

SUPPLEMENTARY FILE 4. Figure legend for Supplemental File 3.

File 1: Gene Regions. Gene regions determined to be differentially expressed in *mec-8* animals as compared with wild type. Genes for which all exons were up or down regulated are in bold. **Region** indicates the specific exons or introns of a transcript that were up or down regulated in *mec-8* animals. Note that exon or intron numbering is specific to individual isoforms (as indicated) and may differ between isoforms. For example, the region encompassing intron 14 in *fbn-1b,d,e* corresponds to introns 14–15 in *fbn-1a,k* and the region encompassing intron 15 in *fbn-1e* corresponds to introns 16–18 in *fbn-1a,k*. **Start** and **End** indicate the flanking genomic positions of the differentially expressed exons or introns. **Difference** is the length in nucleotides of the exons or introns that were differentially expressed. **Probes** indicate the actual number of 25-nt probes that hybridized the indicated region. **D/25** is the theoretical number of 25-nucleotide (nt) probes that cover the length of the genomic fragment. **N2 avg** and **mec-8 avg** are the averaged intensities from three replicates. **N2 SD** and **mec-8 SD** are the standard deviation of the three replicates. **Ratio** is the average intensity of *mec-8* divided by the average intensity of N2. **SD ratio** is the standard deviation of the *mec-8*/N2 ratio of intensity. **AS** (alternatively spliced) indicates whether the gene is alternatively spliced. Gene ratios are color coded according to groups: orange, introns up; green, exons down; red, exons up. *fbn-1* and *mec-8* gene names are highlighted in red. In some cases different regions from the same gene are separated based on ratio rankings.

File 2: Transcripts. Transcripts differentially expressed in *mec-8* animals compared to wild type. **Average ratio** is the average of the ratios of each gene region of the transcript.

File 3: Gene lists. Alphabetical list of all differentially expressed genes including category subdivisions.

File 4. Alternatively (Alt.) Spliced Genes. Alphabetical list of all differentially expressed genes including category divisions and information regarding alternative splicing.

File 5. Sequences of primers (5'–3') used to amplify candidate gene regions.

Expected sizes for candidates that are differentially expressed in *mec-8* mutants are indicated. Orange indicates introns upregulated in *mec-8*; red, exons upregulated in *mec-8*; blue, exons downregulated in *mec-8*. For genes that contain intronic regions that are upregulated in *mec-8*, sizes with and without, respectively, intronic sequences are shown.