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Supplemental information

SKN-1 regulates stress resistance

downstream of amino catabolism pathways

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Figure S1. amdh-1 mutants do not upregulate gcs-1 expression, Related to Figure 1

(A) Schematic of *amdh-1/T12A2.1* genomic locus showing the location of allele *uth29* engineered using CRISPR/Cas9 (top, arrow). Scale bar, 100 bases. (B) Fluorescent images of SKN-1 reporter worms (*gcs-1p::GFP*) fed RNAi targeting *amdh-1* and *wdr-23*. Scale bar, 100 μ m. (C) Quantification of (B), Data shown are representative of n = 4 biological replicates with n > 60 animals per condition for each replicate. **** = P < 0.0001, n.s. = not significant using a one-way ANOVA non-parametric test (Kruskal-wallis).

Figure S2. *gcn-2* and *let-363* are partially required for SKN-1 activation in *amdh-1* mutants, Related to Figure 2

(A) Fluorescent images of SKN-1 reporter animals (*gst-4p::GFP*) fed RNAi targeting. Scale bar, 100 μ m. (B) Quantification of (A), Data shown are representative of n = 2 biological replicates with n > 123 animals per condition for each replicate. (C) Table of causative mutations mapped using whole genome sequencing.

Figure S3. haly-1 is required for SKN-1 activation in amdh-1 mutants, Related to Figure 3

(A) Schematic of *haly-1* genomic DNA (gDNA) rescue array used for genetic rescue experiments to confirm causality (B) Fluorescent images of *haly-1; amdh-1* double mutants with or without *haly-1* gDNA rescue array. Scale bar, 100 μm.

Figure S4. Stress response pathways are not activated in *amdh-1* mutants, Related to Figure 4

(A) Fluorescent images of heat shock response (HSR) reporter animals (hsp-70p::GFP) with or without heat shock treatments (34C) in wildtype and amdh-1(uth29) mutant animals. Data shown are representative of n = 3 biological replicates. Scale bar, 100 μ m. (B) Fluorescent images of a reporter of the unfolded protein response of the ER (UPR ER) animals (*hsp-4p::GFP*) fed RNAi. Scale bar, 100 μ m. (C) Quantification of (B), Data shown are representative of n = 3 biological replicates with n > 50 animals per condition for each replicate. **** = P < 0.0001, n.s. = not significant using a one-way ANOVA non-parametric test (Kruskal-wallis) (D) Fluorescent images of UPR Mito reporter animals (*hsp-6p::GFP*) fed RNAi. Scale bar, 100 μ m. (E) Quantification of (D), Data shown are representative of n = 3 biological replicates with n > 50 animals (*hsp-6p::GFP*) fed RNAi. Scale bar, 100 μ m. (E) Quantification of (D), Data shown are representative of n = 3 biological replicates with n > 50 animals (*hsp-6p::GFP*) fed RNAi. Scale bar, 100 μ m. (E) Quantification of (D), Data shown are representative of n = 3 biological replicates with n > 50 animals (*hsp-6p::GFP*) fed RNAi. Scale bar, 100 μ m. (E) Quantification of (D), Data shown are representative of n = 3 biological replicates with n > 50 animals per condition for each replicate. **** = P < 0.0001, n.s. = not significant using a one-way ANOVA non-parametric test (Kruskal-wallis)

Figure S1

Α



RNAi





Quantification of SKN-1 activation



Allele	Gene	Mutation
uth89	skn-1	A514T
uth94	elt-3	Q128*
uth112	suco-1	A429M
uth92	haly-1	G134E
uth93	haly-1	G265E
uth95	haly-1	G551V

Figure S3

Α

haly-1 gDNA rescue array

Endogenous Promoter	5' UTR	haly-1 genomic DNA	3' UTR
├─── 1.1 kb ───┤	0.3 kb	2.6 kb —	0.3 kb

В

amdh-1(uth29); haly-1(uth92)







Control + array

Control

ol + array



