

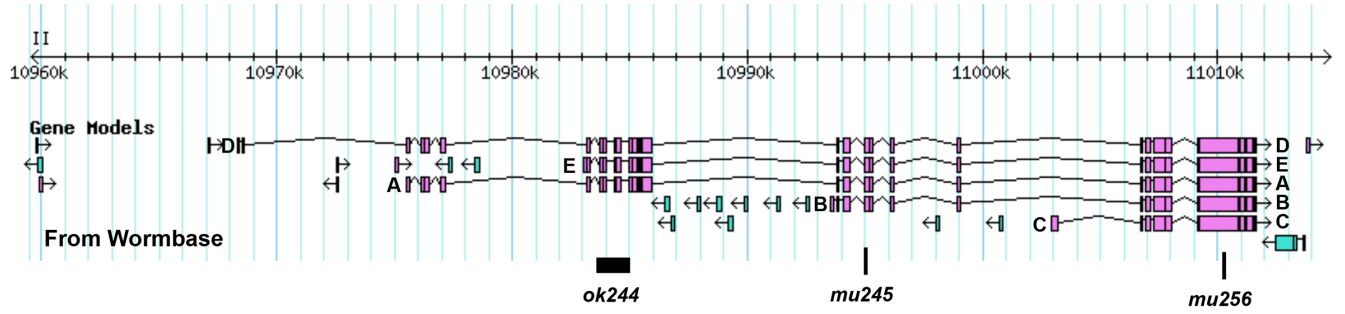
Figure S1 The *mig-21* locus as defined by RNA seq transcript sequencing. Shown is output from the Integrated Genome Viewer 2.0.15 program which aligned RNA seq reads (grey bars) from L1 larvae at 5-5.5 h post hatching to the *C. elegans* genome. The *F01F1.13/mig-21* region is shown, as are the flanking genes *F01F1.12/aldo-1* and *F01F1.2*. Read polarity is indicated by a point at the end of each run, and thin lines between reads indicate that the read aligned across a putative intron. The hatched box represents the region of exon 1 predicted in Middelkoop et al., 2012 but that is not represented by reads in this RNA seq analysis.

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                                gtagaaatttcacttattcagtaagaact
gagtttcatagaaaATGATTGTCATGGTTTTGTTTAAATATCTTCGTTTTTCGTC AATTTCT
1   M I V M V L F N I F V F V N F signal sequence
CATATTCGTTGGCTAATTTAAATGATTTCTAGCATTATATTTCTCAAGTTGTCTCTAATA
16  S Y S L A N L N D S S I L Y S Q V V S N
AGTGTGCATCTAATAATGGTATATTTCTGTGAATGTTTCGAAACAAGGCGGAGAAATTAAGg
36  K C A S N N G I F C E C S K Q G G E I K
ttctacattcaaaaagataaaaaccaattcaataaaatTTTgatgcagATTTGGAATTGC
56                                     I W N C
A in u787 (W to *)
ATCCGTC CAGGAGTTGTCAACGTGGTCAAAATGGTCGAAATGTAGAGAAGGTATCCGA
60  I R P G G W S T W S K W S K C R E G I R TSP1 #1
AAAAGAAGACGAACGTGTAATAATCCTTTACCAATTGGTACC ACTTGTCTGGCCAGAAA
80  K R R R T C N N P L P I G T T C S G Q K
GTTGAGAAGCAATCTTGTGCAATTTCTTCAAATGTACCGGAGTATCTTTTGGATCCTGG
100 V E K Q S C A I S S N V P E Y L F G S W
ACATCCTGGAATCCATGGTCTCGATGCGATTGTGATCGTAGCTGAGGATACGgtaggtt
120 T S W N P W S R C D C D R S L R I R TSP1 #2
caacaattgggaaatgtacagtaaccaagtttcagAACTCGGCACTGCAAAGGTAATT
138                                     T R H C K G N
A in lq37 (C to Y)
CCTGCGAGGGATGTGACAAGGATTACGAAGATTGCCGCCAGATGAGTGTCCAATTAGTA
145 S C E G C D K D Y E D C R P D E C P I S
AAAAATGGTCCGAATGGACAGATTGGGTGAATTATGgtatgggtctcattacgctgaaat
165 K K W S E W T D W V N Y
atatcaacaatTTTgtaatgatttaatttcagGAATTGAGCAAGTACGGTTTTTCAGCCTG
177                                     G I E Q V R F S A W
A in lq78 (G to E)
GTGTTTCGTCATCAAACGTGGCGAATACTGAAGTGGGAATACGGAAGGAGACTCAAGACTC
187 C S S S N V A N T E V G I R K E T Q D S
AATGAAGCATGgtattaatTTtagttaaaaaatTTcgaagaaccataactgaaagactaa
207 M K H
atttgaaagtttcaaagtacaatgtccactttactgtctaaatTTTTgtgtagttaaca
a in lq84 (3' splice site)
acatgataaaaaatTaatgagaataatTTTccagCCAAC TGGTCTGAATGGCATATGCATC
210 A N W S E W H M H
CAGGAGTTGCATACCGTTATCGTCTTCTTCAACTCTTCTATTTCCATCGAACACCATC
219 P G V A Y R Y R L L H N S S I S I E H H
TCTTATCAAGATTCACGTCATCATGTCTTCCCTTGCATTTTGCAATCCAATATTTTGT
239 L L S R F T S S C L P L H F A I P I F C Transmembrane
TTTGTATTCTCACGGGTTTCTTCTCAAATATTATTTATTGTTGTGAATCGTTTTTA
259 F C I L T G F L L Q N I I Y C V V N R F
AAAGGAGATTCATAAGATTGAATTATTCGTATGATTCAAATCCACGTGACTATCCTTCTC
279 K R R R F I R L N Y S Y D S N P R D Y P S
ATTTGATTCGTTCTCCGGTTCCCGAAAGATGAAAGTTTTTGGTGAatttcggatgctt
299 H L I R S P G S P K D E S F W *
tcgagaacagtctctgtctgcccatttctcagccacgataataaaaagttatcattgatc

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Figure S2 The *mig-21* coding region. The DNA sequence of the *mig-21* coding region as determined from cDNAs and transcript sequencing runs on Wormbase, and from our RNA seq analysis. The predicted 5' and 3' untranslated regions and introns are lowercase, and the open reading frame is upper case. A putative poly-A site in the 3' UTR is underlined. Nucleotide lesions associated with *mig-21* alleles are shown in red above the DNA sequence. The putative polypeptide encoded by *mig-21* is shown below the DNA sequence. A potential signal sequence, two potential thrombospondin type I domains, and a potential transmembrane domain and highlighted in grey.



mu245: *ptp-3B* exon 4 **A**
 ACAATCTATGGTTACGCGCACAAGGATATCCGGACT**C**ATATGTCAAGGCGAAGACAGTCGACGGAACCGATCTATCAAC

mu256: *ptp-3B* exon 12 **GA**
 CTGCCACATATGGAGATATCGAGGTGACACTGTTG**GA**AAGCGTTCATTGGCTCATTATACGATGAGAACGATGCGATT

Figure S3 The *ptp-3* locus and mutations. A screen shot from Wormbase 229 of the *ptp-3* locus with the A-E isoforms indicated. The sites of *ptp-3* mutations are shown, with the corresponding nucleotide changes below.

Table S1 Data for Q protrusion and migration in mutants. The table contains data for QR and QL protrusion and migration at three stages: 2-2.5 hours post-hatch when the Q cells have protruded; 3-3.5 h post hatch when the Q cells have migrated; and 4-4.5 h post hatch, when the Q cells have undergone their first division.

Available for download at <http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.112.145706/-/DC1/>.