Supplemental Figure Legends

Figure S1. TILLING screen for *dTrpA1* mutants identified an allele with a premature stop codon. (related to main text Figure 1)

Traces from DNA sequencing reactions of PCR products from wild type and mutant DNA confirm the point mutation (G->A) in *dTrpA1*^{W903*}

Figure S2. Cloning of novel dTRPA1 isoforms and protein alignment of N- and C-terminal TAC regions. (related to main text Figure 4)

(A) Gene structure of *dTrpA1-D*. Green arrows indicate primer placement.

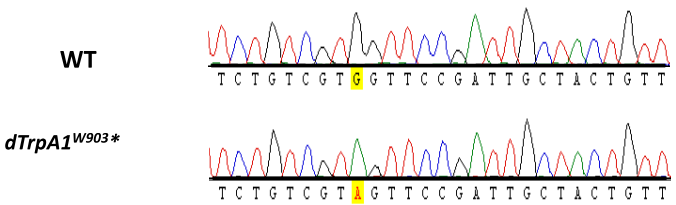
(B) Representative gel used for purification of *dTrpA1-C* and *dTrpA1-D*. Following gel purification RT-PCR products were cloned into the pCR-XL vector (dTRPA1-C) or pENTR vector (dTRPA1-D) (Invitrogen). All four isolated colonies from one cloning experiment contained dTRPA1-C inserts. A single colony isolated in a second experiment contained a dTRPA1-D insert.

(C) Alignment of N-terminal TAC regions dTRPA1-A/B and dTRPA1-C/D with N-terminal regions from *Crotalus atrox* (rattlesnake TRPA1), *Elaphe obsoleta lindheimeri* (rat snake TRPA1), human TRPA1, and mouse TRPA1. The N-terminal TAC regions of dTRPA1 do not align well with each other or with vertebrate TRPA1s. Residue numbers are in reference to the dTRPA1-A sequence. Shading denotes percent identity.

(D) Alignment of N-terminal TAC regions dTRPA1-A/D and dTRPA1-B/C with N-terminal regions from *Crotalus atrox* (rattlesnake TRPA1), *Elaphe obsoleta lindheimeri* (rat snake

TRPA1), human TRPA1, and mouse TRPA1. Residue numbers are in reference to the dTRPA1-A sequence. Shading denotes percent identity.

Supplemental Figure S1



Supplemental Figure S2.