Figure S1.

A

```
HsRIβ          R  R  R  R  G  G  V  S  A  E  101
CeKIN-2        G  G  R  R  T  G  I  S  A  E   99
wt            GGTGGACGCAGAACCGGAATCTCT
cau1(R92H)          CAC
ce179(R92C)         TGC
```

B

pkaPS prediction results

Results

Description	Position	Score	Sequence	Profile	T_1	T_2	T_3	T_4	T_5	T_6	T_7	T_8	T_9	T_{10}	T_{11}	T_{12}	T_{13}	T_{14}
t7	2	0.28	*MTSSSRGYQRVDSSGDGGSLLMEEE	0.31					-0.02	-0.01								
	13	0.31	*MTSSSRGYQRVDSSGDGGSLLMEEEGDNPHEALLHR	0.53		-0.02	-0.02		-0.02	-0.01		-0.01			-0.12			
	81	0.96	MDDRVTEIPEGFHRRQRRSGHEDIDDESDDESKDEDEEEEET	1.11		-0.01			-0.04	-0.05	-0.03		-0.02					
	444	0.68	VLVSELYANLMQKRARNMSREAFIVENLYVSKHIIPFIPTDI	1.42		-0.01						-0.01	-0.01		-0.10	-0.09	-0.36	-0.15
	502	0.64	TSSSAIDMQSCRFCHSRYSLNRAFK*	0.96		-0.02	-0.02				-0.06	-0.01	-0.13		-0.01	-0.06		-0.01

Summary

Submitted sequences:	1
Submitted S/T residues:	67
Number of predicted sites:	5

Figure S1. Analyses of the *C. elegans* KIN-2 amino acid sequence. (A) The inhibitory pseudosubstrate domains of the regulatory subunit of KIN-1/PKA (RIβ/KIN-2) from human and *C. elegans* are aligned. The nucleotide exchanges that result in the $R^{92}H$ and $R^{92}C$ substitution in the *cau1* and *ce179* alleles, respectively, are shown. **(B)** An *in silico* search for putative PKA phosphorylation sites was performed with the *pkaPS* tool adjusted for scores > 0 (http://mendel.imp.univie.ac.at /sat/pkaPS, (NEUBERGER *et al.* 2007)). Five putative PKA-specific phosphorylation sites were predicted along the amino acid sequence of TWK-7, of which the amino acid residues Ser^{81}, Ser^{444} and Ser^{502} were evaluated as highly specific.

Figure S2.

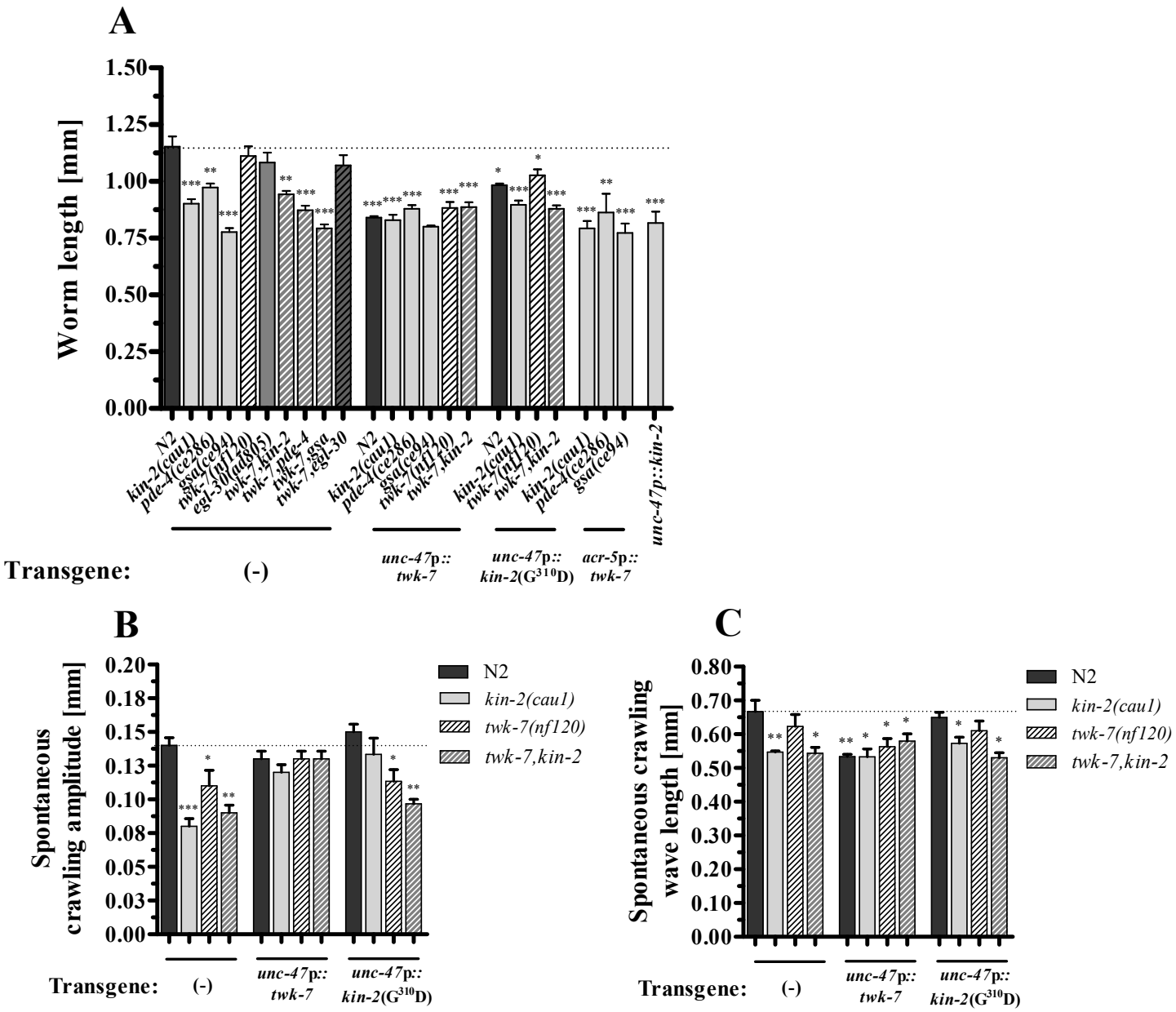

Figure S2. The body lengths and the absolute values of amplitudes and wavelengths during spontaneous crawling. (A) The body lengths of non-transgenic and transgenic animals are depicted. Non-transgenic and transgenic $G\alpha_S$ worms as well as the wild-type and *twk-7(null)* overexpressing the wild-type form of TWK-7 allele in GABAergic neurons are smaller than non-transgenic *twk-7(nf120)* and wild-type animals. In contrast, non-transgenic and transgenic $G\alpha_{q/0}$ mutants have body lengths that are similar to those of non-transgenic wild-type animals. **(B)** The absolute amplitudes and **(C)** wavelengths of transgenic and non-transgenic *C. elegans* strains with alterations in the $G\alpha_S$ and *twk-7* background during spontaneous crawling. For the measurement of wave parameters, N = 3 independent experiments with n = 15 worms per trial were evaluated. *$p < 0.05$; **$p < 0.01$; ***$p < 0.001$ (Student's *t*-test).