Figure S1 - Related to Figure 1

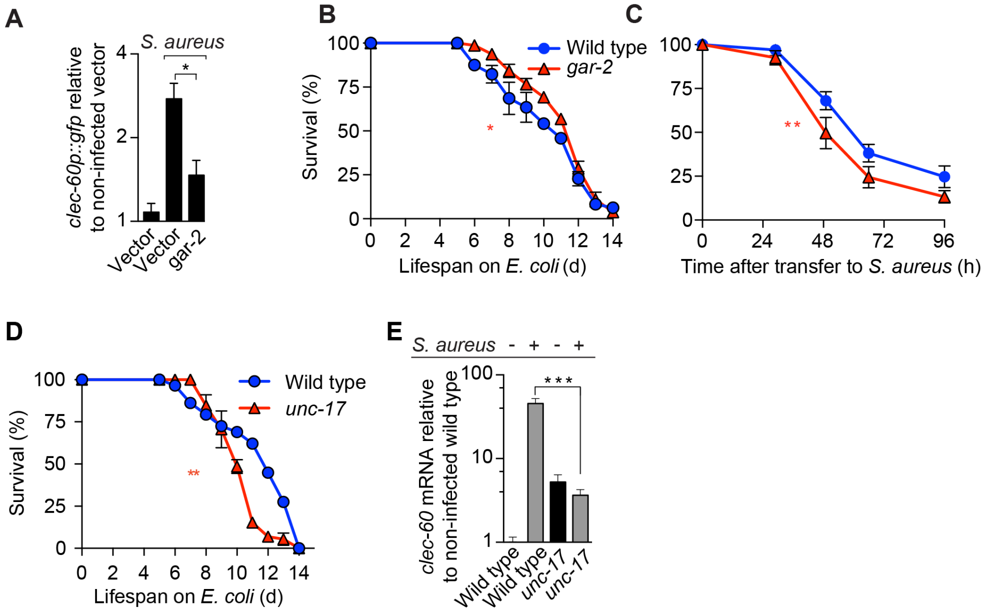

Figure S1- Related to Figure 1: (A) Quantitative analysis of *clec-60::gfp* animals that were reared on *E. coli* carrying empty vector or RNAi against *gar-2* and subsequently infected with *S. aureus* for 16 h. Data are mean ± SEM (at least two biological replicates, n ≥ 50 per condition). * $p \leq 0.05$ (two-sample two-tailed *t* test). **(B)** Survival of wild type and *gar-2* mutant animals infected with *S. aureus*. Results are representative of 2 biological replicates. ** $p \leq 0.01$ (Log-Rank test). **(C)** Lifespan of wild type and *gar-2* mutant animals on *E. coli* OP50. Results are representative of 2 biological replicates. **(D)** Lifespan of wild type and *unc-17* mutant animals on *E. coli* OP50. Results are representative of 2 biological replicates. ** $p \leq 0.01$ (Log-Rank test). **(E)** qRT-PCR of *clec-60* in wild type and *unc-17* mutant animals infected with *S. aureus* for 8 h. Results are normalized to non-infected wild type animals. Data are mean ± SEM (two biological replicates, n ≥ 500 per condition). *** $p \leq 0.001$ (two-sample t test).

Figure S2 - Related to Figure 4

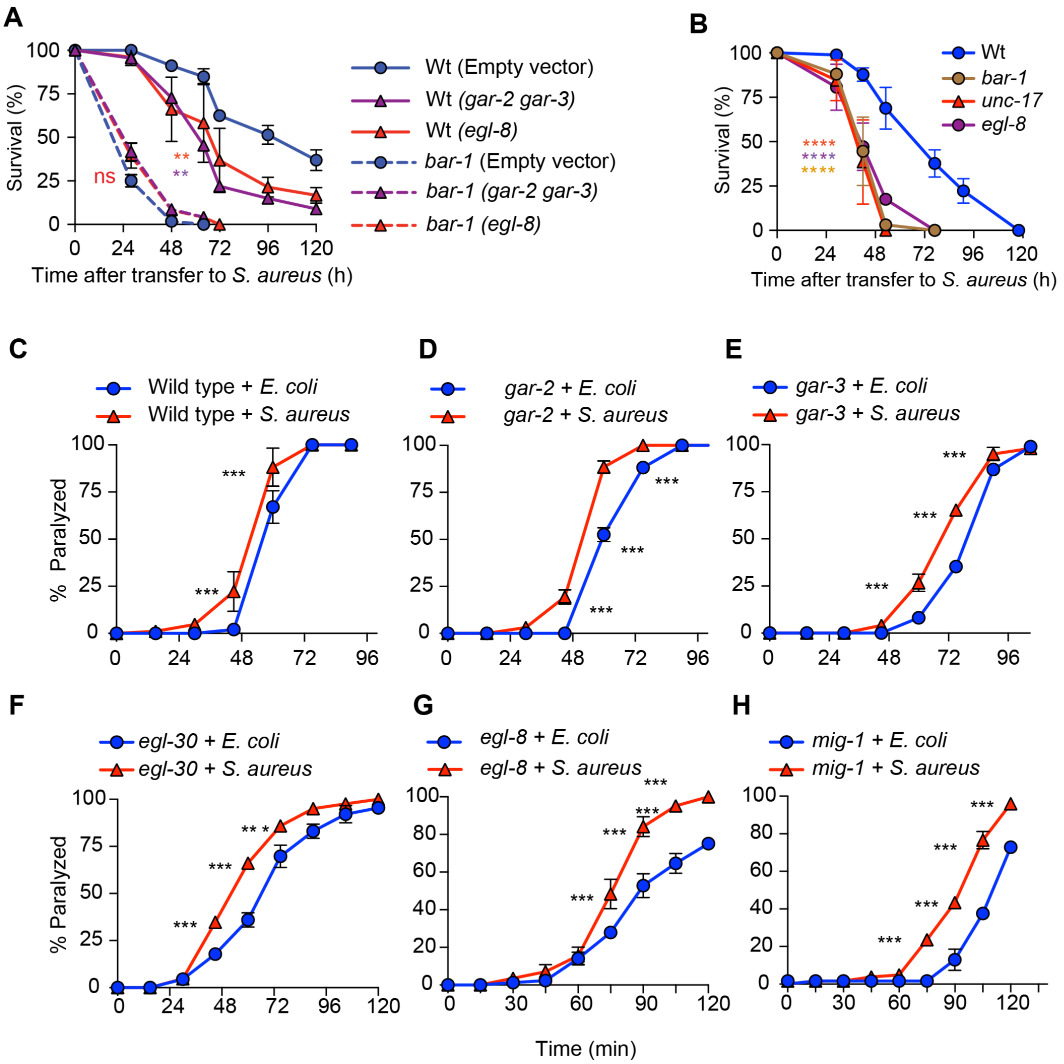

Figure S2-Related to Figure 4: (A) Survival of wild type and *bar-1* mutant animals grown on empty vector, *gar-2* and *gar-3*, or *egl-8* RNAi, and subsequently infected with *S. aureus*. Results are representative of 2 biological replicates. ** $p \leq 0.01$ (Log-Rank test). **(B)** Survival of wild type, *unc-17, egl-8 and bar-1* mutant animals infected with *S. aureus*. Results are representative of 2 biological replicates. **** $p \leq 0.0001$ (Log-Rank test). **(C-H)** Aldicarb paralysis of wild type (C) or mutant animals (D-H) either infected with *S. aureus* or fed with non-pathogenic *E. coli* for 30 min. The error bar at each time point represents the mean of three trials (25-30 animals tested in each trial) and s.e.m. *** $p \leq 0.001$ (two-way ANOVA).

Figure S3 - Related to Figure 6

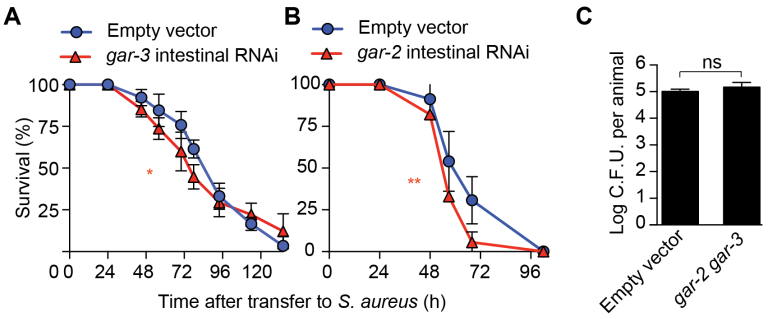

Figure S3-Related to Figure 6: Survival of MGH167 animals, which were subjected to RNAi against *gar-2* **(A)** or *gar-3* **(B)** until young adulthood, and subsequently infected with *S. aureus*. Results are representative of 2 biological replicates. *** $p \leq 0.001$ (Log-Rank test). **(C)** *S. aureus* accumulation in RNAi-treated animals after 8 h of infection, expressed as cfu per animal. Data are mean ± SEM (3 replicates). Differences between groups were not statistically significant (two-sample t test).

Figure S4 - -Related to Star Methods

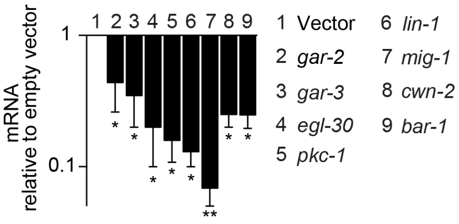

Figure S4-Related to Star Methods: qRT-PCR of *gar-2*, *gar-3, egl-30, pkc-1, lin-1, mig-1, cwn-2* and *bar-1* in lysates from animals treated respectively with, *gar-2, gar-3, egl-30, pkc-1, lin-1, mig-1, cwn-2* and *bar-1.* Results are normalized to empty vector treated animals. Data are mean ± SEM (two biological replicates, two technical replicates, n ≥ 3,000 per condition) * *p* ≤ 0.05 (two-sample t-test).

Figure S5 - Related to Figure 7

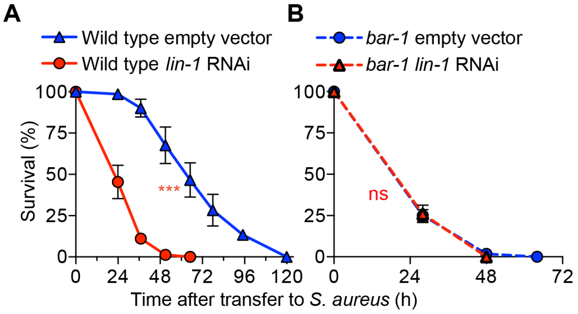

Figure S5-Related to Figure 7: (A) Survival of wild type animals grown on empty vector or *lin-1* RNAi, and subsequently infected with S. aureus. Results are representative of 2 biological replicates. *** $p \leq 0.001$ (Log-Rank test). **(B)** Survival of *bar-1* mutant animals treated as in (H). Results are representative of 2 biological replicates. ns, $p > 0.05$ (Log-Rank test).