Table S4, related to Figures 1, 2, 3, 5, and 6: List of primers used

Gene	Oligonucleutide	Source	Identifier
B2M	Forward: CTGACCGGCCTGTATGCTAT Reverse: CCGTTCTTCAGCATTTGGAT	This paper	N/A
IL-6	Forward: AGCCAGAGTCCTTCAGAGAGAT Reverse: GAGAGCATTGGAAATTGGGGT	This paper	N/A
OPTN	Forward: AGCCTCGCAGTATTCCGATT Reverse: GTCCAGAAGATGCTCTCCCAAGA	This paper	N/A
Rplp0	Forward: GCAGCAGATCCGCATGTCGCTCCG Reverse: ACCAGACGGTTCAGTTCTGC	This paper	N/A
SOCS3	Forward: TAGACTTCACGGCTGCCAAC Reverse: CGGGGAGCTAGTCCCGAA	This paper	N/A
Lys-7	Forward: ATCCAGGGATTGACTGCAAG Reverse: TCATTTCCAATGTTGCTCCA	This paper	N/A
Lys-3	Forward: CCAATGGCTGTGAGAATTGA Reverse: CCTGTCTCCATGGTCCAAAT	This paper	N/A
Hsp-16.41	Forward: TCTTGGACGAACTCACTGGA Reverse: TCCATGTTCCGATTTTGTTTC	This paper	N/A
Thn-1	Forward: TGGTTTCAAGCTCAATGCTG Reverse: ATCCGTCGACAAGGGATACA	This paper	N/A
Thn-2	Forward: CCAACTTACGGCTGGACAAT Reverse: CTGGGAGGTTGTATCCATCG	This paper	N/A
Lys-10	Forward: ATGGCCTGCTAATCATGCTC Reverse: GCCGAAAGCTACGAATTTTG	This paper	N/A
Cyp-13a5	Forward: GCAAGTGCAAAAGGAAAAGC Reverse: AAAGGTAGTTTACGACCATCTTTGA	This paper	N/A
Abtm-1	Forward: ATGGAAAAGCTCCCGAATTT Reverse: GAGCTCCAGTTTGACGGTTC	This paper	N/A
Cyp-35a4	Forward: GAAAACCCGCTGAAGTTTGA Reverse: ATGGTCTCTTTCCGATGCTG	This paper	N/A
Clec-60	Forward: ACGGTGCTCTTCTTGCAGAT Reverse: ACCGTAGCGGTAGGAGTGAA	This paper	N/A
Clec-74	Forward: CCGCCTGTCCTAGCAGTAAG Reverse: GCCCAATCCAAAAGTTTTCA	This paper	N/A
Cdc-42	Forward: GGCAAAGGAATTGAAAGCAG Reverse: GGGGGCTAAGAAAATTTGGA	This paper	N/A
Crp-2	Forward: CCATGAAGTTGATCCGCGAG Reverse: TCCTCCAGTAACGACACCAC	This paper	N/A
Fmo-2	Forward: TGTCACTTGTTTTGAGGCGT Reverse: TGTGACGGAGCTTGATATGC	This paper	N/A
Ilys-3	Forward: ACGTCGGATCCCTTTCTTGT Reverse: TGTGGTTACGAGCCATCACT	This paper	N/A
Asm-3	Forward: CAATGCGAATCCAACAAATG Reverse: TCGACATTGTTGATCGTTGC	This paper	N/A
Spp-1	Forward: ACTCGCATTCTTCCGTGTCT	This paper	N/A

|	Reverse: GCAACAGCATAGTCCAGCAA		
Spp-2	Forward: GATGGATCTGCGGATAAGGA Reverse: CTTGCACACATCCTTTGGTG	This paper	N/A
Tth-1	Forward: AGAATGTTTTGCCGACCAAG Reverse: TGTTGATCTTGTCGGTGAGC	This paper	N/A
Ttr-45	Forward: CACATCACCAGCCAAAAATG Reverse: GAGTCCTGGCTTCAACTTGC	This paper	N/A
Gpdh-1	Forward: CACATCACCAGCCAAAAATG Reverse: GAGTCCTGGCTTCAACTTGC	This paper	N/A
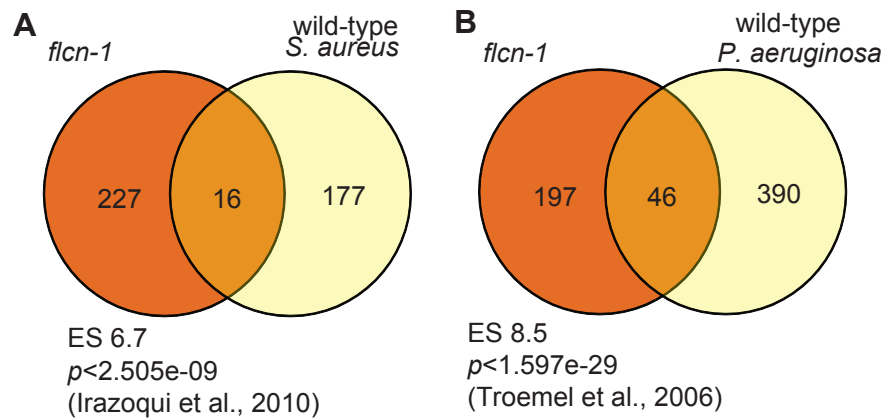
Figure S1, related to Figure 1: Transcriptional profile of *flcn-1* prior to stress overlaps with profiles of wild-type animals infected with pathogens and correlates with a pathogen resistance phenotype.

(A, B) Venn diagrams showing the overlap of genes upregulated in *flcn-1(ok975)* animals at basal level and genes upregulated in wild-type animals following treatment with *S. aureus* from (Irazoqui et al., 2010a) (A) or *P. aeruginosa* from (Troemel et al., 2006) (B). Comparisons were performed using the "compare two lists" online software and the significance and ES (enrichment scores) were obtained using "nemates" software.

A

207 | 36 | 601

■ *flcn-1* no stress
□ *hlh-30 (tm1988)*

ES 4.6
p < 2.13e-14

B

Percent survival vs Time (days)

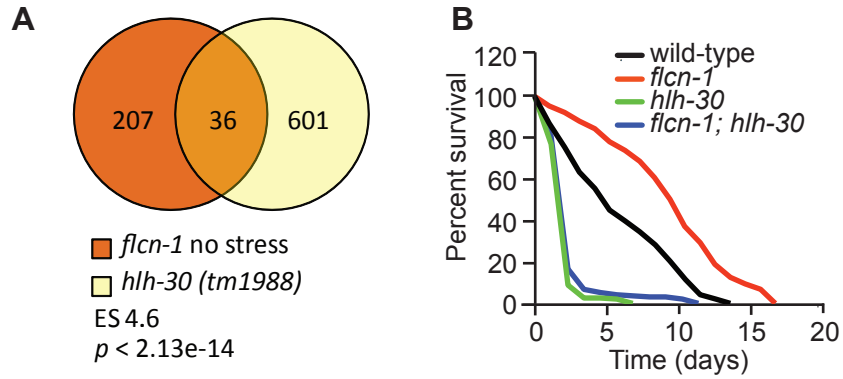— wild-type
— *flcn-1*
— *hlh-30*
— *flcn-1; hlh-30*

Figure S2, related to Figure 2: Role of *hlh-30* downstream of *flcn-1*.

(A) Venn diagrams showing the overlap of genes upregulated in *flcn-1(ok975)* animals at basal level and downregulated in *hlh-30 (tm1978)* mutant nematodes. Comparisons were performed using the "compare two lists" online software and the significance and ES (enrichment scores) were obtained using "nemates" software. (B) Percent survival of indicated strains to 400 mM NaCl stress. Refer to Table S2S9 for details on number of animals utilized and number of repeats Statistics obtained by Mantel-Cox analysis on the pooled curve.
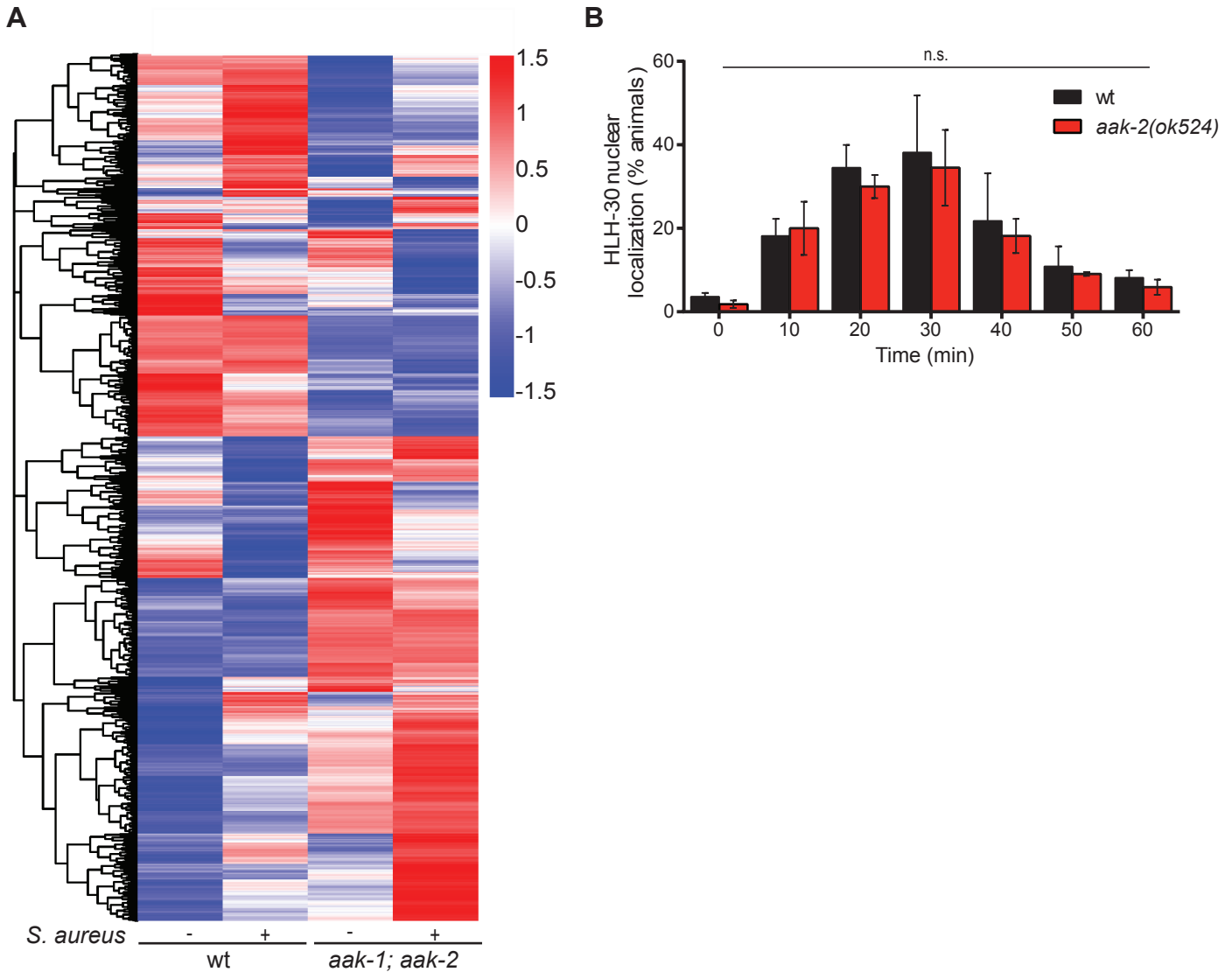
Figure S3, related to Figure 5: RNA Seq heat map and gene ontology analysis in wild-type and *aak-1(tm1944)*; *aak-2(ok524)* at basal level and upon *S. aureus* infection.

(A) Heat map showing differential gene expression in wild-type and *aak-1(tm1944)*; *aak-2(ok524)* mutant animals grown on OP50 or exposed to *S. aureus* for 4 h. Red color indicates genes that are differentially upregulated while blue color indicates gene sets that are downregulated in comparison to untreated wild-type animals. RNAseq data were analysed by Novogene Inc. using DEGseq 1.12.0 (B) Nuclear translocation of HLH-30 in *aak-2(ok524)*; *hlh-30::GFP* at basal level and upon S. aureus infection. Data represent the mean ± SEM with 3 independent repeats, n ≥ 30 animals/condition for every repeat. Significance was determined using student's t-test.