNSLAIPDTHCSPELEEGYQCPPGFKCMDLEDLGLSRQELGYSGFNEIGTSIFTVYE   275
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Danio_rerio                    AASQEGWVFIMYRAIDSFPRWRSYFYFLTLIFFLAWLVKNVFIAVIIETFAEIRVQFQQM   359
Marmota_marmota                    AASQEGWVFLMYRAIDSFPRWRSYFYFITLIFFLAWLVKNVFIAVIIETFAEIRVQFQQM   335
Tachyoryctes_splendens              ASSQEGWVFLMYRAIDSFPHWRSYFYFITLIFFLAWLVKNVFIAVIIETFAEIRVQFQQM   335
Rattus_norvegicus                 ASSQEGWVFLMYRAIDSFPRWRSYFYFITLIFFLAWLVKNVFIAVIIETFAEIRVQFQQM   335
Mus_musculus                      ASSQEGWVFLMYRAIDSFPRWRSYFYFITLIFFLAWLVKNVFIAVIIETFAEIRVQFQQM   335
Nannospalax_galili                ASSQEGWVFLMYRAIDSFPRWRSYFYFITLIFFLAWLVKNVFIAVIIETFAEIRVQFQQM   335
Homo_sapiens                      AASQEGWVFLMYRAIDSFPRWRSYFYFITLIFFLAWLVKNVFIAVIIETFAEIRVQFQQM   335
Pan_troglodytes                   AASQEGWVFLMYRAIDSFPRWRSYFYFITLIFFLAWLVKNVFIAVIIETFAEIRVQFQQM   335
Cavia_porcellus                   ASSQEGWVFLMYRAIDSFPCWRSYFYFITLIFFLAWLVKNVFIAVIIETFAEIRVQFQQM   335
Heterocephalus_glaber              ASSQEGWVFLMYRAIDSFPCWRSYFYFITLIFFLAWLVKNVFIAVIIETFAEIRVQFQQM   335
Georychus_capensis                ASSQEGWVFLMYRAIDSFPCWRSYFYFITLIFFLAWLVKNVFIAVIIETFAEIRVQFQQM   335
Heliophobius_emini                ASSQEGWVFLMYRAIDSFPCWRSYFYFITLIFFLAWLVKNVFIAVIIETFAEIRVQFQQM   335
Fukomys_damarensis                ASSQEGWVFLMYRAIDSFPCWRSYFYFITLIFFLAWLVKNVFIAVIIETFAEIRVQFQQM   335
Cryptomys_hottentotus_hottentotus     ASSQEGWVFLMYRAIDSFPCWRSYFYFITLIFFLAWLVKNVFIAVIIETFAEIRVQFQQM   335
Cryptomys_hottentotus_mahali          ASSQEGWVFLMYRAIDSFPCWRSYFYFITLIFFLAWLVKNVFIAVIIETFAEIRVQFQQM   335
Cryptomys_hottentotus_pretoriae       ASSQEGWVFLMYRAIDSFPCWRSYFYFITLIFFLAWLVKNVFIAVIIETFAEIRVQFQQM   335
Cryptomys_hottentotus_natalensis      ASSQEGWVFLMYRAIDSFPCWRSYFYFITLIFFLAWLVKNVFIAVIIETFAEIRVQFQQM   335
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Danio_rerio                    WGSRSSTTSTATTQMFHEDASGGWQLVAVDVNKPHGRAPACLQQLMRSSVFHMFILSMVA   419
Marmota_marmota                    WGSRSSTTSTATTQMFHEDAAGGWQLVAVDVNKPQGRAPACLQKMMRSSVFHMFILSMVT   395
Tachyoryctes_splendens              WGTRSSTTSTATTQMFHEDTSGGWQLVAVDVNKPQGRAPACLQKMMRSSVFHMFILSMVT   395
Rattus_norvegicus                 WGTRSSTTSTATTQMFHEDAAGGWQLVAVDVNKPQGRAPACLQKMMRSSVFHMFILSMVT   395
Mus_musculus                      WGTRSSTTSTATTQMFHEDAAGGWQLVAVDVNKPQGRAPACLQKMMRSSVFHMFILSMVT   395
Nannospalax_galili                WGTRSSTTSTATTQMFHEDTSGGWQLVAVDVNKPQGRAPACLQKMMRSSVFHMFILSMVT   395
Homo_sapiens                      WGSRSSTTSTATTQMFHEDAAGGWQLVAVDVNKPQGRAPACLQKMMRSSVFHMFILSMVT   395
Pan_troglodytes                   WGSRSSTTSTATTQMFHEDAAGGWQLVAVDVNKPQGRAPACLQKMMRSSVFHMFILSMVT   395
Cavia_porcellus                   WGSRSSTTSTATTQMFHEDAAGGWQLVAVDVNKPQGRAPACLQKMMRSSVFHMFILSMVT   395
Heterocephalus_glaber              WGSRSSTTSTATTQMFHEDAAGGWQLVAVDVNKPQGRAPACLQKMMRSSVFHMFILSMVT   395
Georychus_capensis                WGSRSSTTSTATTQMFHEDAAGGWQLVAVDVNKPQGRAPACLQKMMRSSVFHMFILSMVT   395
Heliophobius_emini                WGSRSSTTSTATTQMFHEDAAGGWQLVAVDVNKPQGRAPACLQKMMRSSVFHMFILSMVT   395
Fukomys_damarensis                WGSRSSTTSTATTQMFHEDAAGGWQLVAVDVNKPQGRAPACLQKMMRSSVFHMFILSMVT   395
Cryptomys_hottentotus_hottentotus     WGSRSSTTSTATTQMFHEDAAGGWQLVAVDVNKPQGRAPACLQKMMRSSVFHMFILSMVT   395
Cryptomys_hottentotus_mahali          WGSRSSTTSTATTQMFHEDAAGGWQLVAVDVNKPQGRAPACLQKMMRSSVFHMFILSMVT   395
Cryptomys_hottentotus_pretoriae       WGSRSSTTSTATTQMFHEDAAGGWQLVAVDVNKPQGRAPACLQKMMRSSVFHMFILSMVT   395
Cryptomys_hottentotus_natalensis      WGSRSSTTSTATTQMFHEDAAGGWQLVAVDVNKPQGRAPACLQKMMRSSVFHMFILSMVT   395
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Danio_rerio                    VDVIVAASNYHRGDH-KLTNDEFYLAEVAFTVLFDLEALLKIWCLGFTGYISSSLHKFES   478
Marmota_marmota                    VDVIVAASNYYKGENFRRQYDEFYLAEVAFTVLFDLEALLKIWCLGFTGYISSSLHKFEL   455
Tachyoryctes_splendens              VDVIVAASNYYKGENFRSQYDEFYLAEVAFTVLFDLEALLKIWCLGFTGYISSSLHKFEL   455
Rattus_norvegicus                 VDVIVAASNYYKGENFRRQYDEFYLAEVAFTVLFDLEALLKIWCLGFTGYISSSLHKFEL   455
Mus_musculus                      VDVIVAASNYYKGENFRRQYDEFYLAEVAFTVLFDLEALLKIWCLGFTGYISSSLHKFEL   455
Nannospalax_galili                VDVIVAASNYYKGENFRRQYDEFYLAEVAFTVLFDLEALLKIWCLGFTGYISSSLHKFEL   455
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Homo_sapiens                    VDVIVAASNYYKGENFRRQYDEFYLAEVAFTVLFDLEALLKIWCLGFTGYISSSLHKFEL    455
Pan_troglodytes                 VDVIVAASNYYKGENFRRQYDEFYLAEVAFTVLFDLEALLKIWCLGFTGYISSSLHKFEL    455
Cavia_porcellus                 VDVIVAASNYYKGENFRRQYDEFYLAEVAFTVLFDLEALLKIWCLGFTGYISSSLHKFEL    455
Heterocephalus_glaber           VDVIVAASNYYKGENFRRQYDEFYLAEVAFTVLFDLEALLKIWCLGFTGYISSSLHKFEL    455
Georychus_capensis              VDVIVAASNYYKGENFRRQYDEFYLAEVAFTVLFDLEALLKIWCLGFTGYISSSLHKFEL    455
Heliophobius_emini              VDVIVAASNYYKGENFRRQYDEFYLAEVAFTVLFDLEALLKIWCLGFTGYISSSLHKFEL    455
Fukomys_damarensis              VDVIVAASNYYKGENFRRQYDEFYLAEVAFTVLFDLEALLKIWCLGFTGYISSSLHKFEL    455
Cryptomys_hottentotus_hottentotus    VDVIVAASNYYKGENFRRQYDEFYLAEVAFTVLFDLEALLKIWCLGFTGYISSSLHKFEL    455
Cryptomys_hottentotus_mahali        VDVIVAASNYYKGENFRRQYDEFYLAEVAFTVLFDLEALLKIWCLGFTGYISSSLHKFEL    455
Cryptomys_hottentotus_pretoriae     VDVIVAASNYYKGENFRRQYDEFYLAEVAFTVLFDLEALLKIWCLGFTGYISSSLHKFEL    455
Cryptomys_hottentotus_natalensis    VDVIVAASNYYKGENFRRQYDEFYLAEVAFTVLFDLEALLKIWCLGFTGYISSSLHKFEL    455
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Danio_rerio                     LLVVGTTLHIYPDLYHSQFTYFQVLRVVRLIKISPALEDFVYKIFGPGKKLGSLVVFTAS    538
Marmota_marmota                 LLVVGTTLHVYPDLYHSQFTYFQVLRVVRLIKISPALEDFVYKIFGPGKKLGSLVVFTAS    515
Tachyoryctes_splendens          LLVVGTTLHVYPGLYHSQFTYFQVLRVVRLIKISPALEDFVYKIFGPGKKLGSLVVFTAS    515
Rattus_norvegicus               LLVIGTTLHVYPDLYHSQFTYFQVLRVVRLIKISPALEDFVYKIFGPGKKLGSLVVFTAS    515
Mus_musculus                    LLVIGTTLHVYPDLYHSQFTYFQVLRVVRLIKISPALEDFVYKIFGPGKKLGSLVVFTAS    515
Nannospalax_galili              LLVIGTTLHVYPGLYHSQFTYFQVLRVVRLIKISPALEDFVYKIFGPGKKLGSLVVFTAS    515
Homo_sapiens                    LLVIGTTLHVYPDLYHSQFTYFQVLRVVRLIKISPALEDFVYKIFGPGKKLGSLVVFTAS    515
Pan_troglodytes                 LLVIGTTLHVYPDLYHSQFTYFQVLRVVRLIKISPALEDFVYKIFGPGKKLGSLVVFTAS    515
Cavia_porcellus                 LLVVGTTLHVYPDLYHSQFTYFQVLRVVRLIKISPALEDFVYKIFGPGKKLGSLVVFTAS    515
Heterocephalus_glaber           LLVIGTTLHVYPDLYHSQFTYFQVLRVVRLIKISPALEDFVYKIFGPGKKLGSLVVFTAS    515
Georychus_capensis              LLVIGTTLHVYPDLYHSQFTYFQVLRVVRLIKISPALEDFVYKIFGPGKKLGSLVVFTAS    515
Heliophobius_emini              LLVIGTTLHVYPDLYHSQFTYFQVLRVVRLIKISPALEDFVYKIFGPGKKLGSLVVFTAS    515
Fukomys_damarensis              LLVIGTTLHVYPDLYHSQFTYFQVLRVVRLIKISPALEDFVYKIFGPGKKLGSLVVFTAS    515
Cryptomys_hottentotus_hottentotus    LLVIGTTLHVYPDLYHSQFTYFQVLRVVRLIKISPALEDFVYKIFGPGKKLGSLVVFTAS    515
Cryptomys_hottentotus_mahali        LLVIGTTLHVYPDLYHSQFTYFQVLRVVRLIKISPALEDFVYKIFGPGKKLGSLVVFTAS    515
Cryptomys_hottentotus_pretoriae     LLVIGTTLHVYPDLYHSQFTYFQVLRVVRLIKISPALEDFVYKIFGPGKKLGSLVVFTAS    515
Cryptomys_hottentotus_natalensis    LLVIGTTLHVYPDLYHSQFTYFQVLRVVRLIKISPALEDFVYKIFGPGKKLGSLVVFTAS    515
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Danio_rerio                     LLIVMSAISLQMFCFVEDLDRFTTFPRAFMSMFQILTQEGWVDVMDQTLVAVGQMWAPVV    598
Marmota_marmota                 LLIVMSAISLQMFCFVEELDRFTTFPRAFMSMFQILTQEGWVDVMDQTLNAVGHMWAPVV    575
Tachyoryctes_splendens          LLIVMSSISLQMFCFVEELDRFTTFPRAFMSMFQILTQEGWVDVMDQTLNAVGHMWAPVV    575
Rattus_norvegicus               LLIVMSAISLQMFCFVEELDRFTTFPRAFMSMFQILTQEGWVDVMDQTLNAVGHMWAPLV    575
Mus_musculus                    LLIVMSAISLQMFCFVEELDRFTTFPRAFMSMFQILTQEGWVDVMDQTLNAVGHMWAPLV    575
Nannospalax_galili              LLIVMSAISLQMFCFVEELDRFTTFPRAFMSMFQILTQEGWVDVMDQTLNAVGHMWAPVV    575
Homo_sapiens                    LLIVMSAISLQMFCFVEELDRFTTFPRAFMSMFQILTQEGWVDVMDQTLNAVGHMWAPVV    575
Pan_troglodytes                 LLIVMSAISLQMFCFVEELDRFTTFPRAFMSMFQILTQEGWVDVMDQTLNAVGHMWAPVV    575
Cavia_porcellus                 LLIVMSAISLQMFCFVEELDRFTTFPRAFMSMFQILTQEGWVDVMDQTLNAVGHMWAPVV    575
Heterocephalus_glaber           LLIVMSAISLQMFCFVEELDRFTTFPRAFMSMFQILTQEGWVDVMDQTLNAVGHMWAPVV    575
Georychus_capensis              LLIVMSAISLQMFCFVEELDRFTTFPRAFMSMFQILTQEGWVDVMDQTLNAVGHMWAPVV    575
Heliophobius_emini              LLIVMSAISLQMFCFVEELDRFTTFPRAFMSMFQILTQEGWVDVMDQTLNAVGHMWAPVV    575
Fukomys_damarensis              LLIVMSAISLQMFCFVEELDRFTTFPRAFMSMFQILTQEGWVDVMDQTLNAVGHMWAPVV    575
Cryptomys_hottentotus_hottentotus    LLIVMSAISLQMFCFVEELDRFTTFPRAFMSMFQILTQEGWVDVMDQTLNAVGHMWAPVV    575
Cryptomys_hottentotus_mahali        LLIVMSAISLQMFCFVEELDRFTTFPRAFMSMFQILTQEGWVDVMDQTLNAVGHMWAPVV    575
Cryptomys_hottentotus_pretoriae     LLIVMSAISLQMFCFVEELDRFTTFPRAFMSMFQILTQEGWVDVMDQTLNAVGHMWAPVV    575
Cryptomys_hottentotus_natalensis    LLIVMSAISLQMFCFVEELDRFTTFPRAFMSMFQILTQEGWVDVMDQTLNAVGHMWAPVV    575
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Danio_rerio                     AIYFILYHLFATLILLSLFVAVILDNLELDEDLKKLKQLKQSEANADTKEKLPLRLRIFE    658
Marmota_marmota                 AIYFILYHLFATLILLSLFVAVILDNLELDEDLKKLKQLKQSEANADTKEKLPLRLRIFE    635
Tachyoryctes_splendens          AIYFILYHLFATLILLSLFVAVILDNLELDEDLKKLKQLKQSEANADTKEKLPLRLRIFE    635
Rattus_norvegicus               AIYFILYHLFATLILLSLFVAVILDNLELDEDLKKLKQLKQSEANADTKEKLPLRLRIFE    635
Mus_musculus                    AIYFILYHLFATLILLSLFVAVILDNLELDEDLKKLKQLKQSEANADTKEKLPLRLRIFE    635
Nannospalax_galili              AIYFILYHLFATLILLSLFVAVILDNLELDEDLKKLKQLKQSEANADTKEKLPLRLRIFE    635
Homo_sapiens                    AIYFILYHLFATLILLSLFVAVILDNLELDEDLKKLKQLKQSEANADTKEKLPLRLRIFE    635
Pan_troglodytes                 AIYFILYHLFATLILLSLFVAVILDNLELDEDLKKLKQLKQSEANADTKEKLPLRLRIFE    635
Cavia_porcellus                 AIYFILYHLFATLILLSLFVAVILDNLELDEDLKKLKQLKQSEANADTKEKLPLRLRIFE    635
Heterocephalus_glaber           AIYFILYHLFATLILLSLFVAVILDNLELDEDLKKLKQLKQSEANADTKEKLPLRLRIFE    635
Georychus_capensis              AIYFILYHLFATLILLSLFVAVILDNLELDEDLKKLKQLKQSEANADTKEKLPLRLRIFE    635
Heliophobius_emini              AIYFILYHLFATLILLSLFVAVILDNLELDEDLKKLKQLKQSEANADTKEKLPLRLRIFE    635
Fukomys_damarensis              AIYFILYHLFATLILLSLFVAVILDNLELDEDLKKLKQLKQSEANADTKEKLPLRLRIFE    635
Cryptomys_hottentotus_hottentotus    AIYFILYHLFATLILLSLFVAVILDNLELDEDLKKLKQLKQSEANADTKEKLPLRLRIFE    635
Cryptomys_hottentotus_mahali        AIYFILYHLFATLILLSLFVAVILDNLELDEDLKKLKQLKQSEANADTKEKLPLRLRIFE    635
Cryptomys_hottentotus_pretoriae     AIYFILYHLFATLILLSLFVAVILDNLELDEDLKKLKQLKQSEANADTKEKLPLRLRIFE    635
Cryptomys_hottentotus_natalensis    AIYFILYHLFATLILLSLFVAVILDNLELDEDLKKLKQLKQSEANADTKEKLPLRLRIFE    635
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Danio_rerio                     KFPNRPQMVKISKLPSDFTVPRIRESFMKQFIDRQQQDPSCLFRRLPSASSSSCDHSKRS    718
Marmota_marmota                 KFPNRPQMVKISKLPSDFTVPKIRESFMKQFIDRQQQDTCCLFRILPSASSSSCDHSKRS    695
Tachyoryctes_splendens          KFPNRPQMVKISKLPSDFTVPKIRESFMKQFIDRQQQDTCCLFRILPSTSSSSSDQAKKA    695
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Rattus_norvegicus                KFPNRPQMVKISKLPSDFTVPKIRESFMKQFIDRQQQDTCCLFRILPSTSSSSCDNPKRP    695
Mus_musculus                     KFPNRPQMVKISKLPSDFTVPKIRESFMKQFIDRQQQDTCCLFRILPSTSSSSCDNPKKP    695
Nannospalax_galili               KFPNRPQMVKISKLPSDFTVPKIRESFMKQFIDRQQQDTCCLFRILPSTSSSSCDQAKKS    695
Homo_sapiens                     KFPNRPQMVKISKLPSDFTVPKIRESFMKQFIDRQQQDTCCLLRSLPTTSSSSCDHSKRS    695
Pan_troglodytes                  KFPNRPQMVKISKLPSDFTVPKIRESFMKQFIDRQQQDTCCLLRSLPTTSSSSCDHSKRS    695
Cavia_porcellus                  KFPNRPQMVKISKLPSDFTVPKIRESFMKQFIDRQQQDTCCLFRILPSASSSSCDHSKRS    695
Heterocephalus_glaber            KFPNRPQMVKISKLPSDFTVPKIRESFMKQFIDRQQQDTCCLFRILPSTSSSSCDHSKRS    695
Georychus_capensis               KFPNRPQMVKISKLPSDFTVPKIRESFMKQFIDRQQQDTCCLFRILPSASSSSCDHSKRS    695
Heliophobius_emini               KFPNRPQMVKISKLPSDFTVPKIRESFMKQFIDRQQQDTCCLFRILPSASSSSCDHSKRS    695
Fukomys_damarensis               KFPNRPQMVKISKLPSDFTVPKIRESFMKQFIDRQQQDTCCLFRILPSASSSSCDHSKRS    695
Cryptomys_hottentotus_hottentotus    KFPNRPQMVKISKLPSDFTVPKIRESFMKQFIDRQQQDTCCLFRILPSASSSSCDHSKRS    695
Cryptomys_hottentotus_mahali         KFPNRPQMVKISKLPSDFTVPKIRESFMKQFIDRQQQDTCCLFRILPSASSSSCDHSKRS    695
Cryptomys_hottentotus_pretoriae      KFPNRPQMVKISKLPSDFTVPKIRESFMKQFIDRQQQDTCCLFRILPSASSSSCDHSKRS    695
Cryptomys_hottentotus_natalensis     KFPNRPQMVKISKLPSDFTVPKIRESFMKQFIDRQQQDTCCLFRILPSASSSSCDHSKRS    695
                     **********.********** .**.* **.:****.*: *:

Danio_rerio                  A-IEDNKYIDQKLRKSVFSIRARNLMEKEITVNKILRACTRQRMLSGSFEGQPTKERSIL    777
Marmota_marmota                  A-IEDNKYIDQKLRKSVFSIRARNLLEKETAVTKILRACTRQRMLSGSFEGQPAKERSIL    754
Tachyoryctes_splendens           T-NEDNKYIDQKLRKSVFSIRARNLLEKEAAVTKILRSCTRQRMLSGSFDGQPAKERSIL    754
Rattus_norvegicus                TV-EDNKYIDQKLRKSVFSIRARNLLEKETAVTKILRACTRQRMLSGSFEGQPAKERSIL    754
Mus_musculus                     TA-EDNKYIDQKLRKSVFSIRARNLLEKETAVTKILRACTRQRMLSGSFEGQPAKERSIL    754
Nannospalax_galili               TGEDNNKYINRRLRKSVFSIRARNLLEKEAAVTKILRACTRQRMLSGSFEGQPAKERSIL    755
Homo_sapiens                     AI-EDNKYIDQKLRKSVFSIRARNLLEKETAVTKILRACTRQRMLSGSFEGQPAKERSIL    754
Pan_troglodytes                  AI-EDNKYIDQKLRKSVFSIRARNLLEKETAVTKILRACTRQRMLSGSFEGQPAKERSIL    754
Cavia_porcellus                  AI-EDNKYIDQKLRKSVFSIRARNLLEKETAVTKILRACTRQRMLSGSFEGQPAKERSIL    754
Heterocephalus_glaber            AI-EDNKYIDQKLRKSVFSIRARNLLEKETAVTKILRACTRQRMLSGSFEGQPAKERSIL    754
Georychus_capensis               AI-EDNKYIDQKLRKSVFSIRARNLLEKETAVTKILRACTRQRMLSGSFEGQPAKERSIL    754
Heliophobius_emini               AI-EDNKYIDQKLRKSVFSIRARNLLEKETAVTKILRACTRQRMLSGSFEGQPAKERSIL    754
Fukomys_damarensis               AI-EDNKYIDQKLRKSVFSIRARNLLEKETAVTKILRACTRQRMLSGSFEGQPTKERSIL    754
Cryptomys_hottentotus_hottentotus    AI-EDNKYIDQKLRKSVFSIRARNLLEKETAVTKILRACTRQRMLSGSFEGQPAKERSIL    754
Cryptomys_hottentotus_mahali         AI-EDNKYIDQKLRKSVFSIRARNLLEKETAVTKILRACTRQRMLSGSFEGQPAKERSIL    754
Cryptomys_hottentotus_pretoriae      AI-EDNKYIDQKLRKSVFSIRARNLLEKETAVTKILRACTRQRMLSGSFEGQPAKERSIL    754
Cryptomys_hottentotus_natalensis     AI-EDNKYIDQKLRKSVFSIRARNLLEKETAVTKILRACTRQRMLSGSFEGQPAKERSIL    754
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Danio_rerio                  SVQHHIRQERRSLRHGSTSQRISRGKSLETLTQDHSSTVRYRNAQREDSEIKMIQEKKEQ    837
Marmota_marmota                  SVQHHIRQERRSLRHGSNSQRISRGKSLETLTQDHSNTVRYRNAQREDSEIKMIQEKKEQ    814
Tachyoryctes_splendens           SVQHHIRQERRSLRHGSNSQRISRGKSLETLTQDHSNTVRYRNAQREDSEIKMIQEKKEQ    814
Rattus_norvegicus                SVQHHIRQERRSLRHGSNSQRISRGKSLETLTQDHSNTVRYRNAQREDSEIKMIQEKKEQ    814
Mus_musculus                     SVQHHIRQERRSLRHGSNSQRISRGKSLETLTQDHSNTVRYRNAQREDSEIKMIQEKKEQ    814
Nannospalax_galili               SVQHHIRQERRSLRHGSNSQRISRGKSLETLTQDHSNTVRYRNAQREDSEIKMIQEKKEQ    815
Homo_sapiens                     SVQHHIRQERRSLRHGSNSQRISRGKSLETLTQDHSNTVRYRNAQREDSEIKMIQEKKEQ    814
Pan_troglodytes                  SVQHHIRQERRSLRHGSNSQRISRGKSLETLTQDHSNTVRYRNAQREDSEIKMIQEKKEQ    814
Cavia_porcellus                  SVQHHIRQERRSLRHGSNSQRISRGKSLETLTQDHSNTVRYRNAQREDSEIKMIQEKKEQ    814
Heterocephalus_glaber            SVQHHIRQERRSLRHGSNSQRISRGKSLETLTQDHSNTVRYRNAQREDSEIKMIQEKKEQ    814
Georychus_capensis               SVQHHIRQERRSLRHGSNSQRISRGKSLETLTQDHSSTVRYRNAQREDSEIKMIQEKKEQ    814
Heliophobius_emini               SVQHHIRQERRSLRHGSNSQRISRGKSLETLTQDHSSTVRYRNAQREDSEIKMIQEKKEQ    814
Fukomys_damarensis               SVQHHIRQERRSLRHGSNSQRISRGKSLETLTQDHSSTVRYRNAQREDSEIKMIQEKKEQ    814
Cryptomys_hottentotus_hottentotus    SVQHHIRQERRSLRHGSNSQRISRGKSLETLTQDHSSTVRYRNAQREDSEIKMIQEKKEQ    814
Cryptomys_hottentotus_mahali         SVQHHIRQERRSLRHGSNSQRISRGKSLETLTQDHSSTVRYRNAQREDSEIKMIQEKKEQ    814
Cryptomys_hottentotus_pretoriae      SVQHHIRQERRSLRHGSNSQRISRGKSLETLTQDHSSTVRYRNAQREDSEIKMIQEKKEQ    814
Cryptomys_hottentotus_natalensis     SVQHHIRQERRSLRHGSNSQRISRGKSLETLTQDHSSTVRYRNAQREDSEIKMIQEKKEQ    814
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Danio_rerio                  AEMKRKVQEEELRENHPYFDKPLFIVGREHRFRNFCRMIVRARFNASNTDPNTGAVNSTK    897
Marmota_marmota                  AEMKRKVQEEELRENHPYFDKPLFIVGREHRFRNLCRVVVRARFNASKTDPVTGAVKNTK    874
Tachyoryctes_splendens           AEMKRKVQEEELRENHPYFDKPLFIVGREHRFRNFCRLVVRARFNVSKTDPVTGAVKNTK    874
Rattus_norvegicus                AEMKRKVQEEELRENHPYFDKPLFIVGREHRFRNFCRVVVRARFNASKTDPVTGAVKNTK    874
Mus_musculus                     AEMKRKVQEEELRENHPYFDKPLFIVGREHRFRNFCRVVVRARFNASKTDPVTGAVKNTK    874
Nannospalax_galili               AEMKRKVQEEELRENHPYFDKPLFIVGREHRFRNFCRVVVRARFNASKTDPVTGAVKNTK    875
Homo_sapiens                     AEMKRKVQEEELRENHPYFDKPLFIVGREHRFRNFCRVVVRARFNASKTDPVTGAVKNTK    874
Pan_troglodytes                  AEMKRKVQEEELRENHPYFDKPLFIVGREHRFRNFCRVVVRARFNASKTDPVTGAVKNTK    874
Cavia_porcellus                  AEMKRKVQEEELRENHPYFDKPLFIVGREHRFRNFCRVVVRARFNASKTDPVTGAVKNTK    874
Heterocephalus_glaber            AEMKRKVQEEELRENHPYFDKPLFIVGREHRFRNFCRVVVRARFNASKTDPVTGAVKNTK    874
Georychus_capensis               AEMKRKVQEEELRENHPYFDKPLFIVGREHRFRNFCRAVVRARFNASKTDPVTGAVKNTK    874
Heliophobius_emini               AEMKRKVQEEELRENHPYFDKPLFIVGREHRFRNFCRAVVRARFNASKTDPVTGAVKNTK    874
Fukomys_damarensis               AEMKRKVQEEELRENHPYFDKPLFIVGREHRFRNFCRAVVRARFNASKTDPVTGAVKNTK    874
Cryptomys_hottentotus_hottentotus    AEMKRKVQEEELRENHPYFDKPLFIVGREHRFRNFCRAVVRARFNASKTDPVTGAVKNTK    874
Cryptomys_hottentotus_mahali         AEMKRKVQEEELRENHPYFDKPLFIVGREHRFRNFCRAVVRARFNASKTDPVTGAVKNTK    874
Cryptomys_hottentotus_pretoriae      AEMKRKVQEEELRENHPYFDKPLFIVGREHRFRNFCRAVVRARFNASKTDPVTGAVKNTK    874
Cryptomys_hottentotus_natalensis     AEMKRKVQEEELRENHPYFDKPLFIVGREHRFRNFCRAVVRARFNASKTDPVTGAVKNTK    874
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Danio_rerio                  YHQLYDLLGLVTYLDWVMIVVTICSCISMMFESPFTRVMHVPTLQIGEYVFVIFMSIELN    957
Marmota_marmota                  YHQLYDLLGLVTYLDWVMIIVTICSCISMMFESPFRRVMHAPTLQIAEYVFVIFMSIELN    934
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Tachyoryctes_splendens            YHQLYDLLGLVTYLDWVMIIVTICSCISMMFESPFRRVMHTPTLQIAEYVFVIFMSIELN   934
Rattus_norvegicus                 YHQLYDLLGLVTYLDWVMITVTICSCISMMFESPFRRVMHAPTLQIAEYVFVIFMSIELN   934
Mus_musculus                      YHQLYDLLGLVTYLDWVMITVTICSCISMMFESPFRRVMHAPTLQIAEYVFVIFMSIELN   934
Nannospalax_galili                YHQLYDLLGLVTYLDWVMIIVTICSCISMMFESPFRRVMHAPTLQIAEYVFVIFMSIELN   935
Homo_sapiens                      YHQLYDLLGLVTYLDWVMIIVTICSCISMMFESPFRRVMHAPTLQIAEYVFVIFMSIELN   934
Pan_troglodytes                   YHQLYDLLGLVTYLDWVMIIVTICSCISMMFESPFRRVMHAPTLQIAEYVFVIFMSIELN   934
Cavia_porcellus                   YHQLYDLLGLVTYLDWVMIIVTICSCISMMFESPFRRVMHAPTLQIAEYVFVIFMSIELN   934
Heterocephalus_glaber             YHQLYDLLGLVTYLDWVMIVVTICSCISMMFESPFRRVMHAPTLQIAEYVFVIFMSIELN   934
Georychus_capensis                YHQLYDLLGLVTYLDWVMIVVTICSCISMMFESPFRRVMHAPTLQIAEYVFVIFMSIELN   934
Heliophobius_emini                YHQLYDLLGLVTYLDWVMIVVTICSCISMMFESPFRRVMHAPTLQIAEYVFVIFMSIELN   934
Fukomys_damarensis                YHQLYDLLGLVTYLDWVMIIVTICSCISMMFESPFRRVMHAPTLQIAEYVFVIFMSIELN   934
Cryptomys_hottentotus_hottentotus YHQLYDLLGLVTYLDWVMIIVTICSCISMMFESPFRRVMHAPTLQIAEYVFVIFMSIELN   934
Cryptomys_hottentotus_mahali      YHQLYDLLGLVTYLDWVMIIVTICSCISMMFESPFRRVMHAPTLQIAEYVFVIFMSIELN   934
Cryptomys_hottentotus_pretoriae   YHQLYDLLGLVTYLDWVMIIVTICSCISMMFESPFRRVMHAPTLQIAEYVFVIFMSIELN   934
Cryptomys_hottentotus_natalensis  YHQLYDLLGLVTYLDWVMIIVTICSCISMMFESPFRRVMHAPTLQIAEYVFVIFMSIELN   934
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Danio_rerio                    LKIMADGLFFTPTAVIRDFGGVMDIFIYLVSLIFLCWLPNNVPPESGAQLLMMLRCFRPL   1017
Marmota_marmota                LKIMADGLFFTPTAVIRDFGGVMDIFIYLVSLIFLCWMPQNVPAESGAQLLMVLRCLRPL   994
Tachyoryctes_splendens         LKIMADGLFFTPTAVIRDFGGVMDIFIYLVSLIFLCWMPQNVPPNSGAQLLMVLRCLRPL   994
Rattus_norvegicus              LKIMADGLFFTPTAVIRDFGGVMDIFIYLVSLIFLCWMPQNVPAESGAQLLMVLRCLRPL   994
Mus_musculus                   LKIMADGLFFTPTAVIRDFGGVMDIFIYLVSLIFLCWMPQNVPAESGAQLLMVLRCLRPL   994
Nannospalax_galili             LKIMADGLFFTPTAVIRDFGGVMDIFIYLVSLIFLCWMPQNVPAESGAQLLMVLRCLRPL   995
Homo_sapiens                   LKIMADGLFFTPTAVIRDFGGVMDIFIYLVSLIFLCWMPQNVPAESGAQLLMVLRCLRPL   994
Pan_troglodytes                LKIMADGLFFTPTAVIRDFGGVMDIFIYLVSLIFLCWMPQNVPAESGAQLLMVLRCLRPL   994
Cavia_porcellus                LKIMADGLFFTPTAVIRDFGGVMDIFIYLVSLIFLCWMPQNVPAESGAQLLMVLRCLRPL   994
Heterocephalus_glaber          LKIMADGLFFTPTAVIRDFGGVMDIFIYLVSLIFLCWMPQNVPAESGAQLLMVLRCLRPL   994
Georychus_capensis             LKIMADGLFFTPTAVIRDFGGVMDIFIYLVSLIFLCWMPQNVPAESGAQLLMVLRCLRPL   994
Heliophobius_emini             LKIMADGLFFTPTAVIRDFGGVMDIFIYLVSLIFLCWMPQNVPAESGAQLLMVLRCLRPL   994
Fukomys_damarensis             LKIMADGLFFTPTAVIRDFGGVMDIFIYLVSLIFLCWMPQNVPAESGAQLLMVLRCLRPL   994
Cryptomys_hottentotus_hottentotus LKIMADGLFFTPTAVIRDFGGVMDIFIYLVSLIFLCWMPQNVRAESGAQLLMVLRCLRPL   994
Cryptomys_hottentotus_mahali   LKIMADGLFFTPTAVIRDFGGVMDIFIYLVSLIFLCWMPQNVRAESGAQLLMVLRCLRPL   994
Cryptomys_hottentotus_pretoriae LKIMADGLFFTPTAVIRDFGGVMDIFIYLVSLIFLCWMPQNVRAESGAQLLMVLRCLRPL   994
Cryptomys_hottentotus_natalensis LKIMADGLFFTPTAVIRDFGGVMDIFIYLVSLIFLCWMPQNVRAESGAQLLMVLRCLRPL   994
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Danio_rerio                    RIFKLVPQMRKVVREVLKGFKEIFLVSILLLTLMLVFATFGVQLFAGKLAKCNDPHISSK   1077
Marmota_marmota                RIFKLVPQMRKVVRELFSGFKEIFLVSILLLTLMLVFASFGVQLFAGKLAKCNDPNIIRR   1054
Tachyoryctes_splendens         RIFKLVPQMRKVVRELFSGFKEIFLVSILLLTLMLVFASFGVQLFAGKLAKCNDPDIIRR   1054
Rattus_norvegicus              RIFKLVPQMRKVVRELFSGFKEIFLVSILLLTLMLVFASFGVQLFAGKLAKCNDPNIIRR   1054
Mus_musculus                   RIFKLVPQMRKVVRELFSGFKEIFLVSILLLTLMLVFASFGVQLFAGKLAKCNDPNIIRR   1054
Nannospalax_galili             RIFKLVPQMRKVVRELFSGFKEIFLVSILLLTLMLVFASFGVQLFAGKLAKCNDPYIIRR   1055
Homo_sapiens                   RIFKLVPQMRKVVRELFSGFKEIFLVSILLLTLMLVFASFGVQLFAGKLAKCNDPNIIRR   1054
Pan_troglodytes                RIFKLVPQMRKVVRELFSGFKEIFLVSILLLTLMLVFASFGVQLFAGKLAKCNDPNIIRR   1054
Cavia_porcellus                RIFKLVPQMRKVVRELFSGFKEIFLVSILLLTLMLVFASFGVQLFAGKLAKCNDPNIIRR   1054
Heterocephalus_glaber          RIFKLVPQMRKVVRELFSGFKEIFLVSILLLTLMLVFASFGVQLFAGKLAKCNDPNIIRR   1054
Georychus_capensis             RIFKLVPQMRKVVRELFSGFKEIFLVSILLLTLMLVFASFGVQLFAGKLAKCNDPNIIRR   1054
Heliophobius_emini             RIFKLVPQMRKVVRELFSGFKEIFLVSILLLTLMLVFASFGVQLFAGKLAKCNDPNIIRR   1054
Fukomys_damarensis             RIFKLVPQMRKVVRELFSGFKEIFLVSILLLTLMLVFASFGVQLFAGKLAKCNDPNIIRR   1054
Cryptomys_hottentotus_hottentotus RIFKLVPQMRKVVRELFSGFKEIFLVSILLLTLMLVFASFGVQLFAGKLAKCNDPNIIRR   1054
Cryptomys_hottentotus_mahali   RIFKLVPQMRKVVRELFSGFKEIFLVSILLLTLMLVFASFGVQLFAGKLAKCNDPNIIRR   1054
Cryptomys_hottentotus_pretoriae RIFKLVPQMRKVVRELFSGFKEIFLVSILLLTLMLVFASFGVQLFAGKLAKCNDPNIIRR   1054
Cryptomys_hottentotus_natalensis RIFKLVPQMRKVVRELFSGFKEIFLVSILLLTLMLVFASFGVQLFAGKLAKCNDPNIIRR   1054
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Danio_rerio                    DDCHGIFRINVSISKNLNLKLKDGEKKPGFWVPRVWANPRNFNFDNVGNAMLALFEVLSL   1137
Marmota_marmota                EDCNGIFRINVSVSKNLNLKLRPGEKKPGFWVPRVWANPRNFNFDNVGNAMLALFEVLSL   1114
Tachyoryctes_splendens         EDCHGIFRINVSVSKNLNLKLKPGQKKPGFWVPRVWANPRNFNFDNVGNAMLALFEVLSL   1114
Rattus_norvegicus              EDCNGIFRINVSVSKNLNLKLRPGEKKPGFWVPRVWANPRNFNFDNVGNAMLALFEVLSL   1114
Mus_musculus                   EDCNGIFRINVSVSKNLNLKLRPGEKKPGFWVPRVWANPRNFNFDNVGNAMLALFEVLSL   1114
Nannospalax_galili             EDCNGIFRINVSVSKNLNLKLKPGEKKPGFWVPRVWANPRNFNFDNVGNAMLALFEVLSL   1115
Homo_sapiens                   EDCNGIFRINVSVSKNLNLKLRPGEKKPGFWVPRVWANPRNFNFDNVGNAMLALFEVLSL   1114
Pan_troglodytes                EDCNGIFRINVSVSKNLNLKLRPGEKKPGFWVPRVWANPRNFNFDNVGNAMLALFEVLSL   1114
Cavia_porcellus                EDCNGIFRINVSVSKNLNLKLKPGEKKPGFWVPRVWANPRNFNFDNVGNAMLALFEVLSL   1114
Heterocephalus_glaber          EDCNGIFRINVSVSKNLNLKLRPGEKKPGFWVPRVWANPRNFNFDNVGNAMLALFEVLSL   1114
Georychus_capensis             EDCNGIFRINVSVSKNLNLKLRPGEKKPGFWVPRVWANPRNFNFDNVGNAMLALFEVLSL   1114
Heliophobius_emini             EDCNGIFRINVSVSKNLNLKLRPGEKKPGFWVPRVWANPRNFNFDNVGNAMLALFEVLSL   1114
Fukomys_damarensis             EDCSGIFRINVSVSKNLNLKLRPGEKKPGFWVPRVWANPRNFNFDNVGNAMLALFEVLSL   1114
Cryptomys_hottentotus_hottentotus EDCSGIFRINVSVSKNLNLKLRPGEKKPGFWVPRVWANPRNFNFDNVGNAMLALFEVLSL   1114
Cryptomys_hottentotus_mahali   EDCSGIFRINVSVSKNLNLKLRPGEKKPGFWVPRVWANPRNFNFDNVGNAMLALFEVLSL   1114
Cryptomys_hottentotus_pretoriae EDCSGIFRINVSVSKNLNLKLRPGEKKPGFWVPRVWANPRNFNFDNVGNAMLALFEVLSL   1114
Cryptomys_hottentotus_natalensis EDCSGIFRINVSVSKNLNLKLRPGEKKPGFWVPRVWANPRNFNFDNVGNAMLALFEVLSL   1114
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Danio_rerio                    KGWVEVRDVIIHRVGPIHGIYIHVFVFLGCMIGLTLFVGVVIANFNENKGTALLTVDQRR    1197
Marmota_marmota                  KGWVEVRDVIIHRVGPIHGIYIHVFVFLGCMIGLTLFVGVVIANFNENKGTALLTVDQRR    1174
Tachyoryctes_splendens           KGWVEVRDVIIHRVGPIHGIYIHVFVFLGCMIGLTLFVGVVIANFNENKGTALLTVDQRR    1174
Rattus_norvegicus                KGWVEVRDVIIHRVGPIHGIYIHVFVFLGCMIGLTLFVGVVIANFNENKGTALLTVDQRR    1174
Mus_musculus                     KGWVEVRDVIIHRVGPIHGIYIHVFVFLGCMIGLTLFVGVVIANFNENKGTALLTVDQRR    1174
Nannospalax_galili               KGWVEVRDVIIHRVGPIHGIYIHVFVFLGCMIGLTLFVGVVIANFNENKGTALLTVDQRR    1175
Homo_sapiens                     KGWVEVRDVIIHRVGPIHGIYIHVFVFLGCMIGLTLFVGVVIANFNENKGTALLTVDQRR    1174
Pan_troglodytes                  KGWVEVRDVIIHRVGPIHGIYIHVFVFLGCMIGLTLFVGVVIANFNENKGTALLTVDQRR    1174
Cavia_porcellus                  KGWVEVRDVIIHRVGPIHGIYIHVFVFLGCMIGLTLFVGVVIANFNENKGTALLTVDQRR    1174
Heterocephalus_glaber            KGWVEVRDVIIHRVGPIHGIYIHVFVFLGCMIGLTLFVGVVIANFNENKGTALLTVDQRR    1174
Georychus_capensis               KGWVEVRDVIIHRVGPIHGIYIHVFVFLGCMIGLTLFVGVVIANFNENKGTALLTVDQRR    1174
Heliophobius_emini               KGWVEVRDVIIHRVGPIHGIYIHVFVFLGCMIGLTLFVGVVIANFNENKGTALLTVDQRR    1174
Fukomys_damarensis               KGWVEVRDVIIHRVGPIHGIYIHVFVFLGCMIGLTLFVGVVIANFNENKGTALLTVDQRR    1174
Cryptomys_hottentotus_hottentotus  KGWVEVRDVIIHRVGPIHGIYIHVFVFLGCMIGLTLFVGVVIANFNENKGTALLTVDQRR  1174
Cryptomys_hottentotus_mahali     KGWVEVRDVIIHRVGPIHGIYIHVFVFLGCMIGLTLFVGVVIANFNENKGTALLTVDQRR    1174
Cryptomys_hottentotus_pretoriae  KGWVEVRDVIIHRVGPIHGIYIHVFVFLGCMIGLTLFVGVVIANFNENKGTALLTVDQRR    1174
Cryptomys_hottentotus_natalensis KGWVEVRDVIIHRVGPIHGIYIHVFVFLGCMIGLTLFVGVVIANFNENKGTALLTVDQRR    1174
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Danio_rerio                    WEDLKSRLKIAQPLHLPPRPENGGFRAKMYDITQHPFFKRGIAVLVLAQSVLLSVKWDEL    1257
Marmota_marmota                  WEDLKSRLKIAQPLHLPPRPDNDGFRAKMYDITQHPFFKRTIALLVLAQSVLLSVKWDVE    1234
Tachyoryctes_splendens           WEDLKSRLKIAQPLHLPPRPDNDGFRAKMYDITQHPFFKRTIALLVLAQSVLLSVKWDVE    1234
Rattus_norvegicus                WEDLKSRLKIAQPLHLPPRPDNDGFRAKMYDITQHPFFKRTIALLVLAQSVLLSVKWDVE    1234
Mus_musculus                     WEDLKSRLKIAQPLHLPPRPDNDGFRAKMYDITQHPFFKRTIALLVLAQSVLLSVKWDVD    1234
Nannospalax_galili               WEDLKSRLKIAQPLHLPPRPDNDGFRAKMYDITQHPFFKRTIALLVLAQSVLLSVKWDVE    1235
Homo_sapiens                     WEDLKSRLKIAQPLHLPPRPDNDGFRAKMYDITQHPFFKRTIALLVLAQSVLLSVKWDVE    1234
Pan_troglodytes                  WEDLKSRLKIAQPLHLPPRPDNDGFRAKMYDITQHPFFKRTIALLVLAQSVLLSVKWDVE    1234
Cavia_porcellus                  WEDLKSRLKIAQPLHLPPRPDNDGFRAKMYDITQHPFFKRTIALLVLAQSVLLSVKWDVE    1234
Heterocephalus_glaber            WEDLKSRLKIAQPLHLPPRPDNDGFRAKMYDITQHPFFKRTIALLVLAQSVLLSVKWDVE    1234
Georychus_capensis               WEDLKSRLKIAQPLHLPPRPDNDGFRAKMYDITQHPFFKRTIALLVLAQSVLLSVKWDVE    1234
Heliophobius_emini               WEDLKSRLKIAQPLHLPPRPDNDGFRAKMYDITQHPFFKRTIALLVLAQSVLLSVKWDVE    1234
Fukomys_damarensis               WEDLKSRLKIAQPLHLPPRPDNDGFRAKMYDITQHPFFKRTIALLVLAQSVLLSVKWDVE    1234
Cryptomys_hottentotus_hottentotus  WEDLKSRLKIAQPLHLPPRPDNDGFRAKMYDITQHPFFKRTIALLVLAQSVLLSVKWDVE  1234
Cryptomys_hottentotus_mahali     WEDLKSRLKIAQPLHLPPRPDNDGFRAKMYDITQHPFFKRTIALLVLAQSVLLSVKWDVE    1234
Cryptomys_hottentotus_pretoriae  WEDLKSRLKIAQPLHLPPRPDNDGFRAKMYDITQHPFFKRTIALLVLAQSVLLSVKWDVE    1234
Cryptomys_hottentotus_natalensis WEDLKSRLKIAQPLHLPPRPDNDGFRAKMYDITQHPFFKRTIALLVLAQSVLLSVKWDVE    1234
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Danio_rerio                    GAVTFPLATMSVVFTFIFVLEVTMKLIAMSPAGYWQSRRNRYDLLVTSLGLIWIILHFAL    1317
Marmota_marmota                    ----VPLATMSVVFTFIFVLEVTMKIIAMSPAGFWQSRRNRYDLLVTSLGVVWVVLHFAL    1290
Tachyoryctes_splendens             ----VPLATMSVVFTFIFVLEVTMKIIAMSPAGFWQSRRNRYDLLVTSLGVVWVVLHFAL    1290
Rattus_norvegicus                  ----VPLATMSVVFTFIFVLEVTMKIIAMSPAGFWQSRRNRYDLLVTSLGVVWVVLHFAL    1290
Mus_musculus                       ----VPLATMSVVFTFIFVLEVTMKIIAMSPAGFWQSRRNRYDLLVTSLGVVWVVLHFAL    1290
Nannospalax_galili                 ----VPLATMSVVFTFIFVLEVTMKIIAMSPAGFWQSRRNRYDLLVTSLGVVWVVLHFAL    1291
Homo_sapiens                     DPVTVPLATMSVVFTFIFVLEVTMKIIAMSPAGFWQSRRNRYDLLVTSLGVVWVVLHFAL    1294
Pan_troglodytes                  DPVTVPLATMSVVFTFIFVLEVTMKIIAMSPAGFWQSRRNRYDLLVTSLGVVWVVLHFAL    1294
Cavia_porcellus                    ----VPLATMSVVFTFIFVLEVTMKIIAMSPAGFWQSRRNRYDLLVTSLGVVWVVLHFAL    1290
Heterocephalus_glaber              ----VPLATMSVVFTFIFVLEVTMKIIAMSPAGFWQSRRNRYDLLVTSLGVVWVVLHFAL    1290
Georychus_capensis                 ----VPLATMSVVFTFIFVLEVTMKIIAMSPAGFWQSRRNRYDLLVTSLGVVWVVLHFAL    1290
Heliophobius_emini                 ----VPLATMSVVFTFIFVLEVTMKIIAMSPAGFWQSRRNRYDLLVTSLGVVWVVLHFAL    1290
Fukomys_damarensis                 ----VPLATMSVVFTFIFVLEVTMKIIAMSPAGFWQSRRNRYDLLVTSLGVVWVVLHFAL    1290
Cryptomys_hottentotus_hottentotus  ----VPLATMSVVFTFIFVLEVTMKIIAMSPAGFWQSRRNRYDLLVTSLGVVWVVLHFAL  1290
Cryptomys_hottentotus_mahali       ----VPLATMSVVFTFIFVLEVTMKIIAMSPAGFWQSRRNRYDLLVTSLGVVWVVLHFAL    1290
Cryptomys_hottentotus_pretoriae    ----VPLATMSVVFTFIFVLEVTMKIIAMSPAGFWQSRRNRYDLLVTSLGVVWVVLHFAL    1290
Cryptomys_hottentotus_natalensis   ----VPLATMSVVFTFIFVLEVTMKIIAMSPAGFWQSRRNRYDLLVTSLGVVWVVLHFAL    1290
                                 .*******************.********.****************:.*:.*****

Danio_rerio                    QNAYTYMMGTCVIVFRFFTICGKHVTLKMLLLTVVVSMYKSFFIIVGMFLLLLCYAFAGV    1377
Marmota_marmota                  LNAYTYMMGACVIVFRFFSICGKHVTLKMLLLTVVVSMYKSFFIIVGMFLLLLCYAFAGV    1350
Tachyoryctes_splendens           QNAYTYMMGACVIVFRFFSICGKHVTLKMLLLTVVVSMYKSFFIIVGMFLLLLCYAFAGV    1350
Rattus_norvegicus                LNAYTYMMGACVIVFRFFSICGKHVTLKMLLLTVVVSMYKSFFIIVGMFLLLLCYAFAGV    1350
Mus_musculus                     LNAYTYMMGACVIVFRFFSICGKHVTLKMLLLTVVVSMYKSFFIIVGMFLLLLCYAFAGV    1350
Nannospalax_galili               LNAYTYMMGACVIVFRFFSICGKHVTLKMLLLTVVVSMYKSFFIIVGMFLLLLCYAFAGV    1351
Homo_sapiens                     LNAYTYMMGACVIVFRFFSICGKHVTLKMLLLTVVVSMYKSFFIIVGMFLLLLCYAFAGV    1354
Pan_troglodytes                  LNAYTYMMGACVIVFRFFSICGKHVTLKMLLLTVVVSMYKSFFIIVGMFLLLLCYAFAGV    1354
Cavia_porcellus                  LNAYTYMMGACVIVFRFFSICGKHVTLKMLLLTVVVSMYKSFFIIVGMFLLLLCYAFAGV    1350
Heterocephalus_glaber            LNAYTYMMGACVIVFRFFSICGKHVTLKMLLLTVVVSMYKSFFIIVGMFLLLLCYAFAGV    1350
Georychus_capensis               LNAYTYMMGACVIVFRFFSICGKHVTLKMLLLTVVVSMYKSFFIIVGMFLLLLCYAFAGV    1350
Heliophobius_emini               LNAYTYMMGACVIVFRFFSICGKHVTLKMLLLTVVVSMYKSFFIIVGMFLLLLCYAFAGV    1350
Fukomys_damarensis               LNAYTYMMGACVIVFRFFSICGKHVTLKMLLLTVVVSMYKSFFIIVGMFLLLLCYAFAGV    1350
Cryptomys_hottentotus_hottentotus  LNAYTYMMGACVIVFRFFSICGKHVTLKMLLLTVVVSMYKSFFIIVGMFLLLLCYAFAGV  1350
Cryptomys_hottentotus_mahali     LNAYTYMMGACVIVFRFFSICGKHVTLKMLLLTVVVSMYKSFFIIVGMFLLLLCYAFAGV    1350
Cryptomys_hottentotus_pretoriae  LNAYTYMMGACVIVFRFFSICGKHVTLKMLLLTVVVSMYKSFFIIVGMFLLLLCYAFAGV    1350
Cryptomys_hottentotus_natalensis LNAYTYMMGACVIVFRFFSICGKHVTLKMLLLTVVVSMYKSFFIIVGMFLLLLCYAFAGV    1350
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Danio_rerio                   VLFGTVKYGENINRHANFSTAGKAITVLIRIVTGEDWNKIMHDCMVQPPFCTPDKHRYWE    1437
Marmota_marmota                    VLFGTVKYGENINRHANFSSAGKAITVLFRIVTGEDWNKIMHDCMVQPPFCTPDEFTYWA    1410
Tachyoryctes_splendens             VLFGTVKYGENINRHANFSSAGKAITVLFRIVTGEDWNKIMHDCMVQPPFCTPDDFTYWA    1410
Rattus_norvegicus                VLFGTVKYGENINRHANFSSAGKAITVLFRIVTGEDWNKIMHDCMVQPPFCTPDEFTYWA    1410
Mus_musculus                     VLFGTVKYGENINRHANFSSAGKAITVLFRIVTGEDWNKIMHDCMVQPPFCTPDEFTYWA    1410
Nannospalax_galili               VLFGTVKYGENINRHANFSSAGKAITVLFRIVTGEDWNKIMHDCMVQPPFCTPDEFTYWA    1411
Homo_sapiens                     VLFGTVKYGENINRHANFSSAGKAITVLFRIVTGEDWNKIMHDCMVQPPFCTPDEFTYWA    1414
Pan_troglodytes                  VLFGTVKYGENINRHANFSSAGKAITVLFRIVTGEDWNKIMHDCMVQPPFCTPDEFTYWA    1414
Cavia_porcellus                  VLFGTVKYGENINRHANFSSAGKAITVLFRIVTGEDWNKIMHDCMVQPPFCTPDEFTYWA    1410
Heterocephalus_glaber                VLFGTVKYGENINRHANFSSAGKAITVLFRIVTGEDWNKIMHDCMVQPPFCTPDEFTYWA    1410
Georychus_capensis                 VLFGTVKYGENINRHANFSSAGKAITVLFRIVTGEDWNKIMHDCMVQPPFCTPDEFTYWA    1410
Heliophobius_emini                 VLFGTVKYGENINRHANFSSAGKAITVLFRIVTGEDWNKIMHDCMVQPPFCTPDEFTYWA    1410
Fukomys_damarensis                   VLFGTVKYGENINRHANFSSAGKAITVLFRIVTGEDWNKIMHDCMVQPPFCTPDEFTYWA    1410
Cryptomys_hottentotus_hottentotus      VLFGTVKYGENINRHANFSSAGKAITVLFRIVTGEDWNKIMHDCMVQPPFCTPDEFTYWA    1410
Cryptomys_hottentotus_mahali         VLFGTVKYGENINRHANFSSAGKAITVLFRIVTGEDWNKIMHDCMVQPPFCTPDEFTYWA    1410
Cryptomys_hottentotus_pretoriae        VLFGTVKYGENINRHANFSSAGKAITVLFRIVTGEDWNKIMHDCMVQPPFCTPDEFTYWA    1410
Cryptomys_hottentotus_natalensis       VLFGTVKYGENINRHANFSSAGKAITVLFRIVTGEDWNKIMHDCMVQPPFCTPDEFTYWA    1410
                    ******************.********.************************.. **

Danio_rerio                   TDCGNYAGALIYFCSFYVIIAYIMLNLLVAIIVENFSLFYSTEEDQLLSYNDLRHFQIIW    1497
Marmota_marmota                    TDCGNYAGALMYFCSFYVIIAYIMLNLLVAIIVENFSLFYSTEEDQLLSYNDLRHFQIIW    1470
Tachyoryctes_splendens             TDCGNYGGALIYFCSFYLIIAYIMLNLLVAIIVENFSLFYSTEEDQLLSYNDLRHFQIIW    1470
Rattus_norvegicus                TDCGNYAGALMYFCSFYVIIAYIMLNLLVAIIVENFSLFYSTEEDQLLSYNDLRHFQIIW    1470
Mus_musculus                     TDCGNYAGALMYFCSFYVIIAYIMLNLLVAIIVENFSLFYSTEEDQLLSYNDLRHFQIIW    1470
Nannospalax_galili               TDCGNYAGALMYFCSFYVIIAYIMLNLLVAIIVENFSLFYSTEEDQLLSYNDLRHFQIIW    1471
Homo_sapiens                     TDCGNYAGALMYFCSFYVIIAYIMLNLLVAIIVENFSLFYSTEEDQLLSYNDLRHFQIIW    1474
Pan_troglodytes                  TDCGNYAGALMYFCSFYVIIAYIMLNLLVAIIVENFSLFYSTEEDQLLSYNDLRHFQIIW    1474
Cavia_porcellus                  TDCGNYAGALMYFCSFYVIIAYIMLNLLVAIIVENFSLFYSTEEDQLLSYNDLRHFQIIW    1470
Heterocephalus_glaber                TDCGNYAGALMYFCSFYVIIAYIMLNLLVAIIVENFSLFYSTEEDQLLSYNDLRHFQIIW    1470
Georychus_capensis                 TDCGNYAGALMYFCSFYVIIAYIMLNLLVAIIVENFSLFYSTEEDQLLSYNDLRHFQIIW    1470
Heliophobius_emini                 TDCGNYAGALMYFCSFYVIIAYIMLNLLVAIIVENFSLFYSTEEDQLLSYNDLRHFQIIW    1470
Fukomys_damarensis                   TDCGNYAGALMYFCSFYVIIAYIMLNLLVAIIVENFSLFYSTEEDQLLSYNDLRHFQIIW    1470
Cryptomys_hottentotus_hottentotus      TDCGNYAGALMYFCSFYVIIAYIMLNLLVAIIVENFSLFYSTEEDQLLSYNDLRHFQIIW    1470
Cryptomys_hottentotus_mahali         TDCGNYAGALMYFCSFYVIIAYIMLNLLVAIIVENFSLFYSTEEDQLLSYNDLRHFQIIW    1470
Cryptomys_hottentotus_pretoriae        TDCGNYAGALMYFCSFYVIIAYIMLNLLVAIIVENFSLFYSTEEDQLLSYNDLRHFQIIW    1470
Cryptomys_hottentotus_natalensis       TDCGNYAGALMYFCSFYVIIAYIMLNLLVAIIVENFSLFYSTEEDQLLSYNDLRHFQIIW    1470
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Danio_rerio                   NMVDDKREGVIPTSRVKFLLRLLRGRLEVDLDKDKLLFKHMCYEMERLHNGGDVTFHDVL    1557
Marmota_marmota                    NMVDDKREGVIPTFRVKFLLRLLRGRLEVDLDKDKLLFKHMCYEMERLHNGGDVTFHDVL    1530
Tachyoryctes_splendens             NMVDDKREGVIPTFRVKFLLRLLRGRLEVDLDKDKLLFKHMCYEMERLHNAGDVTFHDVL    1530
Rattus_norvegicus                NMVDDN-ERCDPTFRVKFLLRLLRGRLEVDLDKDKLLFKHMCYEMERLHNGGDVTFHDVL    1529
Mus_musculus                     NMVDDKREGVIPTFRVKFLLRLLRGRLEVDLDKDKLLFKHMCYEMERLHNGGDVTFHDVL    1530
Nannospalax_galili               NMVDDKREGVIPTFRVKFLLRLLRGRLEVDLDKDKLLFKHMCYEMERLHNGGDVTFHDVL    1531
Homo_sapiens                     NMVDDKREGVIPTFRVKFLLRLLRGRLEVDLDKDKLLFKHMCYEMERLHNGGDVTFHDVL    1534
Pan_troglodytes                  NMVDDKREGVIPTFRVKFLLRLLRGRLEVDLDKDKLLFKHMCYEMERLHNGGDVTFHDVL    1534
Cavia_porcellus                  NMVDDKREGVIPTFRVKFLLRLLRGRLEVDLDKDKLLFKHMCYEMERLHNGGDVTFHDVL    1530
Heterocephalus_glaber                NMVDDKREGVIPTFRVKFLLRLLRGRLEVDLDKDKLLFKHMCYEMERLHSGGDVTFHDVL    1530
Georychus_capensis                 NMVDDKREGVIPTFRVKFLLRLLRGRLEVDLDKDKLLFKHMCYEMERLHNGGDVTFHDVL    1530
Heliophobius_emini                 NMVDDKREGVIPTFRVKFLLRLLRGRLEVDLDKDKLLFKHMCYEMERLHNGGDVTFHDVL    1530
Fukomys_damarensis                   NMVDDKREGVIPTFRVKFLLRLLRGRLEVDLDKDKLLFKHMCYEMERLHNGGDVTFHDVL    1530
Cryptomys_hottentotus_hottentotus      NMVDDKREGVIPTFRVKFLLRLLRGRLEVDLDKDKLLFKHMCYEMERLHNGGDVTFHDVL    1530
Cryptomys_hottentotus_mahali         NMVDDKREGVIPTFRVKFLLRLLRGRLEVDLDKDKLLFKHMCYEMERLHNGGDVTFHDVL    1530
Cryptomys_hottentotus_pretoriae        NMVDDKREGVIPTFRVKFLLRLLRGRLEVDLDKDKLLFKHMCYEMERLHNGGDVTFHDVL    1530
Cryptomys_hottentotus_natalensis       NMVDDKREGVIPTFRVKFLLRLLRGRLEVDLDKDKLLFKHMCYEMERLHNGGDVTFHDVL    1530
                    *****:.* * ** ***********************************..*********

Danio_rerio                   SMLSYRSVDIRKSLQLEELLAREQLEYTIEEEVAKQTIRMWLKKCLKRIRAKQQQSCSII    1617
Marmota_marmota                    SMLSYRSVDIRKSLQLEELLAREQLEYTIEEEVAKQTIRMWLKKCLKRIRAKQQQSCSII    1590
Tachyoryctes_splendens             SMLSYRSVDIRKSLQLEELLAREQLEYTIEEEVAKQTIRMWLKKCLKRIRAKQQQSCSII    1590
Rattus_norvegicus                SMLSYRSVDIRKSLQLEELLAREQLEYTIEEEVAKQTIRMWLKKCLKRIRAKQQQSCSII    1589
Mus_musculus                     SMLSYRSVDIRKSLQLEELLAREQLEYTIEEEVAKQTIRMWLKKCLKRIRAKQQQSCSII    1590
Nannospalax_galili               SMLSYRSVDIRKSLQLEELLAREQLEYTIEEEVAKQTIRMWLKKCLKRIRAKQQQSCSII    1591
Homo_sapiens                     SMLSYRSVDIRKSLQLEELLAREQLEYTIEEEVAKQTIRMWLKKCLKRIRAKQQQSCSII    1594
Pan_troglodytes                  SMLSYRSVDIRKSLQLEELLAREQLEYTIEEEVAKQTIRMWLKKCLKRIRAKQQQSCSII    1594
Cavia_porcellus                  SMLSYRSVDIRKSLQLEELLAREQLEYTIEEEVAKQTIRMWLKKCLKRIRAKQQQSCSII    1590
Heterocephalus_glaber                SMLSYRSVDIRKSLQLEELLAREQLEYTIEEEVAKQTIRMWLKKCLKRIRAKQQQSCSII    1590
Georychus_capensis                 SMLSYRSVDIRKSLQLEELLAREQLEYTIEEEVAKQTIRMWLKKCLKRIRAKQQQSCSII    1590
Heliophobius_emini                 SMLSYRSVDIRKSLQLEELLAREQLEYTIEEEVAKQTIRMWLKKCLKRIRAKQQQSCSII    1590
Fukomys_damarensis                   SMLSYRSVDIRKSLQLEELLAREQLEYTIEEEVAKQTIRMWLKKCLKRIRAKQQQSCSII    1590
Cryptomys_hottentotus_hottentotus      SMLSYRSVDIRKSLQLEELLAREQLEYTIEEEVAKQTIRMWLKKCLKRIRAKQQQSCSII    1590
Cryptomys_hottentotus_mahali         SMLSYRSVDIRKSLQLEELLAREQLEYTIEEEVAKQTIRMWLKKCLKRIRAKQQQSCSII    1590
Cryptomys_hottentotus_pretoriae        SMLSYRSVDIRKSLQLEELLAREQLEYTIEEEVAKQTIRMWLKKCLKRIRAKQQQSCSII    1590
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Cryptomys_hottentotus_natalensis     SMLSYRSVDIRKSLQLEELLAREQLEYTIEEEVAKQTIRMWLKKCLKRIRAKQQQSCSII    1590
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Danio_rerio                    LSLRESQQQDLRR-LLNPPSIETTVPSEDTNTHNQDNPTQPENSGLQTLLSPTLSDRSGY    1676
Marmota_marmota                     HSLRESQQQELSR-FLNPPSIETTQPSEDTTANSQDPNMPPKTSSQQQLLSPTLSDRGGS    1649
Tachyoryctes_splendens              HSLRESQQQELSR-FLNPPSIETTQPSEDTNANSQDHNAPPETSSQQQLLSPTLSDRGGS    1649
Rattus_norvegicus                HSLRESQQQELSR-FLNPPSIETTQPSEDTNANSQDHNTQPESSSQQQLLSPTLSDRGGS    1648
Mus_musculus                     HSLRESQEQERSRLFLNPPSIETTQPSEDSNANSQDHSMQPETSSQQQLLSPTLSDRGGS    1650
Nannospalax_galili               HSLRESQQQELSR-FLNPPSIETTQPSEDTSANSQDHNTQPETSSQQQLLSPTLSDRGGN    1650
Homo_sapiens                     HSLRESQQQELSR-FLNPPSIETTQPSEDTNANSQDNSMQPETSSQQQLLSPTLSDRGGS    1653
Pan_troglodytes                  HSLRESQQQELSR-FLNPPSIETTQPSEDTNANSQDNSMQPETSSQQQLLSPTLSDRGGS    1653
Cavia_porcellus                  HSLRESQQQELSR-FLNPPSIETTQPSEDTNANSQDHNTQPETSSQQQLLSPTLSDRGGS    1649
Heterocephalus_glaber               HSLRESQQQELSR-FLNPPSIETTQPSEDTNASSQDHNMQPETSSQQQLLSPTLSDRGGS    1649
Georychus_capensis                HSLRESQQQELSR-FLNPPSIETTQPSEDTNASSQDHNMQPETSSQQQLLSPTLSDRGGS    1649
Heliophobius_emini                HSLRESQQQELSR-FLNPPSIETTQPSEDTNASSQDHSMQPETSSQQQLLSPTLSDRGGS    1649
Fukomys_damarensis                  HSLRESQQQELSR-FLNPPSIETTQPSEDTNASSQDHNMHPETSSQQQLLSPTLSDRGGS    1649
Cryptomys_hottentotus_hottentotus     HSLRESQQQELSR-FLNPPSIETTQPSEDTNASSQDHNMQPETSSQQQLLSPTLSDRGGS    1649
Cryptomys_hottentotus_mahali         HSLRESQQQELSR-FLNPPSIETTQPSEDTNASSQDHNMQPETSSQQQLLSPTLSDRGGS    1649
Cryptomys_hottentotus_pretoriae       HSLRESQQQELSR-FLNPPSIETTQPSEDTNASSQDHNMQPETSSQQQLLSPTLSDRGGS    1649
Cryptomys_hottentotus_natalensis      HSLRESQQQELSR-FLNPPSIETTQPSEDTNASSQDHNMQPETSSQQQLLSPTLSDRGGS    1649
                     ******:*:  * :********* ****:.: .**   *:.*. * *********.*

Danio_rerio                    RQDSA--DRPQRKLGQWRLPA----------------GRTSVKSMVCKMNPVTDEASSG    1717
Marmota_marmota                     RQDASEAEKPQRKVGQWCRPSDPSLPSQLPPAVTFPCGERIKMKSVVCKMNPVTDAASCG    1709
Tachyoryctes_splendens              RQDAADPGKPQRKFGQWRLPSAPKPISHSVSSVNLRFGGRTTMKSMVCKMNPMPDTASCG    1709
Rattus_norvegicus                RQDAADTGKPQRKIGQWRLPSAPKPISHSVSSVNLRFGGRTTMKSVVCKMNPMPDTASCG    1708
Mus_musculus                     RQDAADTGKPQRKIGQWRLPSAPKPISHSVSSVNLRFGGRTTMKTVVCKMNPMPDTASCG    1710
Nannospalax_galili               RQDAADPGKPQRKFGQWRLPSAPKPISHSVSSVNLRFGGRTTMKSVVCKMNPMPDTASCG    1710
Homo_sapiens                     RQDAADAGKPQRKFGQWRLPSAPKPISHSVSSVNLRFGGRTTMKSVVCKMNPMTDAASCG    1713
Pan_troglodytes                  RQDAADAGKPQRKFGQWRLPSAPKPISHSVSSVNLRFGGRTTMKSVVCKMNPMTDAASCG    1713
Cavia_porcellus                  RQDAGDAGKPQRKFGQWRLPSAPKPISHSVSSVNLRFGGRSTMKSVVCKMNPMTDTASCG    1709
Heterocephalus_glaber               RQDTGDAGKPQRKFGQWRLPSAPKPISHSVSSVNLRFGGRTTMKSVVCKVSPMTDTASCG    1709
Georychus_capensis                RQDTGDAGKPQRKFGQWRLPSAPKPISHSVSSVNLRFGGRTTVKSVVCKMNPMTDTASCG    1709
Heliophobius_emini                RQDTGDAGKPQRKFGQWRLPSAPKPISHSVSSVNLRFGGRTTMKSVVCKMNPMTDTASCG    1709
Fukomys_damarensis                  RQDTGDTGKPQRKFGQWRLPSAPKPISHSVSSVNLRFGGRTTMKSVVCKMNPMTDTASCG    1709
Cryptomys_hottentotus_hottentotus     RQDTGDAGKPQRKFGQWRLPSAPKPISHSVSSVNLRFGGRTTMKSVVCKMNPMTDTASCG    1709
Cryptomys_hottentotus_mahali         RQDTGDAGKPQRKFGQWRLPSAPKPISHSVSSVNLRFGGRTTMKSVVCKMNPMTDTASCG    1709
Cryptomys_hottentotus_pretoriae       RPDTGDAGKPQRKFGQWRLPSAPKPISHSVSSVNLRFGGRTTMKSVVCKMNPMTDTASCG    1709
Cryptomys_hottentotus_natalensis      RPDTGDAGKPQRKFGQWRLPSAPKPISHSVSSVNLRFGGRTTMKSVVCKMNPMTDTASCG    1709
                     * *:.  :****.*** *:           * .:*::***:.*:.* **.*

Danio_rerio                    SEVKKWWTRQLTVESDESGDDLIDI      1742
Marmota_marmota                     SEVKKWWTRQLTVESDESGDDLLDV      1734
Tachyoryctes_splendens              SEVKKWWTRQLTVESDESGDDLLDL      1734
Rattus_norvegicus                SEVKKWWTRQLTVESDESGDDLLDI      1733
Mus_musculus                     SEVKKWWTRQLTVESDESGDDLLDI      1735
Nannospalax_galili               SEVKKWWTRQLTVESDESGDDLLDI      1735
Homo_sapiens                     SEVKKWWTRQLTVESDESGDDLLDI      1738
Pan_troglodytes                  SEVKKWWTRQLTVESDESGDDLLDI      1738
Cavia_porcellus                  SEVKKWWTRQLTVESDESGDDLLDI      1734
Heterocephalus_glaber               SEVKKWWTRQLTVESDESEDDLLDI      1734
Georychus_capensis                SEVKKWWTRQLTVESDESGDDLLDI      1734
Heliophobius_emini                SEVKKWWTRQLTVESDESGDDLLDI      1734
Fukomys_damarensis                  SEVKKWWTRQLTVESDESGDDLLDI      1734
Cryptomys_hottentotus_hottentotus     SEVKKWWTRQLTVESDESGDDLLDI      1734
Cryptomys_hottentotus_mahali         SEVKKWWTRQLTVESDESGDDLLDI      1734
Cryptomys_hottentotus_pretoriae       SEVKKWWTRQLTVESDESGDDLLDI      1734
Cryptomys_hottentotus_natalensis      SEVKKWWTRQLTVESDESGDDLLDI      1734
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Fig. S7

NALCN alignment, Alignment of NALCN amino acid sequences from *Cryptomys* species against a range of NALCN sequences across the animal kingdom.

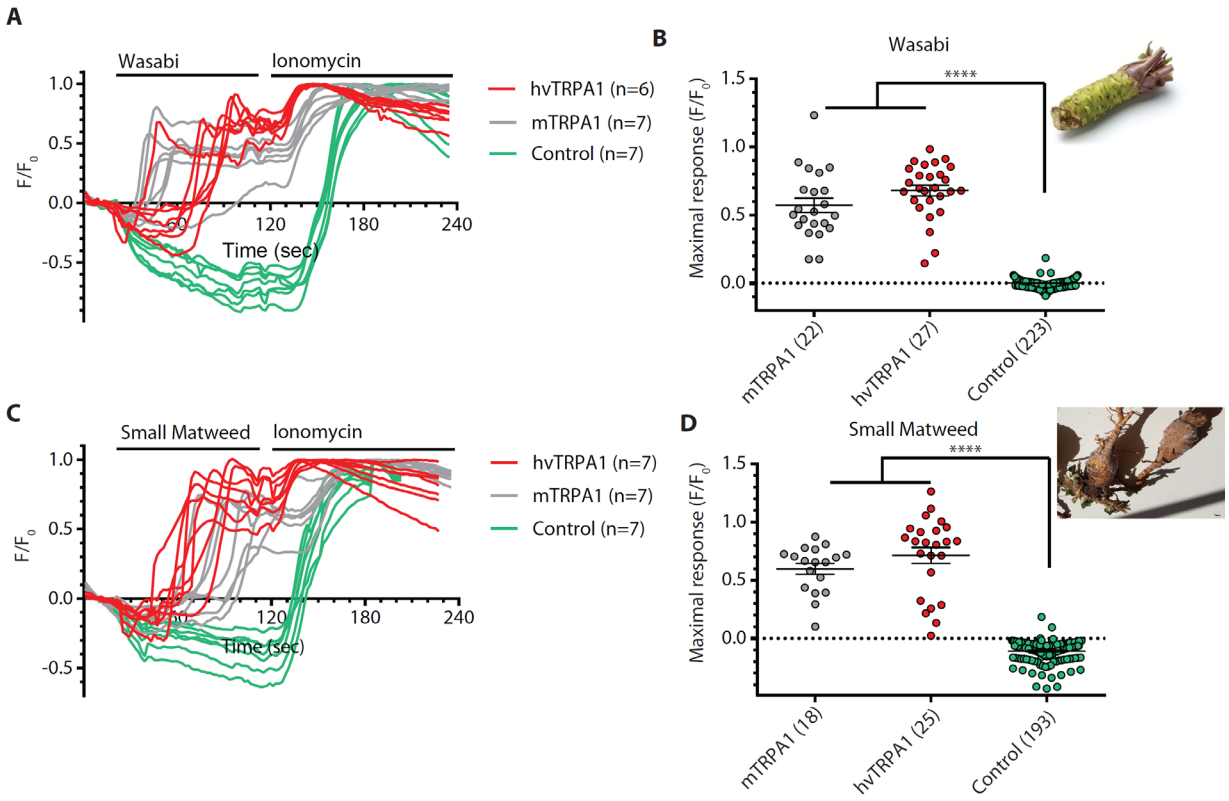

Fig. S8

Root extracts activate TRPA1 A) Representative calcium traces after application of a 10% (w/v) wasabi extract solution on HEK293 cells expressing TRPA1 from mouse (m) or Highveld mole-rats (hv). Every trace represents the data from 1 cell (n). B) Maximal fluorescence intensity was measured after application of the wasabi solution on the cells (n=number of cells from 3 different coverslips) (error bars indicate SEM; ****P ≤ 0.0001; Unpaired *t* test). C) and D) show the same for the Small matweed extract indicating there is a TRPA1 activating substance in plants found in the natural habitat of the Highveld mole-rat. Note that the calcium responses were as large as the ionomycin control indicating that TRPA1 channels were probably maximally activated with the concentration of the ligand found in the extract.

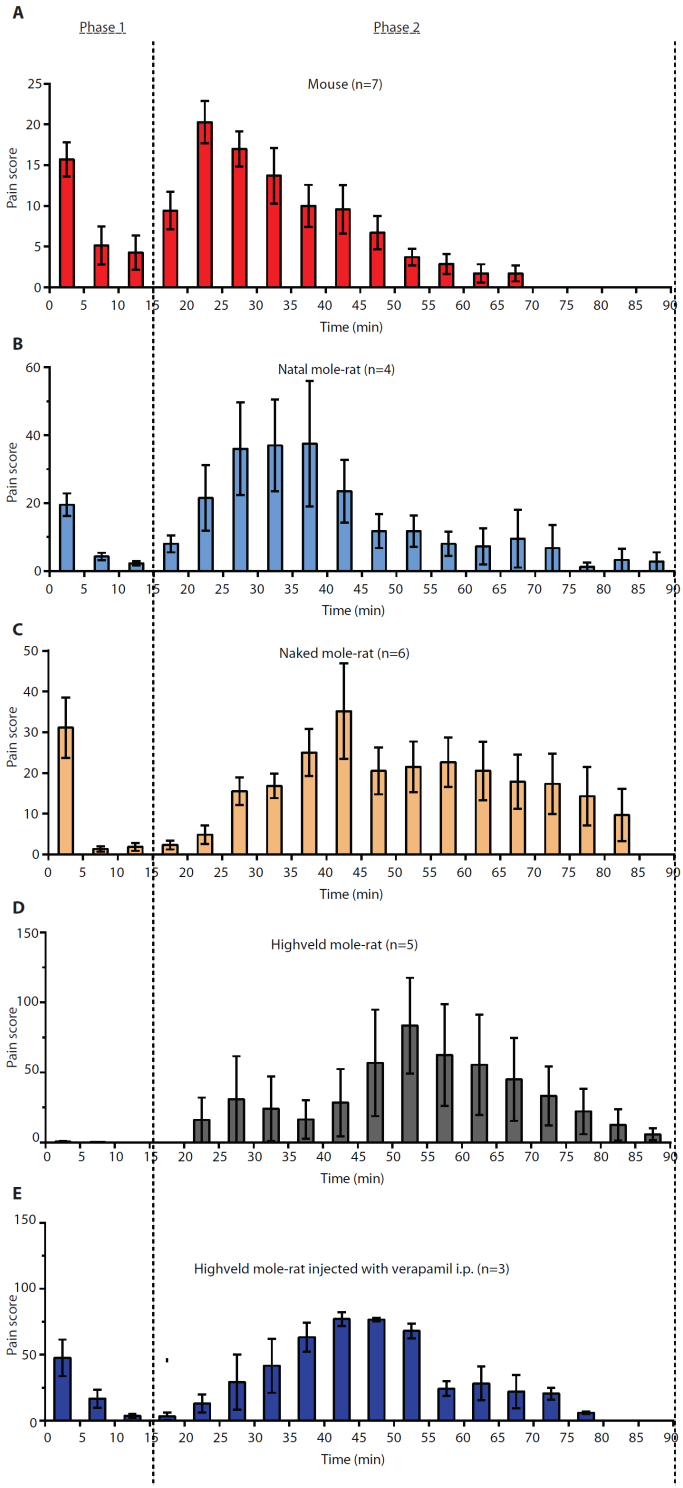

Fig. S9

Formalin Test in different African mole-rats. Frequency of pain behaviors after an injection of 2% Formalin into the paw. Phase 1 was defined as the response from 0-15 minutes, phase 2 from 15-90 minutes. Note that the magnitude of the pain behavior does vary across species but the time course of the response was very similar across species with the notable exception of the Highveld mole-rat.

Species	Number	Sex	Age/weigh t	Tissue sample	#read pairs	De novo assembly	Expression analysis
Mouse *Mus musculus*	M1	m	8 months	DRG, SC	188,962,096	no	yes
	M2	m	8 months	DRG, SC			
	M3	m	8 months	DRG, SC			
East African root rat *Tachyoryctes splendens*	RR1	m	380.8g	DRG, SC	211,112,254	yes	yes
	RR2	m	439.0g	DRG, SC			
	RR4	m	439.0g	DRG, SC			
Naked mole-rat *Heterocephalus glaber*	NMR1	m	6 years	SC	188,470,734	no	yes
	NMR2	m	6 years	SC			
	NMR3	m	6 years	SC			
	NMR1.2	m	59.2g	DRG			
	NMR2.2	m	70.4g	DRG			
	NMR3.2	m	56.6g	DRG			
Emin's mole-rat *Heliophobius emini*	He5	m	60g	DRG	187,929,353	yes	no
	He14	m	ND	DRG			
	He3.2	m	ND	Muscle			
	He5.2	m	ND	Brain			
	He7	m	ND	TGG			
Cape mole-rat *Georychus capensis*	G1	f	100.8g	DRG, SC	172,818,386	yes	yes
	G2	f	147.0g	DRG, SC			
	G3	f	138.7g	DRG, SC			
Common mole-rat *Cryptomys hottentotus hottentotus*	HH3	f	35.6g	DRG, SC	156,707,245	yes	yes
	HH4	f	40.3g	DRG, SC			
	HH5	f	47.1g	DRG, SC			
Mahali mole-rat *Cryptomys hottentotus mahali*	Ma8	m	125g	DRG, SC	229,281,786	yes	no
	Ma9	f	99.4g	DRG, SC			
	Ma10	f	57.5g	DRG, SC			
Natal mole-rat *Cryptomys hottentotus natalensis*	N1	f	72.0g	DRG, SC	181,402,359	yes	yes
	N2	f	74.0g	SC			
	N3	f	99.8g	DRG, SC			
Highveld mole-rat *Cryptomys hottentotus pretoriae*	P1	f	84.3g	DRG, SC	194,791,919	yes	yes
	P2	f	90.0g	DRG, SC			
	P3	f	143.6g	SC			
	P4	f	85.5g	DRG			
Damaraland mole-rat *Fukomys damarensis*	D1	m	70.3g	DRG, SC	181,073,339	no	yes
	D2	f	54.6g	DRG, SC			
	D3	f	57.0g	DRG, SC			

Table S1: Overview of tissues and species used for transcriptome analysis. Sex, weight/age and sequencing depth summed up per species. For most species, these reads were used for de novo transcriptome assembly and transcript quantification. m= male, f=female, dorsal root ganglia (DRG, Spinal cord (SC), Not determined (ND). Sequencing reads were deposited at the NCBI Sequencing Read Archive under accession number PRJNA394865.

species	# full-length protein-coding transcripts	BUSCO score
Tachyoryctes splendens	10,786	76 %
Heliophobius emini	9,553	70 %
Georychus capensis	9,678	71 %
Cryptomys hottentotus hottentotus	9,521	69 %
Cryptomys hottentotus mahali	9,630	70 %
Cryptomys hottentotus natalensis	9,691	70 %
Cryptomys hottentotus pretoriae	9,531	69 %

Table S2 Statistics for de novo transcriptome assemblies. The number of full-length protein-coding transcripts and completeness scores per species for the de novo assembled and annotated transcriptomes.

Capsaicin-insensitive against background

gene name	description	F-value	logFC	p.adj
BMPER	BMP-binding endothelial regulator	42.58	-1.1	0.005333

Acid-insensitive against background

gene name	description	F-value	logFC	p.adj
CROT	carnitine O-octanoyltransferase	44.94	-1.85	0.003654
ANKMY2	ankyrin repeat and MYND domain containing 2	46.93	1.41	0.003654
RGS10	regulator of G-protein signalling 10	41.52	-2.49	0.004759
PHF24	PHD finger protein 24	36.38	-1.44	0.005969
DDX56	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	33.46	-1.16	0.008914
PTPN5	protein tyrosine phosphatase, non-receptor type 5	31.5	3.64	0.0111
WBSCR22	Williams Beuren syndrome chromosome region 22	30.67	1.04	0.0111
UFSP2	UFM1-specific peptidase 2	28.74	-1.29	0.01297
HMCES	5-hydroxymethylcytosine (hmC) binding, ES cell specific	29.01	1.11	0.01297
IMPDH2	inosine 5'-phosphate dehydrogenase 2	27.61	1.01	0.01554
SLC25A30	solute carrier family 25, member 30	26.93	-2.8	0.01613
SLC46A1	solute carrier family 46, member 1	27.07	2.12	0.01613
PLXNC1	plexin C1	25.6	-2.15	0.01694
DOCK11	dedicator of cytokinesis 11	25.48	-1.06	0.01694
FAAP24	Fanconi anemia core complex associated protein 24	24.88	1.2	0.01817
EPB41L4A	erythrocyte membrane protein band 4.1 like 4a	24.36	1.62	0.01898
SPR	sepiapterin reductase	24.06	-1.48	0.01898
STAMBPL1	STAM binding protein like 1	23.65	1.6	0.01971
RAB40B	Rab40B, member RAS oncogene family	23.13	1.48	0.01994
PAQR7	progestin and adipoQ receptor family member VII	23.09	-1.43	0.01994
RNASEH2A	ribonuclease H2, large subunit	23.18	-1.14	0.01994
PEX11G	peroxisomal biogenesis factor 11 gamma	22.88	1.19	0.02
CABLES2	CDK5 and Abl enzyme substrate 2	22.08	1.46	0.02156
ANGEL2	angel homolog 2	22.08	-1.02	0.02156
PTGFR	prostaglandin F receptor	21.57	-1.35	0.02254
TRAF3IP2	TRAF3 interacting protein 2	21.55	1.26	0.02254
ALDH9A1	aldehyde dehydrogenase 9, subfamily A1	21.64	-1.18	0.02254
TCTEX1D2	Tctex1 domain containing 2	21.71	1.1	0.02254
DMAP1	DNA methyltransferase 1-associated protein 1	21.39	1.03	0.02294
GRHPR	glyoxylate reductase/hydroxypyruvate reductase	21.18	1.62	0.02328
RGMA	repulsive guidance molecule family member A	21.25	1.4	0.02328
KCNK1	potassium channel, subfamily K, member 1	20.79	-1.05	0.02462
MED6	mediator complex subunit 6	19.83	1.03	0.0285
CBS	cystathionine beta-synthase	19.26	3.25	0.032
HSD17B7	hydroxysteroid (17-beta) dehydrogenase 7	19.18	-1.21	0.03216
RTKN	rhotekin	18.6	1.22	0.03643
SLC25A48	solute carrier family 25, member 48	18.37	4.15	0.03755
ASIC3	acid-sensing (proton-gated) ion channel 3	18.17	-1.67	0.03859
SLC50A1	solute carrier family 50 (sugar transporter), member 1	17.61	-1	0.04368
PXMP4	peroxisomal membrane protein 4	17.54	-1.34	0.04389
ZBTB6	zinc finger and BTB domain containing 6	17.21	-1.36	0.04745

AITC-insensitive against background

gene name	description	F-value	logFC	p.adj
NALCN	sodium leak channel, non-selective	37.49	2.81	0.03806

Table S3 Differentially expressed genes found in the DRG. Statistical details for all significantly differentially regulated the genes. Data is shown for genes found to be differentially regulated in capsaicin insensitive (top), acid insensitive (middle) and AITC-insensitive species. Transcripts are sorted by adjusted p-value and log fold change.

gene name	description	LR	qval	# sites	ω_2	ω_3
ANO3	anoctamin 3	43.11	8.79e-08	3	0.234	1.280
ATP8B1	ATPase, class I, type 8B, member 1	39.78	3.58e-07	1	0.202	0.962
MAN2B1	mannosidase 2, alpha B1	39.37	3.58e-07	14	0.245	0.965
ST8SIA3	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	32.87	7.17e-06	2	0.104	5.715
MAN2A2	mannosidase 2, alpha 2	32.15	9.10e-06	3	0.232	1.144
CXCR4	chemokine (C-X-C motif) receptor 4	28.86	3.61e-05	2	0.167	1.722
MGAT4C	MGAT4 family, member C	23.57	5.11e-04	1	0.126	0.900
ROPN1L	ropporin 1-like	22.98	5.99e-04	6	0.513	6.411
PLAC8	placenta-specific 8	22.62	6.71e-04	2	0.220	12.375
ANO5	anoctamin 5	22.26	7.16e-04	10	0.248	0.890
HTRA2	HtrA serine peptidase 2	21.62	8.76e-04	1	0.170	3.038
NFE2L2	nuclear factor, erythroid derived 2, like 2	21.56	8.76e-04	1	0.262	26.869
FAM168A	family with sequence similarity 168, member A	21.22	9.95e-04	1	0.035	17.700
NLRX1	NLR family member X1	20.93	1.11e-03	2	0.291	1.260
NXPE3	neurexophilin and PC-esterase domain family, member 3	19.51	1.97e-03	3	0.299	1.953
ADAMTS1	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1	19.22	2.13e-03	6	0.285	0.886
ANO10	anoctamin 10	18.88	2.36e-03	1	0.194	0.616
POGLUT1	protein O-glucosyltransferase 1	18.04	3.16e-03	1	0.183	43.862
SYTL5	synaptotagmin-like 5	18.06	3.16e-03	3	0.345	2.920
QPCTL	glutaminyl-peptide cyclotransferase-like	17.04	4.90e-03	1	0.281	1.598
DNAJB2	DnaJ heat shock protein family (Hsp40) member B2	17.00	4.90e-03	2	0.357	2.451
IFT57	intraflagellar transport 57	16.85	4.94e-03	1	0.016	0.233
RET	ret proto-oncogene	16.84	4.94e-03	7	0.232	0.568
ZBTB33	zinc finger and BTB domain containing 33	15.80	7.66e-03	1	0.351	1.142
UBE3A	ubiquitin protein ligase E3A	15.38	8.98e-03	1	0.188	1.748
FAM57B	family with sequence similarity 57, member B	15.10	9.65e-03	1	0.325	8.273
SPRED2	sprouty-related, EVH1 domain containing 2	15.10	9.65e-03	1	0.146	1.232
DAGLB	diacylglycerol lipase, beta	14.41	1.32e-02	13	0.385	1.141
SLC44A2	solute carrier family 44, member 2	13.98	1.52e-02	1	0.233	0.832
SLC7A8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	13.69	1.63e-02	1	0.224	115.042
FURIN*	furin (paired basic amino acid cleaving enzyme)	13.40	1.86e-02	2	0.460	0.000
CERK	ceramide kinase	13.14	2.11e-02	5	0.203	0.768
CNKSR3	Cnksr family member 3	12.57	2.67e-02	1	0.187	0.798
ALKBH4	alkB homolog 4, lysine demethylase	12.37	2.83e-02	3	0.160	1.327
LRRCC1	leucine rich repeat and coiled-coil domain containing 1	12.39	2.83e-02	4	0.260	2.621
FGG	fibrinogen gamma chain	12.32	2.86e-02	2	0.293	0.956
NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1	11.93	3.31e-02	1	0.098	0.459
QSOX2	quiescin Q6 sulfhydryl oxidase 2	11.96	3.31e-02	11	0.305	0.945
MANEA	mannosidase, endo-alpha	11.87	3.40e-02	3	0.282	0.886
IMMT	inner membrane protein, mitochondrial	11.81	3.47e-02	2	0.487	2.798
TXNDC15	thioredoxin domain containing 15	11.46	4.04e-02	1	0.238	1.107
PARS2	prolyl-tRNA synthetase (mitochondrial)(putative)	11.21	4.33e-02	1	0.338	1.196
FAM193B	family with sequence similarity 193, member B	11.06	4.65e-02	1	0.837	2.318

Table S4 Divergent selection in the acid-insensitive East African root rat. Genes under divergent selection in the east African root rat (*Tachyoryctes splendens*). LR (likelihood ratio)

indicates the signal strength of the divergent selection model. Genes are sorted by adjusted p-value. # sites reports the number of amino acids under divergent selection pressure. ω2 (background) and ω3 (foreground) depict the non-synonymous to synonymous substitution rates. ω2 < ω3 indicates negative selection, ω2 > ω3 implies positive selection. FURIN as the only gene under negative selection is highlighted with an asterisk.

Movie S1

Movie showing positive nocifensive behaviors in African Rodent Species that lack a response to one of the three algogens used. For each species one video is shown with an algogen that provokes behavior and one that does not.

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