

Figure S1

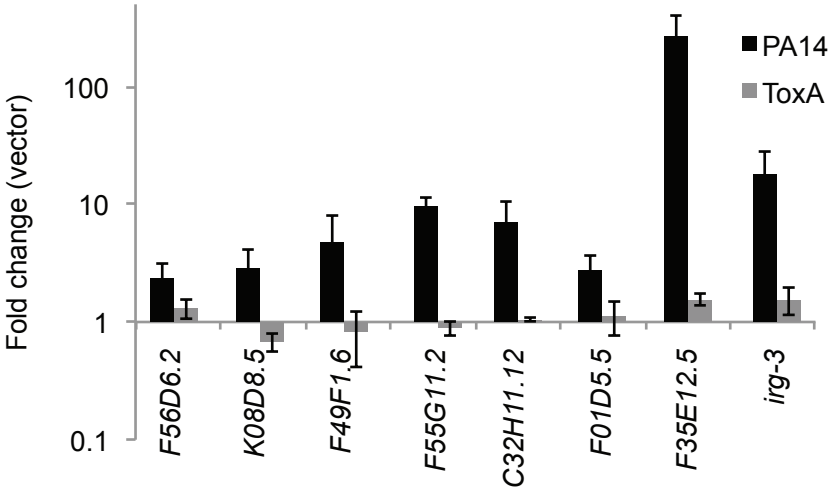
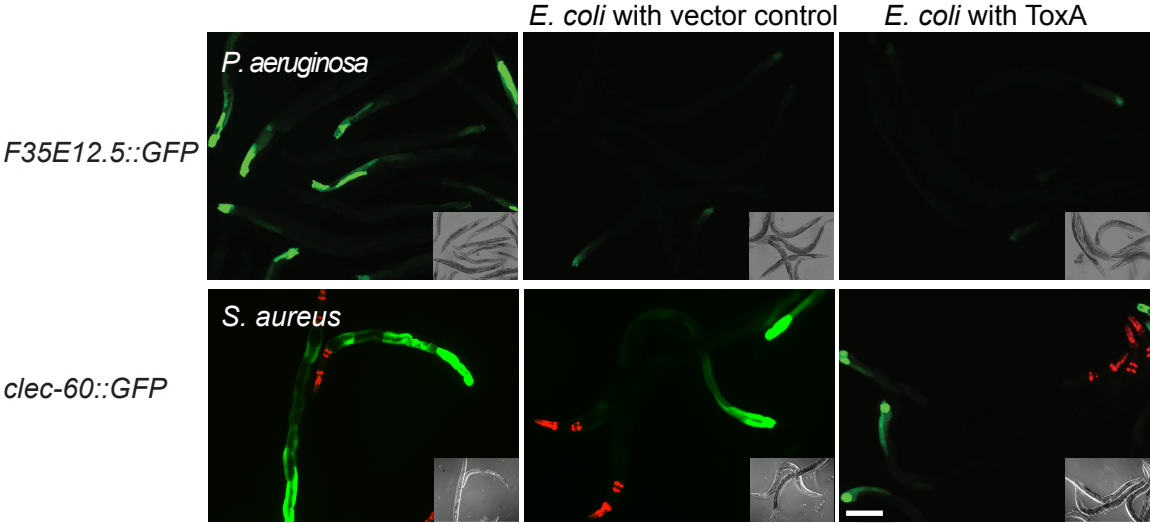


Figure S2

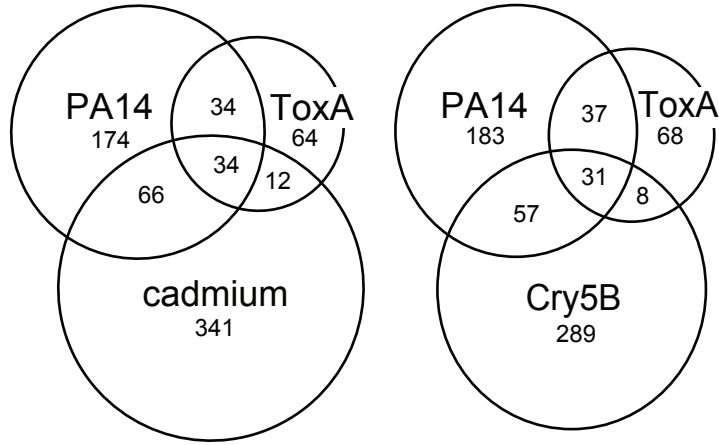


Figure S3

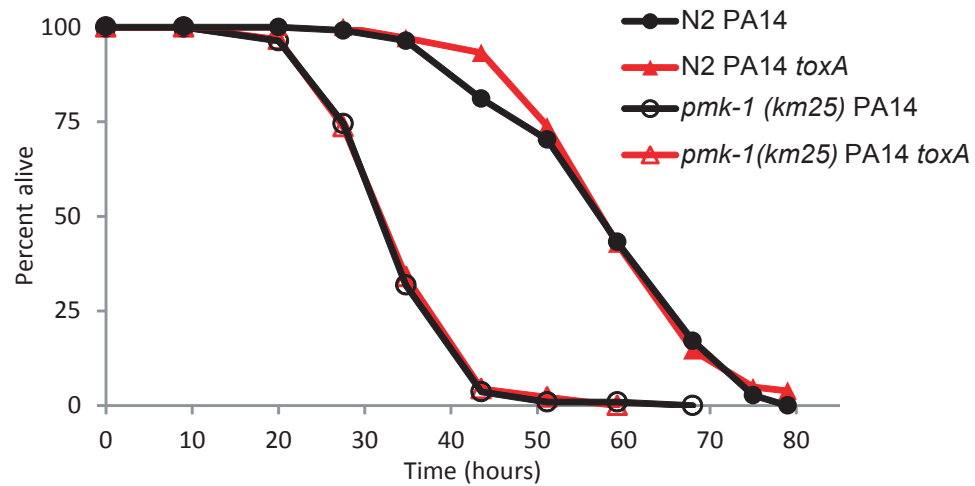


Figure S4

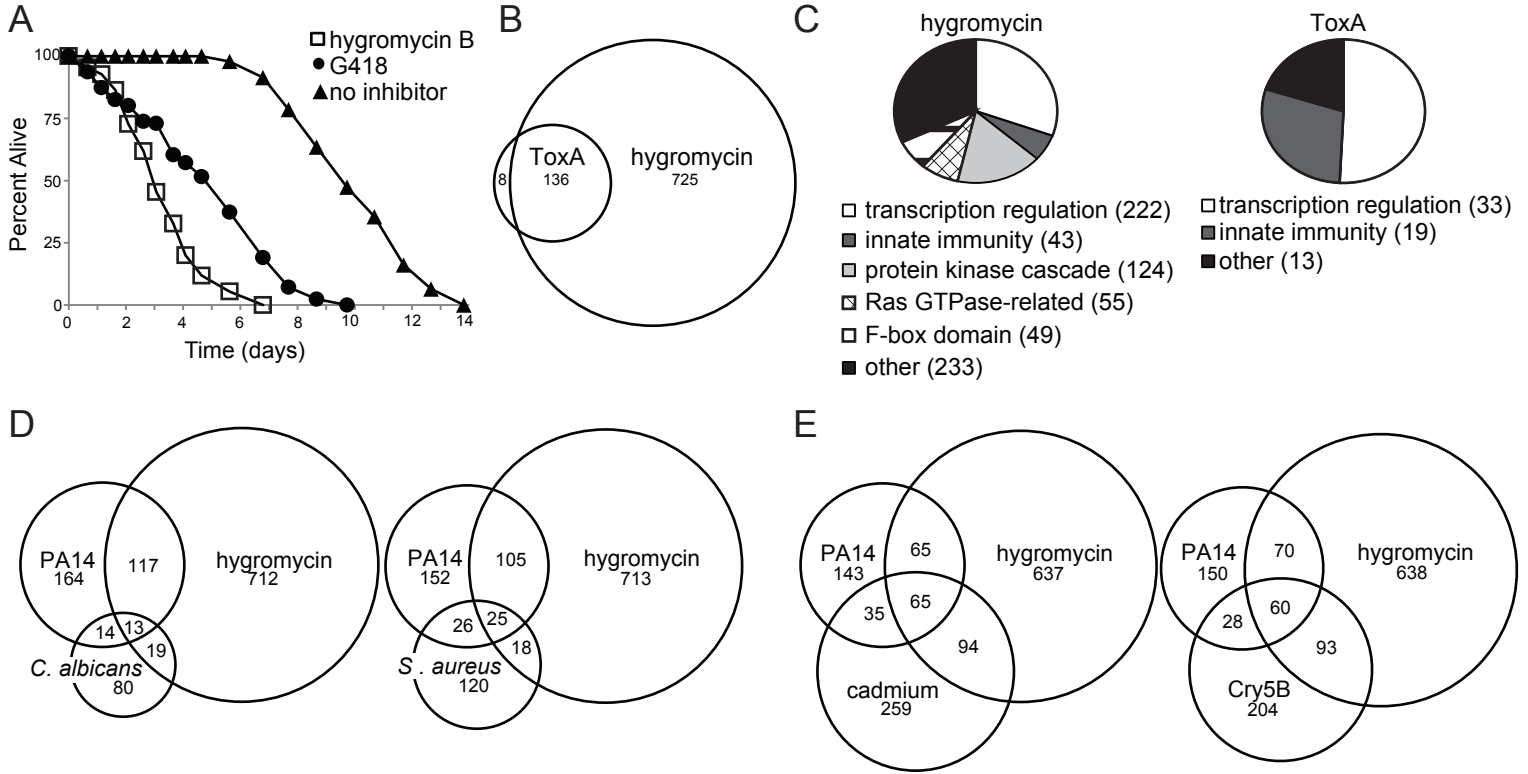


Figure S1: ToxA does not broadly activate *C. elegans* immune genes. (A and B) *C. elegans* strains containing the *P. aeruginosa* reporter *F35E12.5::GFP* (A) or the *S. aureus* reporter *clec-60::GFP* (B) were exposed for 24 hours to *P. aeruginosa* PA14, *S. aureus* NCTC8325, or *E. coli* expressing ToxA or an empty expression vector. Images for each strain were taken at the same time using the same camera settings. Red pharyngeal expression is due to the co-injection marker *myo-2::mCherry* which confirms the transgene is present. Scale bar represents 100 μm . Insets are the corresponding bright field image. (B) qRT-PCR analysis of genes that respond to *P. aeruginosa* but not ToxA. Results shown are an average of 3 biological replicates. Error bars represent SEM.

Figure S2: The ToxA response does not mimic other intestinal stressors. Venn diagrams summarizing the overlap between genes upregulated by ToxA, *P. aeruginosa* PA14, and the heavy metal cadmium (left) or the pore-forming toxin Cry5B (right) (Huffman et al., 2004). All microarrays were conducted with the Affymetrix platform using animals infected at the L4/young adult stage and collected after 24 hours (ToxA), 4 hours (PA14), or 3 hours (cadmium, Cry5B).

Figure S3: ToxA is dispensable for *P. aeruginosa* PA14-mediated *C. elegans* lethality. Lifespan comparison between N2 and *pmk-1(km25)* animals exposed to either wild-type *P. aeruginosa* PA14 or a *toxA* mutants starting at the L4 stage.

Figure S4: Hygromycin upregulates ToxA-induced genes and a subset of *P. aeruginosa*-induced genes. (A) Lifespan comparison of N2 animals exposed hygromycin or G418 starting at the L4 stage. (B) Venn diagram summarizing the overlap between genes upregulated by hygromycin and ToxA. (C) Functional classes enriched in each data set as determined by DAVID analysis. Number of genes in each category is indicated in parenthesis. Classes with few genes [<40 (hygromycin) or <5 (ToxA)] are categorized as “other”. (D-E) Venn diagrams

summarizing the overlap between genes upregulated by hygromycin and the pathogens *P. aeruginosa* PA14 (Troemel et al., 2006), *C. albicans* (Pukkila-Worley et al., 2011), and *S. aureus* (Iraozqui et al., 2010a) (D); or hygromycin, PA14, and cadmium or Cry5B (Huffman et al., 2004) (E). All microarrays were conducted with the Affymetrix platform using animals infected at the L4/young adult stage and collected after 24 hours (ToxA), 8 hours (*S. aureus*), 4 hours (PA14, *C. albicans*), or 3 hours (cadmium, Cry5B).

Table S1: *C. elegans* genes differentially expressed following ToxA exposure. This table lists all the Affymetrix probe sets differentially expressed in N2 animals fed *E. coli* expressing ToxA or an empty vector for 24 hours (≥ 2 -fold change and a modified Wilcoxon rank test > 1.45).

Table S2: *C. elegans* genes differentially expressed following hygromycin treatment. This table lists all the Affymetrix probe sets differentially expressed in N2 animals fed *E. coli* with an empty vector and exposed to hygromycin or no inhibitor for 24 hours (≥ 2 -fold change and a modified Wilcoxon rank test > 1.45).