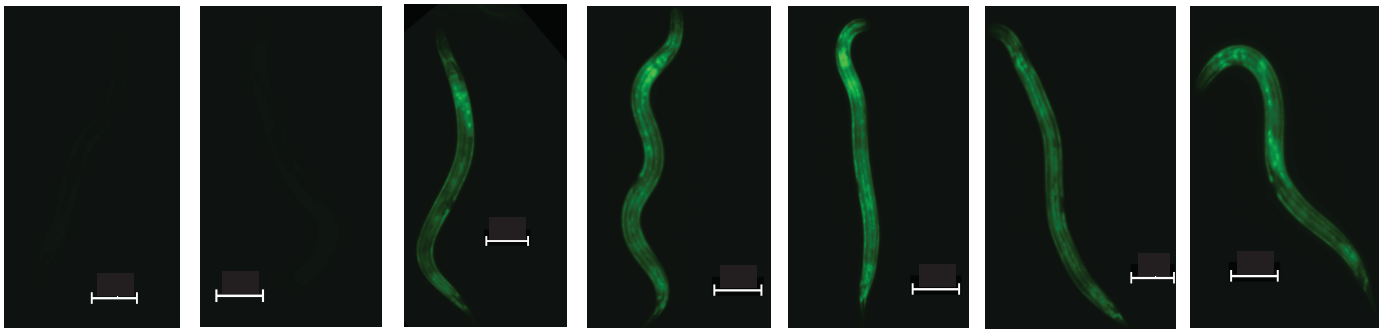
♂ \ ♀

	uwa02	uwa06	uwa05	uwa13	uwa15	uwa14	hif-1(ia04)
uwa02	+	+	-	-	-	-	-
uwa06	+	+	+	+	+	+	+
uwa05	-	+	+	+	+	-	-
uwa13	-	+	+	+	+	-	-
uwa15	-	+	+	+	+	-	-
uwa14	-	+	-	-	-	+	-
hif-1(ia04)	-	+	-	-	-	-	-

Figure S1. Complementation analysis of *suh* alleles. Progeny of matings between males (left column) and hermaphrodites (top) were exposed to H_2S. If a majority of heterozygous animals survived H_2S, indicating non-complementation, cells are marked with +. Complementing crosses are indicated with –. The two independent complementation groups are colored in cyan and magenta. The *uwa06* allele is dominant, but is included in the yellow group because it is also a gain-of-function allele of *skn-1*.



hif-1(ia04) | *hif-1(ia04)* 50 ppm H_2S | *hif-1(ia04); skn-1*(uwa02) | *hif-1(ia04); skn-1(uwa06)* | *hif-1(ia04); wdr-23(uwa05)* | *hif-1(ia04); wdr-23(uwa13)* | *hif-1(ia04); wdr-23(uwa15)*

Figure S2. *suh* mutations increase SKN-1 activity. Representative images of animals with the *Pgst-4::gfp* transgene. There was no expression of GFP in *hif-1(ia04)* animals, even after exposure to 50 ppm H_2S. All other animals were in room air without H_2S. Scale bar is 100 μM.

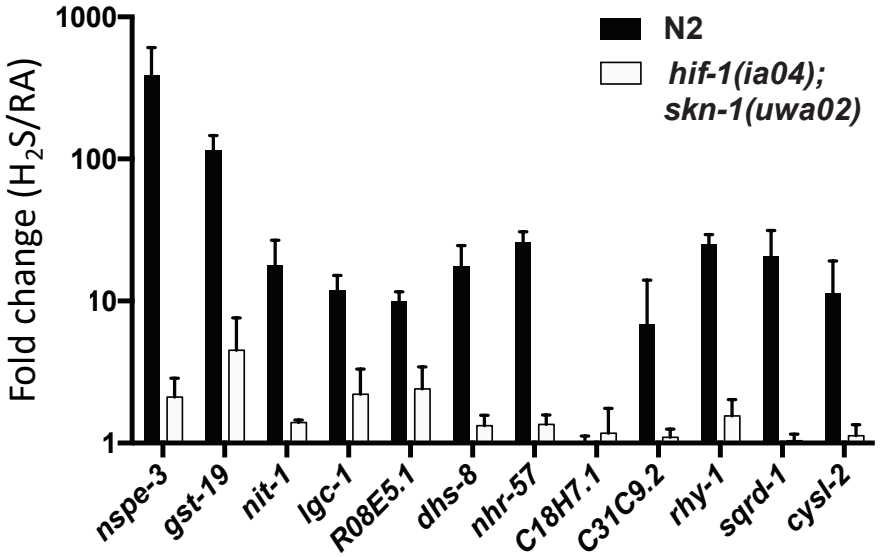


Figure S3. H_2S-induced gene expression is not restored in *skn-1(uwa02gf)* mutant animals. Change in transcript abundance of H_2S-inducible gene products measured by qRT-PCR after exposure to 50 ppm H_2S for 1 h. Average fold change calculated from $\Delta\Delta C_t$ (ΔC_t^{H2S}- ΔC_t^{RA}), error bars show standard deviation. RA is room air without H_2S. N=3 independent experiments, each with three technical replicates.

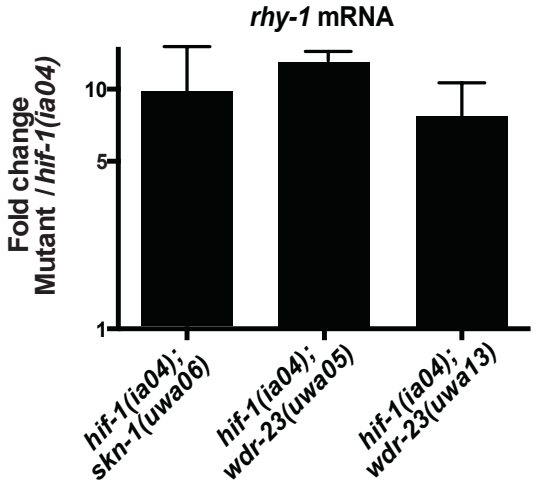


Figure S4. *rhy-1* expression is increased in *suh* mutants. *rhy-1* mRNA abundance in *suh* mutant animals, as measured by qRT-PCR. Average fold change in *rhy-1* expression between the indicated Suh strain compared to *hif-1(ia04)*. Bars indicated one standard deviation.