

Supplemental Data

Supplementary Fig. 1. PINK-1 is evolutionarily conserved from nematodes to mammals. A, The sequence alignment of PINK-1/PINK1 proteins. Sequence identity is highlighted in black; grey shading indicates sequence similarity. Predicted amino acid sequences were aligned with ClustalW: Ce, *C. elegans* PINK-1 (accession number: Q09298); hs, human PINK1 (accession number: NP_115785); ds, *Drosophila* PINK1 (accession number: JU0270). B, Schematic comparison of *C. elegans* PINK-1 and human PINK1 proteins. MTS: Mitochondrial targeting sequence. Identity and similarity values of amino acid sequences of the kinase domain are shown.

Supplementary Fig. 2: *tm1779* represents a loss-of-function allele for *pink-1*. A, Genomic structure of the *pink-1* locus. Exons and introns are indicated by boxes and lines, respectively. The promoter region is presented in the upper panel by boxed arrow. The genomic region that is removed in the *tm1779* deletion mutant is indicated in the lower panel. The solid line in the upper panel represents the probe used for northern blot analysis. B, Northern blot analysis reveals that the transcription of the *pink-1* gene is completely abolished in the *tm1779* mutant. *act-1* was used as loading control.

Supplementary Fig. 3: *lrk-1* is expressed ubiquitously in *C. elegans*. The expression pattern of *lrk-1* was investigated by transgenic expression of a $P_{lrk-1}::lrk-1::gfp$ construct in four independent lines (BR4118, BR4119, BR4120, and BR4121). *lrk-1* is ubiquitously expressed in all body regions including head and tail neurons (A and I), the pharynx (A), the distal tip cells (arrowheads), the canal-associated neurons (CAN; open arrowheads) and vulva epithelium (asterisk). A-B, Head region (head neurons, pharyngeal muscles). C-D, Mid body region (vulva epithelium, DTCs). E-F, Expression in the hypodermis. G-H, Mid body region (CAN, vulva epithelium). I-J, Tail region (tail neurons). The corresponding DIC pictures are shown (B, D, F, H and J). Scale bars represent 20 μ m.

Supplementary Fig. 4. *pink-1* mutant animals display CAN neurite pathfinding defects. Fluorescence micrographs of GFP expression in the CAN neurons of L4 larval animals carrying the integrated transgene *lqls4[ceh-10::gfp]* (20). A, Wild type (wt) animals showed normal posterior CAN axon pathfinding and CAN cell migration. B, *pink-1(tm1779)* animals displayed CAN axon pathfinding defects, a representative animal is displayed. The enlarged sector shows a 40-fold magnified view of the misguided CAN axon. Scale bar: 50 μ m.

Supplementary Fig. 1

A

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hs 1 MAVRQALGRG LQLGRALLLR FTGKPGRAYG LGR.....
ce 1 MSMKRFKAA YRIANELVAK GGRLPVFORF LPR.....
dm 1 MSVRLTLVRL IKHGRVILRS YCKRDHANI LDQNQLKTRS KRGFPLPSTA ANVLR

hs 34 ..FGP AAGCVRGERP GWAAGPGAEF RRVG.....
ce 34 ...IF PATYNLCVHV VLKKAP.....
dm 56 TTPQQ AAKSVVNVVP RTINSRSGSP FNGSGSSPTS SSGIFRVQGH ARKLEIDNIL

hs 75 AGLAARLQRO FVVRWGCAG PCGRAVFLAF G.LGLGLIEE KQAESRRRAVS ACOE
ce 58 LRRLARLVTRH GRVFRPFSSV IERHRFQNG N...DWRK FQPIRKELPR NVDL
dm 111 SRVTTTYSER LQRATRKLK FGDSPFPFAL IGVSASGSG VLSKEDLELEG VQWE

hs 128 HQAHFT QSKPG.PDP LDTRRLQGFR LEEVLIQOSI GKGCSSAAVYE ATMPITLQON
ce 108 VERIRQ IFGNGLRYNE DLKSTEWPNR IDSYEFCGEP GQGCNAAVYS ARLANSDAE
dm 165 TREAAAS RLQNAWNHDE ISDTLDSKFT IDBLEIGPPI AKGCAAVVYA ADFKDVVSS

hs 182 L EGTKSTGLLP GRGPTSAAPG EGQERAPG..
ce 163 S SGNTHYAGAF NEVTNLLAEI PPVSKVAQ..
dm 220 D GASLHDAQF QATPAFAPNS WSTHEMMSPL QNMSRFVHNF GGSVDNVPHY SQP

hs 211 .....
ce 192 .....
dm 274 SAASDFV GAQSREQDQR HHEQQHQHQ BQEQQHQQEP SSSAFNVTSP ANSNINSS

hs 211 AP AFPLAIKMMW NISAGSSS.E ALLNTMSQEL VPASRVLAG EYGAVTYRKS KR
ce 192 .K KFPLAIKMF NFEHHRDGDG HLLKSMGNEL APYPNAKLL NGQMGTRRPT P.
dm 329 VD SYPLAIKMMF NYDIOGNA.L SLIRAMYKET VPARQRGMN. EAADWEVRL QN

hs 264 GPKQLAPH PNIRVLRAP TSSVPLPGA LVDYDPVLES RHHPEGLG.H GRTLELV
ce 244 ...AKH PNIVRIQTAF IDSLKVLPGA IERYPDALHT ARWYBSIASE PKTMYVV
dm 381 QTVHLPRH PNIVCMFGFF CDVVRNFPDG HLLYFVAQEQ RINPQCYG.R NMSLYLV

hs 318 MKN YPCTLRQYLC VNTPSPLAA MMLLQLEGV DHLVQGGIAH RDLKSDNLLV E
ce 294 MRR YRQTLHEVWV TRHRNYWTGR VILIAQLLEAC TYHHEHVAQ RDMKSDNILL E
dm 435 MKR YDHSRGLLD SODLSTRNRI LLLAOMLEAV NHRSRHGVVAH RDLKSDNLLI E

hs 372 LD.PFGCPW LVHADFGCCL ADESIQLQLP FSSWYVDHGG NGCLMAPEVS TARPGP
ce 348 YDPDDEIPQ LVHADFGCAL ACDN.WQVD YESDEVSLGG NAKTRAPETA TAVPGK
dm 489 LQ.DDAAPV LVLSDFGCCL ADKVHQLRLE YVSHDVDHGG NAALMAPEIF NTMPGP

hs 426 RAVI DYKADAWAV GALAYEIFGL VNPFFGQKA HLESRS....
ce 401 NVKV NEEMADTAA GGLSYEVLTR SNPFYKLLDT AT.....
dm 543 FAVI NYCKADPWAC GALAYEIFGN RNPFYSSSGG MARERGEMTL SLRNSDYRQD

hs 470 QLPALPESVP PDVRLVRL LQREASKRPS ARVAANVLHL SLWG..EHL ALKNL
ce 441 ELPALPSRVN FVARDVIFDL LKRDPNERVK PNIAANLNL SLFRMGEDVK QMMEK
dm 597 QLPMSDACP ELLOQLVYNI LNPNSKRVS PDIAANVQL FLWAPSNEWK AGGMP

hs 523 KLDKM VGWLLQSSAA TLANR.....
ce 496 CGISQ MTTLLAGSSK VLSQKINSRL DKVMNLTAE TIMANLAPHL ISRAEQLRA
dm 652 NSPEI LQWLLSLTK IMCEGR.....
PQMAG LMPVASCGR RAYVEVLLIC

hs 557 LFLANLECET LCQALLLCS WRAAF.....
ce 551 TFLSRMNRER TWRSTQYFFP AGVQDTPAT SSDCLETISS LMSSFSNDSE NYEK
dm 699 SPLARARLRR IRGALNWIQN VVA.....

hs .....
ce 605 QQKPAK NGYNNVPLL RNVIRTDADG INGIVHRVRS K
dm .....

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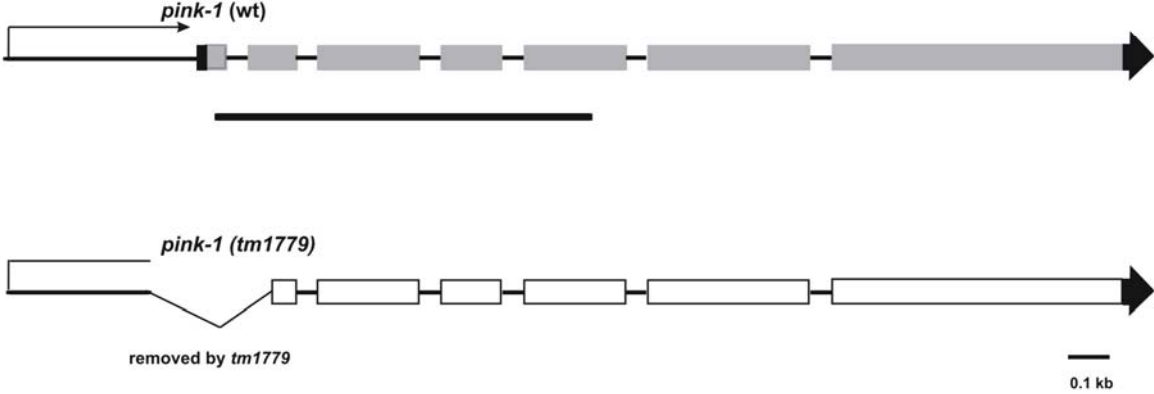
B



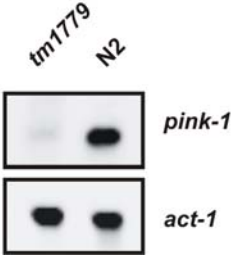
36 (54) % identity (similarity)

Supplementary Fig. 2

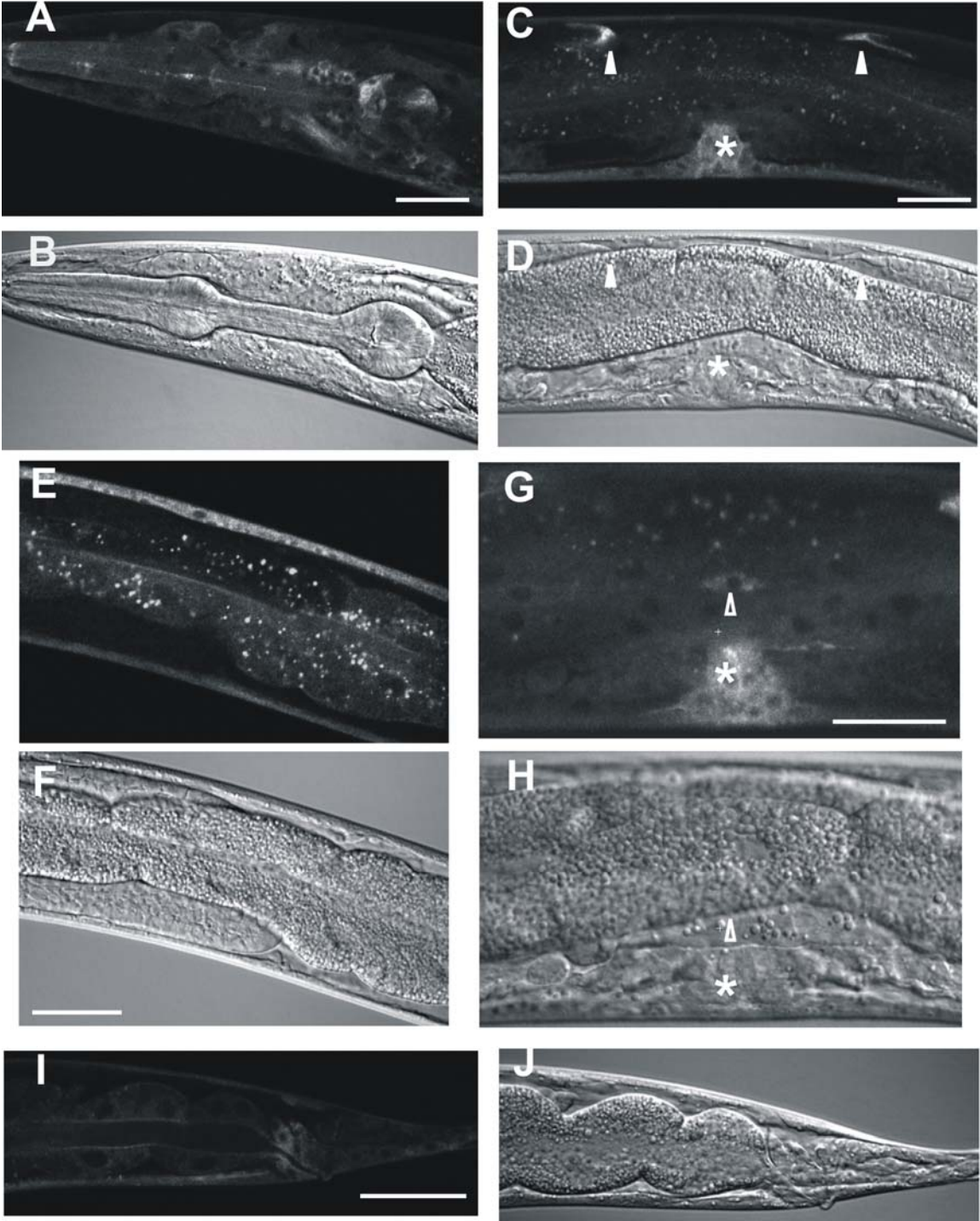
A



B



Supplementary Fig. 3



Supplementary Fig. 4

