## SUPPLEMENTAL DATA



FIGURE S1. Summary of the sites required for Ce-GRK2 chemosensory function *in vivo*. Sitedirected mutagenesis revealed that Ce-GRK-2 residues Asp3, Leu4, Val7/Leu8, Asp10, Arg195, Lys220, Lys567 and Arg587 (shown in red) contribute to its chemosensory function. Changing Ce-GRK-2 residues Arg106, Tyr109 or Asp110 (shown in black, bold) did not disrupt its ability to restore ASHmediated chemosensory responses to *Ce-grk-2* mutant animals. Each residue targeted by site directed mutagenesis is indicted by an asterisk.

## Figure S2.

	2	56	263
$bG\alpha_q$	VLVESDNENRMEESKALF	RTIITY	PWFQNSSVILFLNKKDLLE
$hGlpha_q$	VLVESDNENRMEESKALF	RTIITY	PWFQNSSVILFLNKKDLLE
hGa11	VLVESDNENRMEESKALF	RTIITY	PWFQNSSVILFLNKKDLLE
EGL-30	VLVECDNENRMEESKALF	RTIITY	PWFTNSSVILFLNKKDLLE
ODR-3	VLFEDETTNRMIESMQLF	NSICNS	TWFLSTAMILFMNKKDLFM
GPA-3	VLFEDETTNRMIESMRLF	ESICNS	RWFINTSMILFLNKKDLFA
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FIGURE S2. Alignment of the GRK2-binding domain of mammalian  $G\alpha_{q/11}$  subunits with *C. elegans* ASH G $\alpha$  subunits. The GRK2-binding domain of bovine  $G\alpha_q$  (bG $\alpha_q$ ), human  $G\alpha_q$  (hG $\alpha_q$ ) and human  $G\alpha_{11}$  (hG $\alpha_{11}$ ) is conserved in the *C. elegans*  $G\alpha_{q/11}$  ortholog EGL-30. The described mammalian GRK2-binding site is highlighted by the grey box. Residues in mammalian  $G\alpha_{q/11}$  that form hydrogen bonds with the GRK2 RH domain, and are required for interaction *in vitro* and in cell culture (1,2), are indicated by an asterisk. Key GRK2-binding residues within this domain are not conserved in the primary ASH sensory Gas ODR-3 and GPA-3 (shown in white), which are both most similar to the  $G\alpha_{i/o}$  family.

## **Plasmid Construction**

All constructs were sequenced following site-directed mutagenesis.

Site-directed mutagenesis (QuikChange, Stratagene) was used to correct amino acid 20 to serine in *Ce-grk-2* cDNA in pHA#343 (3) to make pFG8. pHA#343 incorrectly contains a glycine at this position.

pFG44: The ~3kb upstream promoter sequence of *Ce-grk-2* (3) was amplified from genomic sequence using primers JFW3 (5'- gcgcgcctgcaggcgacagtttccatagtgattgg-3') and DMF3 (5'- aaaggatccttttgttctgcaaaatcgaattg-3') to incorporate 5' SbfI and 3' BamHI sites, respectively. The promoter was inserted into these sites of pPD49.26 (Fire Lab *C. elegans* Vector Kit, Addgene).

grk-2p::grk-2 (pFG45): The ~3kb upstream promoter sequence of *Ce-grk-2* (3) was isolated by SbfI/BamHI digest of pFG44 and placed between the corresponding sites in pFG8.

grk-2p::grk-2(D3K) (pFG46), grk-2p::grk-2(L4K) (pFG47), grk-2p::grk-2(V7A/L8A) (pFG48), grk-2p::grk-2(D10A) (pFG49), grk-2p::grk-2(R195A) (pFG84), and grk-2p::grk-2(K567E) (pFG89): Sitedirected mutagenesis was used to introduce amino acid changes in the wild-type *Ce-grk-2* cDNA in pHA#343 (3). An additional round of site-directed mutagenesis was used to correct Gly20 to serine. Mutant *Ce-grk-2* cDNAs were isolated by Asp718/Sac1 digest and inserted into these sites in pPD49.26 (Fire Lab *C. elegans* Vector Kit, Addgene). The ~3kb *Ce-grk-2* upstream promoter sequence (3) was isolated by SbfI/BamHI digest of pFG44 and placed between the corresponding sites in pPD49.26, upstream of the *Ce-grk-2* cDNAs.

*grk-2p::grk-2(R016A)* (pFG85), *grk-2p::grk-2(Y109I)* (pFG86), and *grk-2p::grk-2(D110A)* (pFG86): Sitedirected mutagenesis was performed in pMST258, pMST259 and pMST260 to correct Gly20 to serine. Mutant *Ce-grk-2* cDNAs were isolated by Asp718/Sac1 digest and inserted into these sites in pPD49.26 (Fire Lab *C. elegans* Vector Kit, Addgene). The ~3kb *Ce-grk-2* upstream promoter sequence (3) was isolated by SbfI/BamHI digest of pFG44 and placed between the corresponding sites in pPD49.26, upstream of the *Ce-grk-2* cDNAs.

grk-2p::grk-2(K220R) (pFG88): Site-directed mutagenesis used to correct Gly20 to serine in pHA#348 (*Ce-grk-2(K220R)* cDNA in pPD49.26). The corrected mutant grk-2(K220R) cDNA was isolated by Asp718/SacI digest and inserted into these sites in pPD49.26 (Fire Lab *C. elegans* Vector Kit, Addgene). The ~3kb *Ce-grk-2* upstream promoter sequence (3) was isolated by Sbfl/BamHI digest of pFG44 and placed between the corresponding sites in pPD49.26, upstream of the *Ce-grk-2(K220R)* cDNA.

*grk-2p::grk-2(R587Q)* (pFG90) and *grk-2p::grk-2(K576E/R587Q)* (pFG91): Site-directed mutagenesis was used to introduce the R587Q change into pFG45 and pFG89. The R587Q change introduces a Sac1 restriction site into the *Ce-grk-2* cDNA sequence.

## SUPPLEMENTAL REFERENCES

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