Supplemental Methods

Strains

The following strains were obtained from the *Caenorhabditis* Genetics Center (University of Minnesota, USA): N2 Bristol, PY1589 *cmk-1(oy21),* GN244 *cmk-1(pg58),* VC691 *ckk-1(ok1033),* RB1468 *dkf-2(ok1704),* VC567 *arf-1.2(ok796)*, VC127 *pkc-2(ok328)*, KG532 *kin-2(ce179)*, RB918 *acr-16(ok789)*, RB818 *hum-1(ok634)*, RB781 *pkc-1(ok563)*, RB1447 *chd-3(ok1651)*, RB830 *epac-1(ok655)*, HA865 *grk-2(rt97)*, NW1700 *plx-2(ev773)*; *him-5(e1490)*, PR678 *tax-4(p678)*, KG744 *pde-4(ce268)*, RB758 *hda-4(ok518)*, RB1625 *par-1(ok2001)*, DA596 *snt-1(ad596)*, XA406 *ncs-1(qa406)*, CB109 *unc-16(e109)*, RB653 *ogt-1(ok430)*, TU3568 *sid-1*(*pk3321*) him-5(*e1490*); *lin-15B*(*n744*); *uIs71*[*Pmyo-2*::mCherry; *Pmec-18*::*sid*-1], BC10002 *dpy-5(e907),* and VC40557 (which harbors *cmk-1(gk691866)* among many other mutations (Thompson et al. 2013); outcrossed strain is VG834 *cmk-1(gk691866)*). The following strains were obtained from the National BioResource Project for the nematode (Tokyo Womens Medical Hospital, Japan): FX01046 *ogt-1(tm1046),* FX01282 *T23G5.2(tm1282),* FX03075 *pdhk-2(tm3075),* FX00870 *nhr-6(tm870),* FX04733 *syx-6(tm4733),* FX05136 *R11A8.7(tm5136)*, and FX02653 *rab-30(tm2653).* *Transgenic strains.* The transgenic *C. elegans* strain VH905 *hdIs30*[P*glr-1*::DsRed2] was a gift from H. Hutter (Simon Fraser University, Canada). The plasmid containing *Pmec-7*::mRFP was a gift from J. Rand (University of Oklahoma Health Sciences Center, USA). The transgenic *C. elegans* strains YT1128 *lin-15(n765); tzEx*[P*ckk-1*::GFP; *lin-15*(+)] and YT2016 *tzIs2*[P*cmk-1*::GFP; *rol-6(su1006)*] and plasmids

containing *cmk-1* cDNA were gifts from Y. Kimura (Mitsubishi Kagaku Institute of Life Sciences, Japan) and D. Glauser (University of Fribourg, Switzerland).

The following strains were created for this work: VG183 *yvEx64*[P*cmk-1*::GFP; P*mec-7*::mRFP], VG12 *hdIs30*[P*glr-1*::DsRed2]; *tzIs2*[P*cmk-1*::GFP; *rol-6*(*su1006*)], VG19 *tzEx*[P*ckk-1*::GFP; *lin-15*(+)]; *hdIs30*[P*glr-1*::DsRed2], VG92 *cmk -1(oy21)*; yvEx49[P*cmk-1*::CMK-1; P*myo-2*::GFP], VG160 *cmk -1(oy21)*; *yvEx57*[P*cmk-1*::CMK-1; P*myo-2*::GFP], VG260 *yvEx73*[P*ogt-1*::GFP; P*mec-7*::RFP; *rol-6(su1006)*], VG214 *yvEx70*[P*ogt-1*::GFP; *rol-6(su1006)*] and VG261 *yvEx74*[P*ogt-1*::GFP; P*mec-7*::RFP; *rol-6(su1006)*], VG271 *cmk-1(oy21); dpy-5(e907),* VG279 *cmk-1(gk691866); dpy-5(e907),* VG245 *cmk-1(oy21); ogt-1(ok430),* VG708 *cmk -1(oy21)*; *yvEx*707[P*mec-3*::CMK-1::SL2::GFP; P*unc-122p::*RFP].

PCR fusion construct primers. The primer sequences for the PCR fusion construct P*cmk-1*::GFP were a gift from D. Baillie (Simon Fraser University, Canada). The forward and reverse primer sequences used to amplify the *cmk-1* promoter were TATCCAAAATCTTGCCGAAAGTA and agtcgacctgcaggcatgcaagctTAAAAAGGGGGATTGGGC, respectively. The forward and reverse primer sequences used to amplify GFP were AGCTTGCATGCCTGCAGGTCGACT and AAGGGCCCGTACGGCCGACTAGTAGG, respectively.

The forward and reverse primer sequences used to amplify the promoter-GFP fusion construct were AGAATGCCGTATCATAAGCGTAA and GGAAACAGTTATGTTTGGTATATTGGG, respectively.

The forward and reverse primer sequences used to amplify the *ogt-1* promoter were CTGTTTTCGATTTGATTCTTCAATCAC and agtcgacctgcaggcatgcaagctCTTCTCGATCGTCTAATCCATTCG, respectively.
The forward and reverse primer sequences used to amplify GFP were the same as those used for P*cmk-1*::GFP (see above).
The forward and reverse primer sequences used to amplify the promoter-GFP fusion construct were CGGTTCGCCTTTTATTATGTG and GGAAACAGTTATGTTTGGTATATTGGG, respectively.

Kinase and phosphosite prediction and evolutionary analyses. The kinase substrate specificity prediction matrices (KSSPM) for *C. elegans* CMK-1, human CaMK1 isoforms and human CaMK4 were generated using an updated version of the algorithm originally described in Safaei *et al*. (Safaei et al. 2011). The *C. elegans* CMK-1 KSSPM was used to score all of the hypothetical peptides surrounding each of the serine and threonine residues in the 20,470 known *C. elegans* protein sequences. The top 597 scoring phosphopeptides were examined for their conservation in humans using the algorithm described in Safaei *et al*. (Safaei et al. 2011). The identified human phosphosites were then scored with the KSSPMs for human CaMK1 isoforms and human CaMK4.

Behavioral testing of mutant strains. Worms were synchronized for behavioral testing on Petri plates containing Nematode Growth Media (NGM) seeded with 50 μl of OP50 liquid culture 12-24 hours before use. Five gravid adults were picked to

plates and allowed to lay eggs for 3-4 hours before removal. The animals were maintained in a 20°C incubator for 72, 96, or 120 hours. Plates of worms were placed into the tapping apparatus and after a 100s acclimatization period, 30 taps were administered at either a 60s or a 10s ISI.

For CMK-1 rescue strains, twelve hours prior to testing, 40-60 worms carrying the selection marker were transferred using a platinum pick to a fresh NGM plate. Plates were seeded with 50 μl of OP50 liquid culture 12-24 hours before use.