

Fig. S1. The AVM migration defects of *unc-40* **mutants.** Photomicrographs (A-C) and corresponding schematics (D-F) of animals showing the AVM cell body (arrow) and axon projections as marked by *mec-4::gfp*. Anterior is to the left and dorsal is up. In wild-type animals (A,D), the AVM axon first migrates ventrally and then turns anteriorly to migrate along the ventral nerve cord. (B,C,E,F) Examples of AVM axon migration defects in *unc-40* mutants.

human RGMa	48	CK	(1	LK	(<mark>C</mark> ł	4 S	EF	W	S A	Т	S G	SI	I A	Ρí	A S	DC) Т	P-			-							EF	C .	A F	۱L I	R S	Y F	۱L	ст	R 87
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DRAG-1	22	CR	ŧ٧	ΕE	: <mark>C</mark> /	AA	WF	Q	КΤ	K	DY	E	4 L	٧F	P K	A 1	ГΕ	R			-							- 1	r <mark>C</mark>	Q١	/L	QΤ	ΥL	. К	C MI	N 60
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human RGMa	88	RT	A	RT	CF	۲G	DL	A	Y H	S	ΑV	H (GΙ	ΕI	DL	.MS	s Q	H	I C	S K	D	GΡ	ΤS	S Q	P R	LF	۹-	- 1		P F	۲ <mark>Α</mark>	G D	S Q) E (RSI	D 140
human RGMc	92	R T	A	R T	ĊF	۲G	DL	A	FH	S,	ΑV	H (GΙ	ΕI	DL	M	I Q	H	I C	S R	Q	GΡ	Τł	۱P	P P	ΡF	۲G	P #	۱L	ΡĢ) A (G S	GL	. P		- 143
human RGMb	135	RT	S	K A	I C F	۲G	N L	v	Y H	S	ΑV	L (GΙ	S I	DL	.MS	S Q	R	I C	S K	D	GΡ	ΤS	S S	T N	ΡI	ΕV	Tŀ	1 D	P C	2 N 1	ΥH	S P	I A I	G -	- 187
DRAG-1	61	DT	Q	RY	′ <mark>C</mark> ł	1 G	N L	R	FH	S	SE	L	I M	R	RH	W	< E	FI	EC	EK	W	E S	Cł	4 D	N S	H١	γĸ	Rŀ	(H)	VK	IT (СY	ΕŇ	I P I	Р-	- 113
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human RGMc	144	AP	D	ΡC) D Y	ł E	GF	۱F	S R	L	H G	R	P P	GI	FL	. H (CA	SI	F G	DP	H	۷R	SI	H	HH	Fł	I T	CF	٤V	Q	; A (ŴР	LL	. D	N D	F 198
human RGMb	188				· - ·	- A	RE	H	RR	G	DQ	N	P P	S١	ΥL	. F (G	LI	F G	DP	H	L R	T	K	D N	ΕC	2 T	C	٤V	E	; A (NΡ	LI	D	N N 1	<mark>Y</mark> 235
DRAG-1	114				· - ·			-		-	- P	SI	4 R	КI	LK	Y (C S	LI	F G	DP	H	LI	M	F N	GS	V	2 T	C S	5 E	E 🤇	; A (R P	L۷	/ D /	N R	<mark>Y</mark> 153
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human RGMc	199	LF	v	Q A	<mark>۲</mark> ۲	S S	ΡN	1A	L G	AI	N A	Т	A T	R	ΚL	T	11	FF	C N	MC	E	сı	DQ	ЭK	V Y	Q/	٩E	V) N		· L !	PV	A F	E	DG	S 251
human RGMb	236	L S	; V	QV	/ T	٩V	P١	٧V	ΡG	S :	S A	T /	A T	N	ĸI	Τļ	11	Fł	(A	НH	E	ст	DQ	QΚ	V Y	Q/	٩V	T C	D		· L !	P A	AF	۰V	DG	T 288
DRAG-1	154	FL	V,	QV	/ T	I R	N١	/ R	GE	A	LT	T	ΓV	Т	KΝ	۲ <mark>۲</mark> ۱	/L	VF	۲- ۶	КH	IN	ст	A٩	βL	RY	E /	۹S	S I) E	ΕØ	;L	P R	. G F	٠V	D G '	T 207
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human RGMa	248	KN	I G	GD	I K F	ł G	AN	IS	L K	L	ΤE	К١	٧S	G	QH	VI	EI	Q/	٩K	ΥI	G	ТΤ	٦١	/ V	RQ	V	G R	ΥL	. Т	F P	۱V	RM	ip e	E	VVI	N 302
human RGMc	252	I N	I G	GD	RF	P G	GS	S	L S	L,	QT	AI	4 P	Gł	N H	VI	E	Q/	٩	ΥI	G	ТΤ	11		RQ	T/	٩G	QL	. S	FS	; I J	ĸν	A	D	V AI	M 306
human RGMb	289	T S	G G	GD	- 5	S D	AK	S	L R	Ц	V E	RI	E S	Gł	HY	٧I	EM	IH /	۱R	ΥI	G	ТΤ	٧ł	۶V	RQ	V	G R	Y L	. T I	LP	11	RM	ip e	D	LA	M 342
DRAG-1	208	TF	Q	МT	SI	(H	S١	/ E	۷L	W	QD	_		D	NY	۷I	E	ΑL	. н	FI	H	S S	I F	11	<mark>r</mark> r	Q	G P	ΥL	. S '	VS	; V	<mark>r</mark> A	PT	[V L	E 259
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human RGMa	303	Α١	/Ε	D٧	/D 5	6 Q	GL	Y.	LС	LI	R <mark>G</mark>	сı	PL	N (0 0) I () F	- () A	FΗ	T	N A	E (G T	GA	R	۲L	A /	۱A:	S P	' A I	РТ	AP) E (TF	P 356
human RGMc	307	A F	S		A	E Q	DL	Q	L C	V	G <mark>G</mark>	СI	P P	S (Q R	LS	s -				-	R S	EF	۱		RF	۲G	A I	Т							- 339
human RGMb	343	S Y	ľ E		- E S	S Q	DL	Q	LC	VI	N G	СI	PL	S I	E R	1 I I) D	GQ	Q G	QV	S.	ΑI	L	GH	S L	PF	۲S	S L	. γ	Q /	W	ΡG	i		- Y)	T 391
DRAG-1	260	ΤĢ	GG		- C) V	AR	ξE	LC	W	S G	C	R K	S S	s R	t I F	P A	ΕL	. A	V E	М	ТΚ	Κł	F A	EC	Y	۲R	R١	/Н	V P) -					- 302
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numan KGMa	357	ΥE	T	A٧	/ A P	٢C	KE	K	L P	۷	E D	Ľ	Y	0/	A C	V I	F D	LL	. Т	ΤG	D	V N	F 1	ΓL	A A	Y١	í A	LE	D	V K	(M	LH	S			406
human RGMc	340	10) T	A R	RI	- C	KE	G	L P	۷	E D	A	Y F	H \$	s c	V I	F D	٧L	- 1	S C	D	P N	F 1	۲V	A A	Q/	٩A	LE	E D .	AF	ξ Α	FL	Р			389
human RGMb	392	LE	T	A N	т	2 C	H E	K	MP	۷	КD	I I	Y F	Q	s c	V I	F D	LL	. Т	те	D	A N	F 1	Α	A A	H S	6 A	LE	E D '	V E	: Al	LH	Р			441
DRAG-1	303	КК	(۷	A E	DF	۲C	KD	1	GN	L,	G -	۷I	FF	D /	A C	V I	FD	LN	ΛF	ΤG	D	DY	L١	/Н	LS	R /	٩A	E S	5 D	FR	L R I	LA	Р			351

Fig. S2. DRAG-1 shares conserved features with human RGM proteins. Sequence comparison between mature human RGMa, RGMb and RGMc (HFE2) and *C. elegans* DRAG-1 proteins, highlighting conserved residues (blue). The N- and C-terminal signal sequences are not shown. The black line underlines the partial vWF type D domain. The three JH (juvenile hemochromatosis) disease-associated hypomorphic mutations discussed in this paper are boxed in red (Lanzara et al., 2004).

Table S1. Plasmid constructs	
Constructs for tissue-specific ex	pression of unc-40
pCXT261, unc-40p::unc-40 cDNA::	gfp::unc-54 3'UTR
pCXT262, elt-3p::unc-40 cDNA::gf	p::unc-54 3'UTR
pCXT264, rol-6p::unc-40 cDNA::gf	p::unc-54 3'UTR
pCXT266, hlh-8p::unc-40cDNA::qf	p::unc-54 3'UTR
pCXT265, unc-119p::unc-40cDNA:	.gfp::unc-54 3'UTR
pCXT289, myo-3p::unc-40 cDNA::c	yfp::unc-54 3'UTR
Mammalian cell culture express	ion constructs (all cloned into the pSecTag vector)
pCXT239 (DRAG-1-FLAG), pCMV:::	signal peptide::DRAG-1 mature region (aa22-360)::FLAG
pJKL962 (Myc-DRAG-1), pCMV::sig	nal peptide::cMyc-His::DRAG-1 mature region (aa22-360)
pCXT271 (DRAG-1 ^{G272V} -FLAG), pCA	IV::signal peptide::DRAG-1 mature region (aa22-360) ^{G272Y} ::FLAG
pCXT245 (Myc-FN5,6), pCMV::sign	al peptide::cMyc-His-UNC-40 FNIII 5-6 (aa852-1081)
pCXT249(Myc-FN5,6 C-C'loop), pC	MV::signal peptide::cMyc-His-UNC-40 FNIII 5-6 (aa852-1081) with aa987-993 mutated from DRASLAD to LDKNIPI
pCXT299 (Myc-FN5,6 C'strand), pC	W::signal peptide::cMyc-His-UNC-40 FNIII 5-6 (aa852-1081) with aa997-1002 mutated from TINYVA to IMETIS
pCXT300 (Myc-FN5,6 E-Floop), pC/	MV::signal peptide::cMyc-His-UNC-40 FNIII 5-6 (aa852-1081) with aa1011-1014 mutated from SNLL to MDLN
pJKL964 (Myc-SMA-6), pCMV::sigr	al peptide::cMyc-His-SMA-6 full length (aa27–stop)
pCXT230 (Myc-DAF-4), pCMV::sigr	nal sequence::cMyc-His-DAF-4 EXD- TM-partial ICD (aa33–468)
pCXT241 (FLAG-DBL-1), pCMV::sig	nal sequence::DBL-1 prodomain (aa32-238)::FLAG-DBL-1 mature region (aa239–stop)
Constructs for making DRAG-1 a	and UNC-40 vertebrate and <i>C. elegans</i> hybrids
pCXT161, drag-1p (–3977 to –1 ar	nd 4 to 1123)::drag-1 signal sequence:: mRgmb mature region::drag-1 C-signal sequence::unc-54 3'UTR, has aa23-375 of
DRAG-1 replaced by aa59-414 o	of mouse Rgmb in pCXT15 (Tian et al., 2010)
pCXT185, drag-1p (–3977 to –1 ar	nd 4 to 1123)::drag-1 signal sequence:: hHJV mature region::drag-1 C-signal sequence::unc-54 3'UTR, has aa23-375 of DRAG-1
replaced by aa38-398 of human	RGMc/HJV in pCXT15
pCXT278, unc-40p (–610 to –1)::u	nc-40 signal sequence::mDCC mature region::unc-54 3'UTR, has aa36-stop of UNC-40 replaced by aa34-stop of mDCC
pCXT279, unc-40p (–610 to –1)::u	nc-40 signal sequence::mNeo1 mature region::unc-54 3'UTR, has aa36-stop of UNC-40 replaced by aa58-stop of mouse Neo1
Constructs for in vivo structure-	function analysis of UNC-40
All constructs are derived from pZF2	22, a functional <i>unc-40::gfp</i> fusion described by Chan et al. (Chan et al., 1996)
pCXT253(△FN5), unc-40::gfp with	out aa852-939
pCXT254(△FN6), unc-40::gfp with	out aa946-1041
pCXT255(△FN5,6), unc-40::gfp wit	hout aa852-1041
pCXT260 (UNC-40 EXD), unc-40 (a	a1-1079)::gfp
pCXT269(UNC-40 C-C' loop), unc-4	40::gfp with aa987-993 mutated from DRASLAD to LDKNIPI
pCXT285(UNC-40 C' strand), unc-4	10::gfp with aa997-1002 mutated from TINYVA to IMETIS
pCXT286(UNC-40 E-F loop), unc-40	0::gfp with aa1011-1014 mutated from SNLL to MDLN
Constructs for expressing wild-t	sype and mutant <i>drag-1</i> using the MosSCI technique
pCXT208: wildtype DRAG-1 in pCl	FJ151
pCXT224: DRAG-1G68V (GGT to G	iTT) in pCFJ151
pCXT225: DRAG-1D117E (GAT to	GAA) in pCFJ151
pCXT223: DRAG-1G272V (GGA to	GTA) in pCFJ151