SUPPLEMENTAL FIGURES

Supplemental Figure 1: *mec-10(tm1552)* deletion structure and potential deleted translation product. *mec-10(tm1552)* deletes 448 bp and removes exon 5 and part of exon 6, which encode part of the conserved extracellular domain (the amino acids encoded by the deleted nucleotides are indicated by blue underline). Normal translation of the mutant sequence would induce a frameshift with three premature stop codons (the first one is TAA at the end of the sequence below) close to the deletion site (…tctattcatattttt-deletion-TTTATGCAGCAAAAAAAGCTAA) such that if the theoretical transcript were translated, most of the extracellular domain and the pore-forming 2nd transmembrane domain of MEC-10 would be missing. However, an alternatively spliced transcript that joins exon 3 in-frame to exon 7 (detected in RT/PCR experiments with multiple primer sets) would, if translated, encode a MEC-10 protein lacking 153 amino acids from the extracellular domain (indicated by purple underline). Since the deleted region includes highly conserved sequences known to be essential for MEC-4 function, *tm1552* is likely to be a loss-of-function allele. Primers designed to avoid the homologous sequences between *mec-4* and *mec-10* and identify the deletion were: 5'GTAGGGTCTGCAACTAGCTC-3' and 5'-TGGGAGGGAGCTTCATCTTA-3'. Green lines indicate the 1st and 2nd transmembrane domains.

Supplemental Figure 2: Effect of *mec-10(e1515)* on anterior touch response. a. Animals were touched with an eyelash at the indicated positions; escape responses (reversals) were scored as described. *mec-10(e1515)* animals were significantly less responsive than wild-type at all positions (***p<.001) according to the Student's t test

(n= 100 for each genotype over five different days). One way analysis of variance (ANOVA) demonstrated a statistically significant difference in the responses of *mec-10(e1515)* animals at different positions along the anteroposterior axis ($p<.001$).

b. Averaged calcium response to gentle touch. Each red trace represents the average percentage change in R/R_0, where R is the fluorescence emission ratio at a given time point and R_0 is its initial value. The number of individual recordings averaged for each trace were n=22 (all positions). Gray shading indicates SEM of the mean response. Scale bars are indicated in upper left. The green bar indicates the time of the stimulus. **c. Scatter plot of peak calcium responses.** Red lines indicate the mean response at each of the four stimulus points; error bars indicate SEM. Each other line indicates the response for a single animal. Half the animals were stimulated from anterior to posterior, and half from posterior to anterior. Wild-type, *mec-10(tm1552)* and *mec-4(u253)* data from Figure 2 are shown for comparison. One way analysis of variance (ANOVA) demonstrated a statistically significant difference in the calcium and behavioral responses of *mec-10(e1515)* animals at different positions along the anteroposterior axis ($p<.001$).

Supplemental Figure 3: Rescue of *mec-10(tm1552)* by *pmec-10::mec-10(+)*. a. Stimulus positions for imaging experiments. Animals were given a 1 second gentle (buzz) stimulus at the indicated position, as described in Experimental Procedures. **b. Averaged calcium responses of *mec-10(tm1552)* (red trace), and *mec-10(tm1552); Ex[pmec-10::mec-10; pmyo-2::GFP]* (green traces) animals.** Each trace represents the average percentage change in R/R_0, where R is the fluorescence emission ratio at a given time point and R_0 is its initial value. The number of individual recordings averaged for

each trace were n=13 (*mec-10(tm1552)* and n=20 (*pmec-10::mec-10* rescue). Gray shading indicates SEM of the mean response. Scale bars are indicated in upper right The green bar indicates the time of the stimulus. **c. Scatter plot of peak calcium responses for each genotype.** Red lines indicate the mean response at each of the four stimulus points; error bars indicate SEM. Each other line indicates the response for a single animal. Statistical significance (*** $p < .0005$; ** $p < .005$) is according to the Mann-Whitney rank sum test. Half the animals were stimulated from anterior to posterior, and half from posterior to anterior.

Supplemental Figure 4: Effect of *mec-10(u20)* on posterior touch response. a, b. Animals were touched with an eyelash at the indicated positions; escape responses (forward accelerations) were scored as described. *mec-10(e1515)* animals were significantly less responsive than wild-type at all positions (***$p<.001$, **$p<.01$) according to the Student's t test (n= 100 for each genotype). One way analysis of variance (ANOVA) demonstrated a statistically significant difference in the responses of *mec-10(u20)* animals at different positions along the anteroposterior axis ($p<.001$). **c. Scatter plot of peak calcium responses.** Red lines indicate the mean response at each of the four stimulus points; error bars indicate SEM. Each other line indicates the response for a single animal. Half the animals were stimulated from anterior to posterior, and half from posterior to anterior. Wild-type data from Figure 6 are shown for comparison.

Supplemental Figure 5: Rescue of *mec-10(tm1552)* gentle touch defects by *mec-10::gfp*. Animals were touched with an eyelash at the indicated positions. Escape

responses to anterior (reversals, A) or posterior (forward accelerations, B) were scored as described. *pmec-4::mec-10::gfp* animals were significantly more responsive than non-rescued *mec-10(tm1552)* animals at all positions (***p<.001, **p<.01) according to the Student's t test (n= 100 for each genotype).

Supplemental Figure 6: Effects of *degt-1::RNAi* and *mec-10(tm1552)* on localization of MEC-10 protein fusions in body touch neurons. Shown are images of MEC-10::GFP fluorescence in the ALM neurons of *pmec-4::degt-1RNAi* (A) and *mec-10(tm1552)* (B) animals. MEC-10::GFP fluorescence only in the cell body in about 65% of observations; in the rest some staining can be observed in the posterior-projecting dendrite. The *pmec-4::degt-1RNAi* array (*ljEx240*) was described previously (Chatzigeorgiou et al., 2010).