The *C. elegans* NF2/Merlin Molecule NFM-1 Non-Automously Regulates Neuroblast Migration and Interacts Genetically with the Guidance Cue SLT-1/Slit

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Abstract

During nervous system development, neurons and their progenitors migrate to their final destinations. In *Caenorhabditis elegans*, the bilateral Q neuroblasts and their descendants migrate long distances in opposite directions, despite being born in the same posterior region. QR on the right migrates anteriorly and generates the AQR neuron positioned near the head, and QL on the left migrates posteriorly, giving rise to the PQR neuron positioned near the tail. In a screen for genes required for AQR and PQR migration, we identified an allele of *nfm-1*, which encodes a molecule similar to vertebrate NF2/Merlin, an important tumor suppressor in humans. Mutations in NF2 lead to Neurofibromatosis Type II, characterized by benign tumors of glial tissues. These molecules contain Four-point-one Ezrin Radixin Moesin (FERM) domains characteristic of cytoskeletal-membrane linkers, and vertebrate NF2 is required for epidermal integrity. Vertebrate NF2 can also regulate several transcriptional pathways including the Hippo pathway. Here we demonstrate that in *C. elegans*, *nfm-1* is required for complete migration of AQR and PQR, and that it likely acts outside of the Q cells themselves in a non-autonomous fashion. We also show a genetic interaction between *nfm-1* and the *C. elegans* Slit homolog *slt-1*, which encodes a conserved secreted guidance cue. In vertebrates, NF2 can control Slit2 mRNA levels through the hippo pathway in axon pathfinding, suggesting a conserved interaction of NF2 and Slit2 in regulating migration.
Introduction

A critical process in nervous system development is the directed migration of neurons to precise destinations. Directed migration is a complex process that requires integration of extracellular cues into cytoskeletal changes which guide the cell to a specific location. In *C. elegans* the Q neuroblasts are an established system to study directed cell migrations (MIDDELKOOP AND KORSWAGEN 2014). The QR and QL neuroblasts are born in the posterior region of the worm yet migrate in opposite directions (SULSTON AND HORVITZ 1977; SALSER AND KENYON 1992; SALSER *et al.* 1993). QL is born on the left side of the animal and migrates posteriorly over the seam cell V5 before dividing. During this initial migration QL detects a posteriorly derived EGL-20/Wnt signal which through canonical Wnt signaling initiates transcription of *mab-5/Hox* (SALSER AND KENYON 1992). MAB-5 drives further posterior migration of the QL lineage, resulting in the QL.a descendant PQR migrating to the tail near the anus and posterior phasmid ganglion. QR is born on the right side of the animal and migrates anteriorly over the seam cell V4 and away from the EGL-20/Wnt signal (SALSER *et al.* 1993; HARRIS *et al.* 1996; SALSER AND KENYON 1996). QR does not initiate *mab-5* expression in response to Wnt and continues to migrate anteriorly. After division, QR.a undergoes an identical pattern of cell divisions and cell death as QL.a while migrating anteriorly, with AQR completing migration near the posterior pharyngeal bulb in the head (Figure 1)(MALOOF *et al.* 1999; WHANGBO AND KENYON 1999). Initial Q migrations are controlled autonomously by the receptor molecules UNC-40/DCC and PTP-3/LAR (HONIGBERG AND KENYON 2000; SUNDARARAJAN AND LUNDQUIST 2012) and non-autonomously by the Fat-like cadherin CDH-4 (SUNDARARAJAN *et al.* 2014). Later Q
descendant migrations are controlled by Wnt signaling (Whangbo and Kenyon 1999; Zinovieva and Forrester 2005; Zinovieva et al. 2008; Harterink et al. 2011), which appears to not be involved in initial migration (Josephson et al. 2016), and by the transmembrane receptor MIG-13 in parallel with SDN-1/Syndecan (Wang et al. 2013; Sundararajan et al. 2015).

To identify additional molecules that regulate Q migrations, a forward genetic screen for mutations affecting AQR and PQR migration was previously performed. Here we report that this screen identified an allele of nfm-1, which encodes a C. elegans Neurofibromatosis Type II (NF2)/Merlin molecule. NF2 acts as a tumor suppressor in humans, and mutations in the gene lead to development of neurofibromatosis type II (Gusella et al. 1996; Gutmann et al. 1997), a disease of benign Schwannomas that must be removed surgically. NF2/Merlin is involved in signaling pathways involving hippo, mTOR and PI3K-Akt (Zhao et al. 2007; Striedinger et al. 2008; James et al. 2009; Okada et al. 2009). Additionally, NF2 is involved in nervous system maintenance, corpus callosum development, and axon guidance (Schulz et al. 2013; Lavado et al. 2014; Schulz et al. 2014). In corpus callosum development, NF2 inhibits the hippo pathway component Yap. In NF2 mutants, this inhibition is relieved, resulting in increased expression of Slit2, a secreted axon guidance cue that prevents midline crossing. This leads to defects in midline crossing of axons in the callosum (Lavado et al. 2014).

In C. elegans, RNAi against nfm-1 results in embryonic lethality (Skop et al. 2004), and an nfm-1::gfp transgene is reported as being localized to the basolateral region of gut epithelium (Zhang et al. 2011). Here we report that two likely hypomorphic
mutations in nfm-1 display AQR and PQR migration defects. Mosaic analysis and expression studies indicated that NFM-1 might not act in the Q cells themselves (i.e. that it acts non-autonomously). Finally, we show a genetic interaction between NFM-1 and the secreted guidance cue SLT-1 in AQR migration. In vertebrates, Slit1 and Slit2 are required for guidance of many axons, acting through the Robo family receptors (Nguyen Ba-Charvet et al. 1999; Piper et al. 2000; Bagri et al. 2002; Unni et al. 2012; Kim et al. 2014). The Slit-Robo guidance pathway is conserved in C. elegans where SLT-1 acts as a guidance cue for several neurons through SAX-3/Robo (Hao et al. 2001; Chang et al. 2006; Quinn et al. 2006; Xu and Quinn 2012). In general, detection of extracellular guidance cues such as Slit cause cytoskeletal changes that result in directed migration of cells and axonal growth cones, most typically repulsion. We show that slt-1 mutations enhance AQR migration defects of nfm-1 mutations, and that sax-3 mutants display defects in AQR and PQR migration. These results are consistent with a model in which NFM-1 regulates AQR and PQR migration by controlling the production of an extracellular cue, either SLT-1 itself or an unidentified cue that acts in parallel to SLT-1.
Materials and Methods

Nematode Strains and genetics

*C. elegans* were grown under standard conditions at 20°C on Nematode Growth Media (NGM) plates (Sulston and Brenner 1974). N2 Bristol was the wild-type strain.

Alleles used include LG III: *nfm-1(ok754)*, *nfm-1(lq132)*, LG X: *sax-3(ky123)*, *slt-1(ok255)*, *slt-1(eh15)*. Standard gonadal injection was used to create the following extrachromosomal arrays: *lqEx773* [*nfm-1::gfp* fosmid (5ng/µL), *Pgcy::32::yfp* (50ng/µL)], *lqEx782* [*Pnfm-1::gfp* (10ng/µL), *Pgcy-32::cfp* (25ng/µL)]. Ultraviolet Trimethylpsoralen (UV/TMP) techniques (Mello and Fire 1995) were used to integrate extrachromosomal arrays to generate the following transgenes: LGII: *lqIs244* [*lqEx737*, *Pgcy-32::cfp* (25ng/µL)], unknown chromosomal location *lqIs247* [*lqEx773*, *nfm-1::gfp*], *lqIs274* [*lqEx834*, *Pegl-17::myr-mCherry* (20ng/µL) *Pegl-17::mCherry::his-24* (20ng/µL)]. The *nfm-1::gfp* fosmid was obtained from the TransgeneOme project, clone 7039520022144752 D02 (Sarov et al. 2006). *nfm-1(ok754)* was maintained as a heterozygote over the *hT2* balancer because homozygous *ok754* animals arrest during larval stages, but positions of AQR and PQR could be scored in these arrested animals.

Genotypes with M+ had maternal contribution from the *hT2* balancer.

Scoring migration of AQR and PQR

AQR migrates to a position near post-deirid ganglia in the region of the posterior pharyngeal bulb, and PQR migrates posteriorly to a position near the phasmid ganglia posterior to the anus. We used a method as described previously to score AQR and PQR position using *Pgcy-32* to drive expression of fluorescent proteins (Shakir et al. 2006;
Five positions in the anterior-posterior axis of the animal were used to score AQR and PQR position. Position 1 was the wild-type position of AQR and is the region around the posterior pharyngeal bulb. Neurons anterior to the posterior pharyngeal bulb were not observed. Position 2 was posterior to position 1, but anterior to the vulva. Position 3 was the region around the vulva, position 4 was the birthplace of Q cells, and position 5 was posterior to the anus, the wild-type position of PQR (see Figure 2D). A Leica DM550 equipped with YFP, CFP, GFP, and mCherry filters, was used to acquire all micrographs, and for visualization of A/PQR for scoring. Micrographs were acquired using a Qimaging Retiga camera. Significances of difference were determined using Fisher’s Exact test.

Mosaic analysis.

Mosaic analysis was conducted as previously described (CHAPMAN et al. 2008; SUNDARARAJAN et al. 2014). A rescuing nfm-1(+) extrachromosomal array was generated using the nfm-1::gfp fosmid with a Pgcy-32::yfp marker. This array was crossed into nfm-1(ok754)/hT2; lqIs58 (Pgcy-32::cfp) to create the rescuing array lqEx773, referred to as nfm-1(+). Presence of the rescuing array was determined by Pgcy-32::yfp expression, and position of AQR and PQR was determined by Pgcy-32::cfp expression. nfm-1(ok754)III; nfm-1(+) animals were viable and fertile and had wild-type AQR and PQR position, indicating rescue of nfm-1(ok754). Presence of YFP in AQR or PQR indicated nfm-1(+) was present in those cells during their migrations. Pgcy-32 is also expressed in URX, and presence of YFP in the URX neurons indicates other tissues have inherited nfm-1(+). Animals that lost nfm-1(+) in AQR or PQR, and retained nfm-
I(+), in the other Q descendant (PQR and AQR respectively) and URX were scored for AQR and PQR position.

Synchronization of L1 larvae for expression analysis.

L1 Animals carrying Pnfm-1::gfp or nfm-1::gfp fosmid were synchronized as described previously to the time of Q cell migration (3-5h post hatching) (CHAPMAN et al. 2008; SUNDARARAJAN AND LUNDQUIST 2012). Gravid adults were allowed to lay eggs overnight. Plates were washed with M9 buffer, and eggs remained attached to plate. Hatched larvae were collected every half hour using M9 washes and placed onto clean NGM plates for later imaging. Pegl-17::mCherry was used as a Q cell marker to determine overlapping expression of nfm-1 expression constructs.
Results

*nfm-1* mutants have defective AQR and PQR migration.

QL and QR undergo identical patterns of cell division, cell death, and neuronal differentiation, but migrate in opposite directions (Figure 1). To identify genes required for AQR and PQR migration, a forward genetic screen using the mutagen ethyl methanesulfonate (EMS) was conducted (Sulston and Hodgkin 1988). This screen identified a new mutation with defective AQR and PQR migration, *lq132* (10% AQR defects and 6% PQR defects, Figure 2). The genome of the *lq132*-bearing strain was sequenced and variants were detected using Cloudmap (Minevich et al. 2012). The strain contained a contained a splice-donor mutation after the fifth exon in the *nfm-1* gene (Figure 2A) (GTATGTGT to ATATGTGT). We scored AQR and PQR migration in the *nfm-1(ok754)* mutant generated by the *C. elegans* gene knock-out consortium. *nfm-1(ok754)* is an in-frame 1042-bp deletion with breakpoints in exons 3 and 7 that removes all of exons 4, 5, and 6 (Figure 2A and B). *nfm-1(ok754)* homozygotes arrested as larvae, but we were able to score AQR and PQR position in arrested larvae. *nfm-1(ok754)* had strong AQR defects, with 88% of AQR failing to migrate to the head, and occasional (1%) posterior AQR migration (Figure 2C and E). *nfm-1(ok754)* also had significant PQR defects, with 15% of PQR failing to migrate into the wild-type position 5 posterior to the anus (Figure 2F). An *nfm-1::gfp* fosmid transgene rescued AQR and PQR defects of both *lq132* and *ok754*, indicating that mutations in *nfm-1* were causative for the migration deficiencies of *lq132* and *ok754* (Figure 2E and F).

*nfm-1* encodes a protein similar to human NF2/Merlin (43% identity), and contains Four-Point-One Ezrin Radixin and Moesin (FERM) N, B, and C domains at the
N-terminus (Figure 2B). The lq132 splice donor mutation occurred after the conserved FERM domain regions, and the ok754 in-frame deletion removes the entire FERM C domain, including the putative actin-binding site (Figure 2B). RNAi of nfm-1 caused embryonic lethality (SKOP et al. 2004). Thus, both lq132 and ok754 are likely not null alleles and retain some function. AQR migration defects in ok754 were significantly strong than lq132, suggesting that ok754 is a stronger allele than lq132.

Mosaic analysis indicates a non-autonomous requirement for nfm-1 in anterior AQR migration

Genetic mosaic analysis using a rescuing nfm-1(+) extrachromosomal array was used to test if nfm-1 was required in the Q cells themselves (see Methods). In C. elegans, extrachromosomal arrays are not stably inherited meiotically, and can be lost during mitotic cell divisions, creating genetically mosaic animals. We used an established strategy to score mosaic animals that had lost an nfm-1(+) rescuing transgene in AQR or PQR lineage (see Methods and (CHAPMAN et al. 2008; SUNDARARAJAN et al. 2014)). This strategy uses a stable Pgcy-32::cfp integrated transgene to visualize AQR and PQR in all animals, and an unstable array nfm-1(+) carrying the rescuing nfm-1::gfp fosmid and Pgcy-32::yfp (Figure 4.3). Non-mosaic nfm-1(ok754) animals that harbored the nfm-1(+) array were viable, fertile, and were rescued for AQR and PQR migration (Figure 2E and F). We analyzed 89 mosaic animals in which the nfm-1(+) array was lost from the AQR lineage, but retained in PQR and URX lineages as shown in Figure 3. These animals were rescued for AQR migration defects despite loss of nfm-1(+) in AQR, suggesting that nfm-1 is required non-autonomously for anterior AQR migration (Figures
3B and C and 4A). Similarly, PQR migration defects were still rescued in 75 mosaic animals in which PQR that had lost the nfm-1(+) array (Figure 4B). Animals mosaic for nfm-1(+) in AQR or PQR rescued nfm-1(ok754) defects to a similar level as non-mosaics (nfm-1(+) in AQR and PQR) (Figure 4A and B). In sum, this mosaic analysis indicates that nfm-1 function was not required in AQR and PQR for their proper migration, and that nfm-1 might act non-autonomously in this process.

Using this method, it was impossible to determine which tissues require nfm-1.

Based on cell lineages (Figure 3A), presence of nfm-1(+) array in URX and either AQR or PQR suggests it is present broadly in AB-derived lineages. P lineages were not assayed in this study, but mosaic nfm-1(ok754) animals, which normally arrest as sterile larvae, grew to viable and fertile adults, again suggesting broad nfm-1 distribution in the mosaics, possibly including P-derived germ line and gonad lineages. It is possible that perdurance of NFM-1 protein, or array loss in the Q lineages themselves led to nfm-1 function in the Q lineages despite loss in AQR or PQR. To account for these rare but possible events, we scored at least 70 mosaic animals. Overall, mosaic analysis suggests that nfm-1 acts non-autonomously in AQR and PQR migration, as loss of the rescuing array in AQR or PQR did not correlate with mutant phenotype.

nfm-1::gfp transcriptional and translational reporter expression was not apparent in Q lineages.

A Pnfm-1::gfp transcriptional reporter was created by using a 2.1-kb region upstream of nfm-1 to drive expression of GFP. This 2.1-kb region was the entire upstream region between nfm-1 and the next gene anmt-2. At the time of Q migration, this
construct showed expression in posterior cells near the anus, including posterior intestinal cells, the three rectal gland cells, and other unidentified cells that might be the anal sphincter muscle and the stomatointestinal muscle (Figure 5A-C). Variable expression in the hypodermis was also observed (Figure 5A-C). Overlap between Pnfm-1::gfp and Pegl-17::mCherry, a Q cell marker, was not observed, consistent with nfm-1 not being expressed in the Q neuroblasts during their migrations (Figure 5A-C). Likewise, full length NFM-1::GFP expression from the rescuing fosmid was not observed in migrating Q cells (Figure 6). NFM-1::GFP was detected in the posterior gut region. In sum, no nfm-1 transgene expression was observed in the Q cells during their migration.

**slt-1 mutations enhance AQR defects of nfm-1(lq132).**

Previous studies suggested that NF2 can non-autonomously affect axon guidance in the developing mouse brain (LAVADO et al. 2014). This guidance mechanism occurs through regulation of Slit2 mRNA levels, suggesting a transcriptional role of NF2 (LAVADO et al. 2014). Slit2 is a secreted guidance cue for developing neurons, and is detected by the Robo receptor. Because of interactions between Slit2 and NF2 we investigated the interaction of nfm-1 and the *C. elegans* Slit2 homolog slt-1 in Q descendant migration. In this study we used one null allele slt-1(eh15), and one strong loss-of-function in frame deletion allele slt-1(ok255) (HAO et al. 2001; STEIMEL et al. 2013). slt-1 mutations had no effect on AQR and PQR migration on their own, but enhanced AQR migration defects of nfm-1(lq132) and nfm-1(ok754) (Figure 7). slt-1 had no effect on PQR migration in double mutants. We tested the SLT-1 receptor SAX-3/Robo, and sax-3(ky123) mutants
showed weak but significant defects in both AQR and PQR migration, consistent with SAX-3 promoting migration of the Q lineages (Figure 7).
Discussion

The NF2/Merlin molecule NFM-1 promotes migration of AQR and PQR.

Complete migration of the QR and QL descendants AQR and PQR requires the coordination of many genes (Middekoop and Korswagen 2014). Although numerous molecules have been identified that act in the Q cells to promote migration, such as the transmembrane receptors UNC-40/DCC, PTP-3/LAR, and MIG-13 (Sundararajan and Lundquist 2012; Wang et al. 2013; Sundararajan et al. 2015), fewer have been identified that act outside the Q cells to control their migration. Of the non-autonomous genes that have been implicated in Q descendant migration, most are secreted molecules such as Wnts (Hunter et al. 1999; Whangbo and Kenyon 1999; Korswagen 2002; Pan et al. 2006), although some transmembrane genes such as CDH-4 have been demonstrated to non-autonomously affect Q cell migration (Sundararajan et al. 2014).

Here we present data identifying a non-autonomous role for the FERM domain-containing molecule NFM-1 in promoting Q migration. NFM-1 is similar to human NF2/Merlin, the molecule affected in Neurofibromatosis type II. We found that mutations in nfm-1 resulted in severe AQR migration defects, and to a lesser extent PQR migration defects. These defects typically manifested as incomplete migrations, suggesting that these nfm-1 mutations did not affect direction of migration along the anterior/posterior axis, but rather the migratory capacity of these cells.

Loss of NF2/Merlin function in either mouse or Drosophila results in embryonic lethality (Feigon et al. 1997; McClatchey et al. 1997). In C. elegans, nfm-1 appears to be required in embryonic development similar to other animals, as RNAi against nfm-1 is reported as embryonic lethal (Skop et al. 2004), and no null alleles of nfm-1 have been
The two \textit{nfm-1} mutations studied here are not complete loss of function and likely retain some NFM-1 function. The 5' splice site mutant \textit{nfm-1(lq132)} was viable and fertile, and the in-frame deletion allele \textit{nfm-1(ok754)} caused larval arrest. It is possible that complete loss of \textit{nfm-1} function results in more severe AQR and PQR migration defects, possibly even directional defects, not observed in these alleles. The \textit{nfm-1(ok754)} in-frame deletion removes part of the FERMB domain and the entire FERMC domain, suggesting that these domains are important in AQR and PQR migration.

\textbf{NFM-1 acts non-autonomously in AQR and PQR migration.}

As a cytoskeletal-membrane linker with a potential actin-binding domain, we hypothesized that NFM-1 might regulate actin-based membrane protrusion in migrating cells. However, a genetic mosaic analysis indicated that NFM-1 was not required in AQR or PQR for their migration. Furthermore, expression of transgenes of the \textit{nfm-1} promoter and a rescuing full-length \textit{nfm-1::gfp} were not observed in Q lineages. Rather, expression was observed in in posterior region near the anus, including posterior intestine, the rectal gland cells and potentially the anal sphincter muscle and stomatointestinal muscle. While the mosaic analysis was unable to discern the tissue in which NFM-1 acts, these expression studies suggest that NFM-1 function in the posterior region of the gut near the anus might regulate AQR and PQR migration. However, hypodermal expression is also a possibility. In sum, mosaic analysis and expression studies indicate that NFM-1 acts outside of the AQR and PQR, non-autonomously, to regulate their migration.
nfm-1 and slt-1 interact genetically to promote anterior AQR migration.

In Drosophila and mice, NF2/Merlin is known to regulate several signaling pathways, including stimulating the Hippo pathway to inhibit the Yorkie transcription cofactor (HAMARATOGLU et al. 2006; MOROISHI et al. 2015). In mice, loss of NF2 in neural progenitor cells results in upregulation of Yap (LAVADO et al. 2014). High Yap activity leads to ectopic levels of the secreted guidance cue Slit2 which causes defects in midline axon guidance (LAVADO et al. 2014). Interestingly, this is a non-autonomous role of NF2 in midline axon guidance, similar to our observation of nfm-1 in C. elegans neuronal migration. The Hippo pathway in C. elegans is poorly conserved, and the C. elegans genome does not encode a clear Yap homolog (HILMAN AND GAT 2011). We tested the role of the single C. elegans Slit gene slt-1 in AQR/PQR migration and interaction with nfm-1. slt-1 regulates the anterior-posterior migration of the CAN neurons in embryos (HAO et al. 2001). Although no migration defects were detected in slt-1 mutants alone, they did enhance AQR migration defects of nfm-1(lq132) and nfm-1(ok754). This enhancement is consistent with NFM-1 and SLT-1 acting in parallel pathways, but since we do not know the null phenotype of NFM-1 with regard to AQR and PQR, the possibility that they act in the same pathway cannot be excluded.

Interestingly no enhancement of nfm-1 PQR migration defects was seen in slt-1; nfm-1 double mutants. This suggests that slt-1 and nfm-1 interact in AQR migration but not PQR migration. This is of note because nfm-1 is expressed in posterior tissues where PQR migrates, and away from which AQR migrates. sax-3/Robo mutants displayed both AQR and PQR migration defects. Possibly, SAX-3/Robo acts with SLT-1 in AQR migration, and with an unidentified ligand in PQR migration. In mice, midline axon
defects are due to excess Slit2 expression in NF2 mutants. The phenotypic enhancement that we observe between slt-1 and nfm-1 suggests that these molecules are both required for AQR migration. Further studies of the interaction between nfm-1 and slt-1 will be required to understand the role of these molecules in AQR migration.

Our results, combined with those in vertebrates, are consistent with the idea that NFM-1 promotes the production of a signal or signals that regulate AQR and PQR migration. This could be SLT-1 itself, such as in vertebrates, or a molecule that acts in parallel to SLT-1. The slt-1 expression pattern is dynamic throughout development, but slt-1 is expressed in posterior cells including body wall muscles and the anal sphincter muscle (HAO et al. 2001). Whether nfm-1 can control pathways that regulate transcription as it does in vertebrates, or maintains epidermal integrity to control migration, is unclear, but our studies suggest that NFM-1 interacts with cues that guide AQR and PQR migrations.
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Figure 1. Migration of QR and QL descendants. A-B) Diagrams representing the migration and cell division pattern of QR on the right side (A) and QL on the left side (B) in the L1 animal, showing birthplace of the Q neuroblasts, and approximate locations of the Q descendants. Maroon shading represents the posteriorly derived EGL-20/Wnt signal. White ovals are hypodermal seam cells V1-V6. Circles with black x indicate cells that undergo programmed cell death after cell division. Dorsal is up, anterior to the left. 

C) Merged DIC and fluorescent micrograph showing location of Q descendants AQR and PQR in an adult wild-type animal. Pgcy-32::cfp is expressed in AQR, PQR and URXL/R. The scale bar represents 10µM.

Figure 2. Position of Q descendants AQR and PQR in nfm-1 mutants. A) A diagram of the nfm-1 locus and alleles used. The ok754 deletion (dashed line), and lq132 splice site mutation (arrow) are noted. B) NFM-1 isoform A domain structure and allele locations are shown. The FERM domain lobes N (gray), B (black), and C (white) are shown. The black bar under FERM C represents predicted actin-binding motif. The dashed line is ok754 in frame deletion, and lq132 splice donor mutation location is marked by an arrow. C) Merged DIC and fluorescent micrograph of an nfm-1(ok754) arrested larval mutant animal. Both AQR and PQR failed to migrate (PQR wild-type position noted by arrowhead). Scale bar represents 10µM. D) Diagram of scoring positions in an L4 animal, with wild-type locations of AQR and PQR shown as magenta circles. E-F) Chart showing percent of AQR (E) or PQR (F) in positions 1-5 in different genotypes. All animals unless otherwise noted were scored using lqIs58 (Pgcy-32::cfp). M+ indicates animals were scored from heterozygous mother and have wild-type
maternal contribution of nfm-1. nfm-1(+) animals harbor the array containing the nfm-
1::gfp fosmid. Asterisks indicate significant (N>100 *p<0.05, **p<0.005, ***p<0.0005 Fisher’s exact test). Pound signs indicate, for that position, a
significant rescue of corresponding nfm-1 mutant (N>100 #p<0.05, ##p<0.005, ###p<0.0005, Fisher’s exact test). Error bars represent two times the standard error of the
proportion.

**Figure 3. nfm-1 mosaic analysis.** A) The abbreviated lineage of cells that express Pgcy-
32 (red). Numbers next to lines indicate the number of cell divisions not shown. The X
next to AQR and PQR indicates the sister of A/PQR (QL/R.aa) that undergoes
programmed cell death. B) Fluorescent micrograph taken with CFP filter of nfm-
1(ok754); nfm-1(+), Pgcy-32::cfp mosaic animal with correct placement of AQR and
PQR. C) Fluorescent micrograph of the same animal from B using a YFP filter. AQR is
not visible in this animal indicating that somewhere in AQR lineage, the nfm-1(+)
transgene was lost. YFP is detected in URXL/R, and PQR indicating many tissues
retained nfm-1(+). Scale bar represent 10μM.

**Figure 4. Analysis of nfm-1(+) mosaic animals.** Quantification of AQR (A), and PQR
(B) migration as in Figure 2, with nfm-1(+) mosaic animals. nfm-1(+) represents
presence of nfm-1 rescuing fosmid. nfm-1(+) rescued ok754 lethality, and animals were
maintained as rescued homozygous ok754 mutants. Mosaic animals have nfm-1(+) in
URX but have lost nfm-1(+) in either AQR or PQR. Pound signs indicate, for that
position, a significant rescue of corresponding nfm-1 mutant (N>100 #p<0.05,
##p<0.005, ###p<0.0005, Fisher’s exact test). Error bars represent two times the standard error of the proportion.

**Figure 5. nfm-1 transcriptional reporter was not expressed in Q cells during their early migrations.** A-C) Ventral view of the posterior region of a Pnfm-1::gfp; Pegl-17::mCherry transgenic animal staged to 3-3.5h post hatching. A) A GFP Micrograph showing expression of Pnfm-1::gfp. Expression was seen in posterior cells near the anus, including posterior intestinal cells (Int) the three rectal gland cells (Rect). Other unidentified cells in the region were possibly the anal sphincter muscle and the stomatointestinal muscle. Variable hypodermal expression was observed along the length of the animal (Hyp). B) An mCherry micrograph shows Q cell specific expression during their migrations. C) Merged. GFP is not observed in Q cells, but is expressed in neighboring tissues and posterior cells. Scale bar is 10µm, anterior is to the left, right is up.

**Figure 6. nfm-1::gfp translational reporter was excluded from Q cells.** A-C) Lateral view of a staged 3-3.5h post hatching L1 nfm-1::gfp; Pegl-17::mCherry animal. A) Fluorescent micrograph of GFP expression from nfm-1::gfp rescuing fosmid. Asterisk marks URX expression of Pgcy-32::yfp in the head that was not excluded by GFP filter. The dashed rectangle indicates the enlarged posterior section in D-F. B) Pegl-17::mCherry, fluorescent micrograph showing location of early Q neuroblasts. QL is out of focus because QL and QR are on different planes, QR on the right side, and QL on left side of the animal. C) Merge of A and B. No overlap of mCherry and GFP was observed.
D-F) Enlarged posterior section of A-C. Anterior is left, dorsal is up. D) Enlargement of A to show nfm-1::gfp present in posterior region near the anus. E) Enlargement of B. QL is outlined to distinguish it from the V5 seam cell that transiently expresses Pegl-17. F) Enlargement of C. Scale bars in C and F represent 10 µm.

Figure 7. slt-1 enhances nfm-1 AQR migration defects. A) Percentage of AQR in each position, quantified as in Figure 2. B) PQR migration. Asterisks indicate significant difference from wild-type (N>100 *p<0.05, **p<0.005, ***p<0.0005 Fisher’s exact test). Pound signs indicate, for that position, a significant enhancement of the corresponding nfm-1 mutant (N>100 #p<0.05, ##p<0.005, ###p<0.0005, Fisher’s exact test). Error bars represent two times the standard error of the proportion.
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Fig. 1
N>100
**p<0.005, ***p<0.0005 compared to wild-type

Fig. 2
Fig. 3

B nfm-1(ok754); nfm-1(+) lost in AQR

C nfm-1(ok754); nfm-1(+) lost in AQR
Fig. 4
Fig. 5

(A) Pnf-1::gfp

(B) Pegl-17::mCherry

(C)
Fig. 6

A \textit{nfm-1::gfp}  

B \textit{Pegl-17::mCherry}  

C

D \textit{nfm-1::gfp}  

E \textit{Pegl-17::mCherry}  

F
**Fig. 7**

Bar graphs showing the percentage of AQR and PQR for different genotypes. The x-axis represents different genotypes: Wild-type, slt-1(eh15), slt-1(ok255), nfm-1(lq132), nfm-1(lq132); slt-1(eh15), nfm-1(ok754)M+; nfm-1(ok754)M+; sax-3(ky123). The y-axis represents the percentage of AQR and PQR.

- **A** shows the percentage of AQR, with error bars indicating standard deviation.
- **B** shows the percentage of PQR, with error bars indicating standard deviation.

Statistical significance:
- *p < 0.05
- **p < 0.005
- ***p < 0.0005

Compared to wild-type and corresponding nfm-1 mutant.