

Supplemental Materials

Molecular Biology of the Cell

Qadota et al.

Figure S1

UNC-89-B (8081 aa)

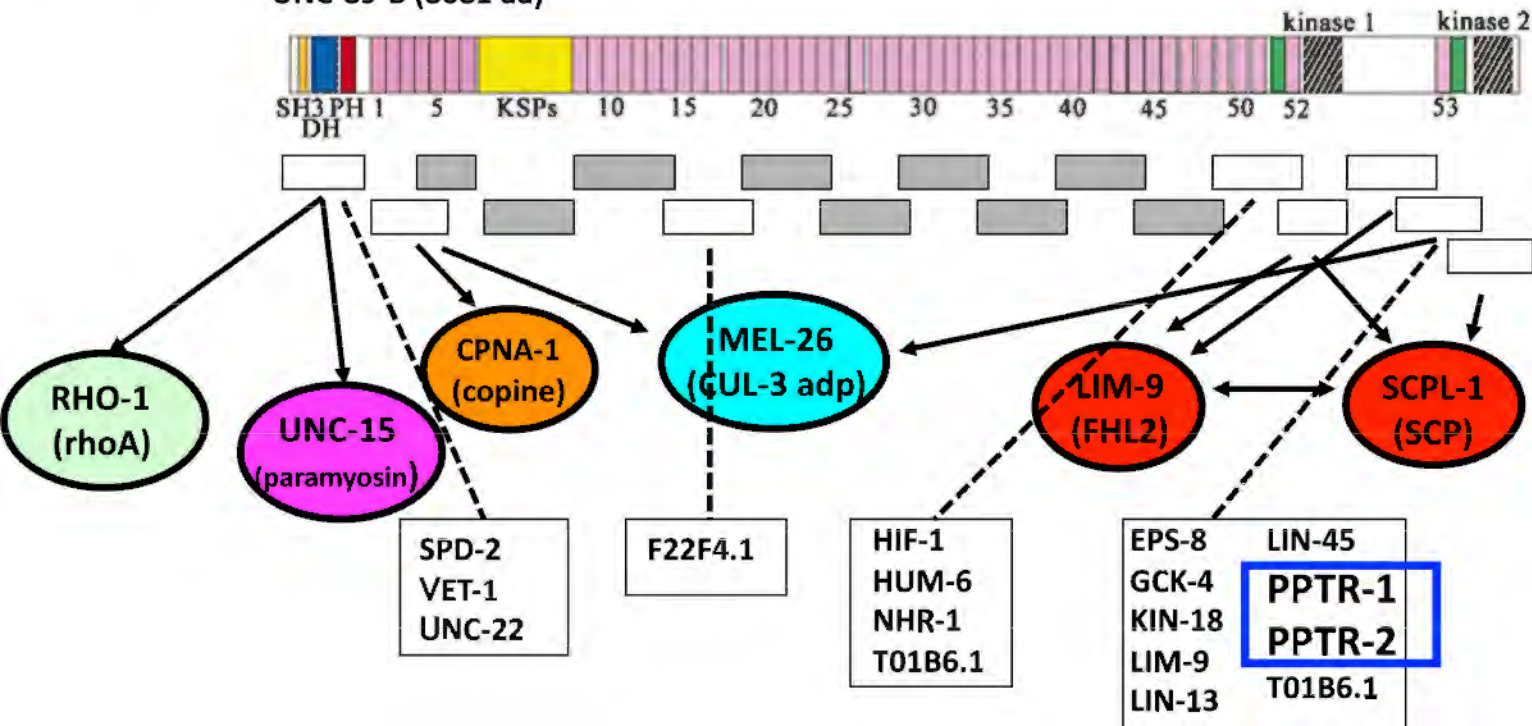


Figure S2

A: alignment of *C. elegans* PPTR-1 and PPTR-2, human B56alpha, B56beta, B56gamma, B56delta, and B56epsilon

```
B56alpha -----MSSSSPPAGAASA
B56epsilon -----MSSAPT
B56beta -----METKLPPASTPTSPSSPGLS
PPTR-1 -----MHGSGHSLTGAPHQIPPPRTQGAATGGQQL
B56gamma -----
B56delta MPYKLLKKEKEPPKVAKCTAKPSSSGKGGGENTEAAQPQPQPQPQAQSQPPSSNKRPS
PPTR-2b -----MIPADAPP
```

```
B56alpha AISASEKVDGFRKSVRKAQRQKRSQGSQFRSQGSQAEHLPLPQLKDATSNEQQELFCQ
B56epsilon TPPSVDKVDGFSRKSVRKAR-QKRSQSSSQFRSQGKPIELTPLPLLKDVPSSEQPELFLK
B56beta PVPPPDKVDGFSRRSLRRAR-PRRSHSSSQFRYQSNQQELTPLPLLKDVFASELHELLSR
PPTR-1 SATANQFVDKIDPFHNKRGTSRRLRINNSRYNVDSAQELVQLALIKDTAANEQPALVIE
B56gamma -----MVVDAANSNGPFQPVVLLHIRDVFPADQEKLFIQ
B56delta NSTPPPTQLSKIKYSGGPQIVKKERRQSSSRFNLSKNRELQKLPALKDSPTQEREELFIQ
PPTR-2b PTNIGRTNTYGGDLISGPVIPRRERRQSSSMFNISQNRELQRLPAIKDADPSERETLEFIQ
. . . : * : * . : * . .
```

```
B56alpha KLQCCILDFDM-DSVSDLKSKEIKRATLNELVEYVSTN-RGVIVESAYSDIVKMISANI
B56epsilon KLQCCVIFDFM-DTSLDLKMKKEYKRSTLNELVDYITIS-RGCLTEQTYPEVVRMVSCNI
B56beta KLAQCGVMFDFL-DCVADLKGKEVKRAALNELVECVGST-RGVLIEPVYPDIIRMISVNI
PPTR-1 KLVQCCQHVDFDY-DPVAQLKCKEIKRAALNELIDHITST-KGAIVETIYPAVIKMKVAKNI
B56gamma KLRQCCVLFDFVSDPLSDLKWEVKRAALSEMVEYITHN-RNVITEPIYPEVVHMFVAVNM
B56delta KLRQCCVLFDFVSDPLSDLKFKVEVKRAGLNEMVEYITHS-RDVVTEAIYPEAVTMFVSNL
PPTR-2b KLRQCCVVFDFANDALSDLKFKVEVKRAALNELVDHVS GAPKGSLSDAVYPEAIGMFSTNL
** ** :*** * :*:** ** **: *.*:*: : :. : : *. :*.* :
```

```
B56alpha FRTLPPSDN---PDFDPEEDEPTLEASWPHIQLVYEFFLRFLESPDFRPSIAKRYIDQKF
B56epsilon FRTLPPSDS---NEFDPEEDEPTLEASWPHLQLVYEFFLRFLESQEFQPSIAKRYIDQKF
B56beta FRTLPPSEN---PEFDPEEDEPNLEPSWPHLQLVYEFFLRFLESPDFQPSVAKRYVDQKF
PPTR-1 FRVLPPSEN---CEFDPEEDEPTLEVSWPHLQLVYELFLRFLESPDFQASIGKKYIDQRF
B56gamma FRTLPPSSNPTGAEFDPEEDEPTLEAAWPHLQLVYEFFLRFLESPDFQPNIAKRYIDQKF
B56delta FRTLPPSSNPTGAEFDPEEDEPTLEAAWPHLQLVYEFFLRFLESPDFQPNIAKRYIDQKF
PPTR-2b FRPLSPPTNPIGAEFDPEEDEPTLEAAWPHLQLVYEFFLRFLECPDFQSQVAKRYIDQNF
** *.*. . :***:****.*** :***:*****:*.****. :*:...*:**.* *
```

```
B56alpha VQQLLELFDSEDPREDFLKTTLHRIYGKFLGLRAFIRKQINNIFLRFIYETEHFNGVAE
B56epsilon VLQLELFDSEDPREDFLKTTLHRIYGKFLGLRAFIRKQINNIFLRFVYETEHFNGVAE
B56beta VLMLLELFDSEDPREDFLKTTLHRIYGKFLGLRAYIRKQCNHIFLRFIYEFEHFNGVAE
PPTR-1 VLKLLDLFDSEDPREDFLKTTLHRIYGKFLGLRAFIRKHINMMFLRFVYETDSFNGVGE
B56gamma VLQLELFDSEDPREDFLKTTLHRIYGKFLGLRAYIRKQINNIFYRFIYETEHNGIAE
B56delta VLALLDLFDSEDPREDFLKTTLHRIYGKFLGLRAYIRKQINNIYRFIYETEHNGIAE
PPTR-2b ILRLLMIMDSEDPREDFLKTTLHRIYGKFLGHRAYIRKQINNIFYSFIYETERHNGIAE
: ** :*:*****:*** ***:***** **:***: :*: * ** : .**.* *
```

```
B56alpha LLEILGSIINGFALPLKAEHKQFLMKVLI PMHTAKGLALFHAQLAYCVVQFLEKDTTLTE
B56epsilon LLEILGSIINGFALPLKAEHKQFLVKVLIPLHTVRSLSLFHAQLAYCIVQFLEKDPSTLE
B56beta LLEILGSIINGFALPLKTEHKQFLVRVLIPLHSVKLSLVFHAQLAYCVVQFLEKDATLTE
PPTR-1 LLEILGSIINGFALPLKQEHKVFLVKVLLPLHKPKCLSLSYHAQLAYCVVQFIEKDSSTLP
B56gamma LLEILGSIINGFALPLKEEHKIFLLKVLLPLHKVKSLSVYHPQLAYCVVQFLEKDTTLTE
B56delta LLEILGSIINGFALPLKEEHKMFLIRVLLPLHKVKSLSVYHPQLAYCVVQFLEKESSTLE
PPTR-2b LLEILGSIINGFALPLKEEHKTFLLRVLLPLHKVKSLSVYHPQLAYCVVQFIEKDSSTLE
***** ** **:***:*. : :*:*.*****:***:***:***:***
```

B56alpha PVIRGLLKFWPKTCSQKEVMFLGEIEEILDVIEPTQFKKIEEPLFKQISKCVSSSHFQVA
 B56epsilon PVIRGLMKFWPKTCSQKEVMFLGELEEEILDVIEPSQFVKIQEPLFKQIAKCVSSPHFQVA
 B56beta HVIRGLLKYWPKTCTQKEVMFLGEMEEILDVIEPSQFVKIQEPLFKQVAVCVSSPHFQVA
 PPTR-1 QVFEALLKFWPRTCSSKEVMFLGEVEEILDIEPEQFKKIIDPLFRQLAKCVSSPHFQVA
 B56gamma PVVMALLKYWPKTHSPKEVMFLNELEEEILDVIEPSEFVKIMEPLFRQLAKCVSSPHFQVA
 B56delta PVIVGLLKFWPKTHSPKEVMFLNELEEEILDVIEPSEFVKIMEPLFRQLAKCVSSPHFQVA
 PPTR-2b PVISGMLRFWPKQHSPKEVMFLNELEEVLDVIEPNEFQKIMTPLFSQIARCVSSPHFQVA
 * . . : : : * * : : * * * * * . * : * * : * * * * * : * * : * * * * * : : * * * * * . * * * * *

B56alpha ERALYFWNNEYILSLIEENINKILPIMFASLYKISKEHWNPTIVALVYNVLKTLMEMNGK
 B56epsilon ERALYYWNNEYIMSLIEENSIVLIPIMFSSLYRISKEHWNPAIVALVYNVLKAFMEMNST
 B56beta ERALYFWNNEYILSLIEDNCHTVLPAVFGTLYQVSKEHWNQTIVSLIYNVLKTFMEMNGK
 PPTR-1 ERALYFWNNEYILSLIEDTSSLVMPIMFPALYRISKEHWNQTIVALVYNVLKTFMEMNGK
 B56gamma ERALYYWNNEYIMSLISDNAAKILPIMFPALYRNSKTHWNKTIHGLIYNALKLFMEMNQK
 B56delta ERALYYWNNEYIMSLISDNAARVLPIMFPALYRNSKSHWNKTIHGLIYNALKLFMEMNQK
 PPTR-2b ERALYYWNNEYVMSLVADNARV IIPIMFPVLFKNSKSHWNKTIHGLIYNALKMFMEMNQK
 * * * * * : * * * * * : * * * * * : . . : : * * : * * : * * * * * : * . * : * * . * * : * * * * * .

B56alpha LFDLDTSSYKAERQREKKKELEREELWKKLEELKLLKKALEKQNSAYNMHSILSNTSAE--
 B56epsilon MFDELATYKSDRQREKKKEREELWKKLEDELKRLRRDGI IPT-----
 B56beta LFDLDTASYKLEKQQEQQAQERQELWQGLEELRLRRLQGTQGAKEAPLQRLTPQVAASG
 PPTR-1 LFDLDTSTYKGERLREKQREKDRDAFWKKMEALELNP AEGKEVTPSLFPEKLTLDYLLKKD
 B56gamma LFDLDTQQYKAEKLEKLEKMKEREAAWVKIENLAKANPQVLKKRIT-----
 B56delta LFDLDTQQYKAEKQKGRFRMKEREEMWQKIEELARLNPQYPMFRAPPPLPVYVSMETETP
 PPTR-2b LFDECSQAYQKDRVQEKTLNEEKERIWNNEIEKQAMGNPQYVEVKALFARFNPDEI ISSRQ
 : * * : : : : : : : : : : : : : : * : * : *

B56alpha -----
 B56epsilon -----
 B56beta GQS-----
 PPTR-1 GPNMTPLPVATAGGGDKSPSVVKKSSSTGSETTTPAKK-----
 B56gamma -----
 B56delta TAEDIQLLKRVTETEAVQMLKDIKKEKVL-----RRKSELQDQVYTIKALEAHKRA
 PPTR-2b QNGVDENMKTSTVLSKDEILKNAVGVSSMKNDMDFGPNHKQSDFPPEQTTRALGEYKRR

B56alpha -----
 B56epsilon -----
 B56beta -----
 PPTR-1 -----
 B56gamma -----
 B56delta EEFLTASQEAL--
 PPTR-2b DPFLKKVTSTDEQ

B: % identities

PPTR-1 to PPTR-2: 55% (12-506)
 PPTR-1 to B56alpha: 78% (39-458)
 PPTR-1 to B56beta: 66% (39-480)
 PPTR-1 to B56gamma: 67% (71-490)
 PPTR-1 to B56delta: 66% (52-482)
 PPTR-1 to B56epsilon: 67% (38-492)
 PPTR-2 to B56alpha: 64% (30-441)
 PPTR-2 to B56beta: 64% (35-460)
 PPTR-2 to B56gamma: 74% (54-470)
 PPTR-2 to B56delta: 65% (5-552)
 PPTR-2 to B56epsilon: 67% (47-441)

Figure S3

PPTR-1

1 73 **B56** 478 543



001, 045,
081, 3-3-1



PPTR-2b

1 51 462 561



19n3-1



27:2-1



**isolated clones of
PPTR-1, and PPTR-2**

Figure S4

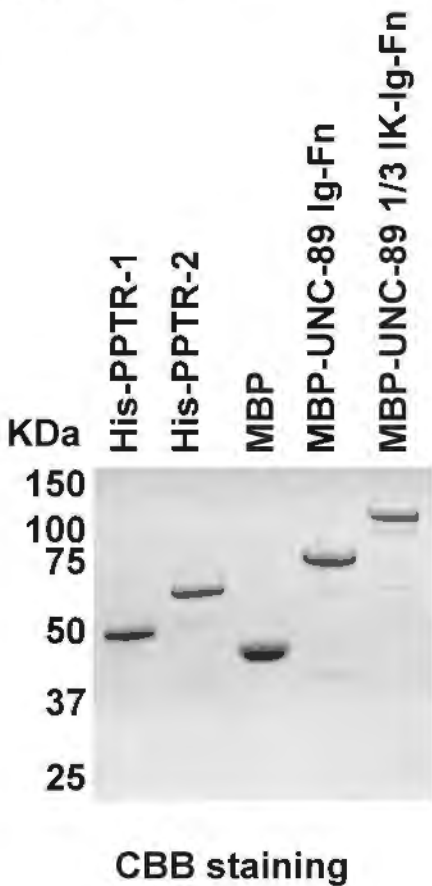
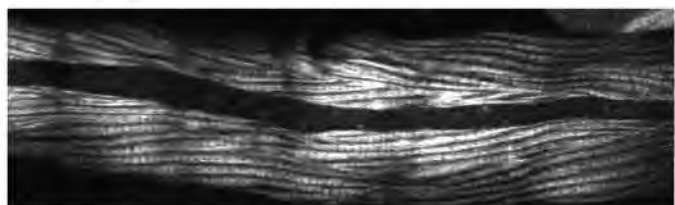
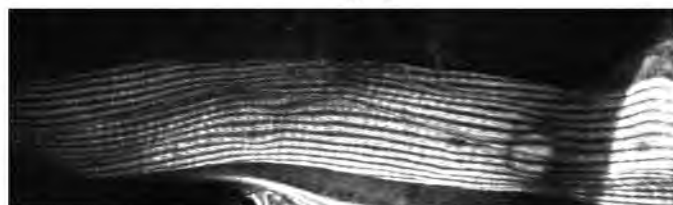


Figure S5

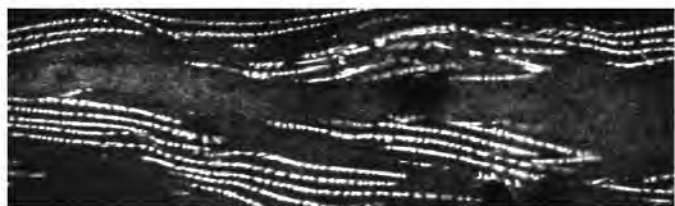
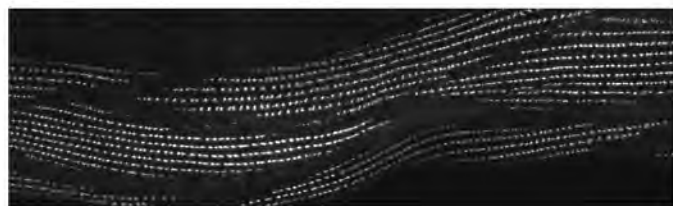
Wild type

pptr-1(tm3103)

Actin



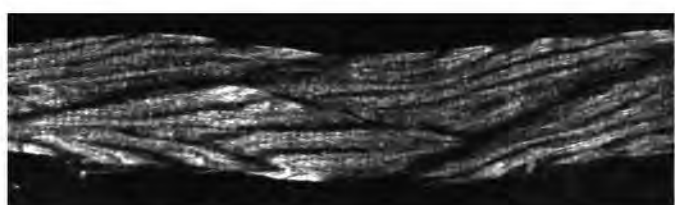
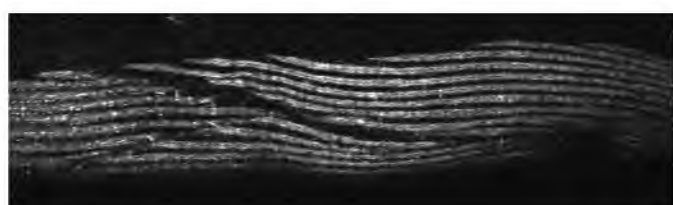
ATN-1



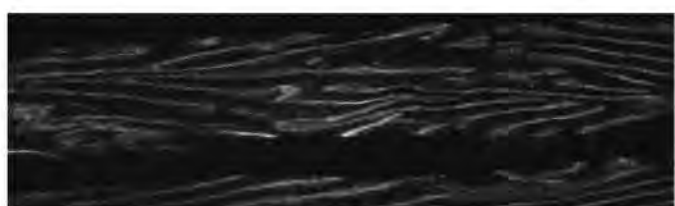
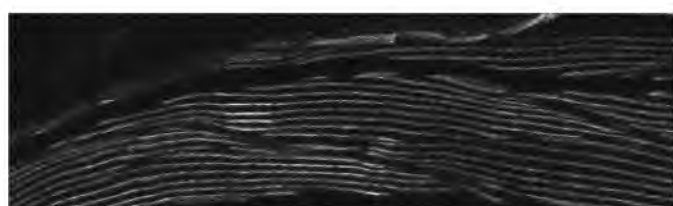
MHC B



UNC-15



UNC-89



UNC-95

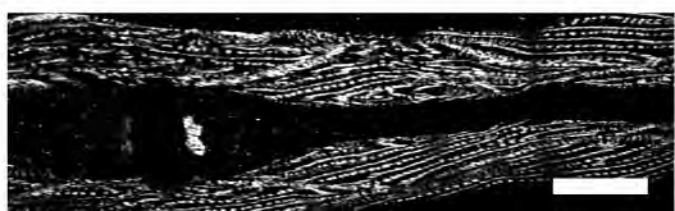
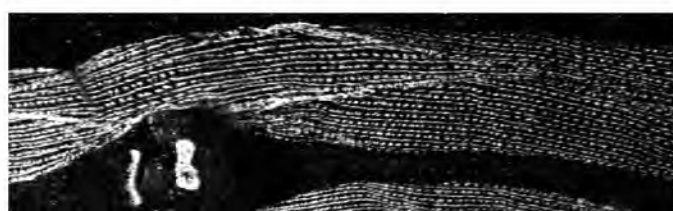


Figure S6. Alignment of MHC A and MHC B sequences with phosphorylation sites

MHC A	9	ENDPGFPFLGISREARAATAARPFDSKKNCWIPDPEDGFVAAEIQSTTGEQVTVVTVKGN	68
		E DPG+ +L +RE ++P+DSKKN WIPDPE+G++A EI +T G+QVT+VT +GN	
MHC B	4	EKDPGWQYLRRRTREQVLEDQSKPYDSKKNWIPDPEEGYLAGEITATKGDQVTIVTARGN	63
MHC A	69	QITVKKDQCQEMNPPKFDKTEDMANLTFLEASVLGNLKDRLMIYTYSGLFCVWINP	128
		++T+KK+ QEMNPPKF+KTEDM+NL+FLN+ASVL NL+ RY ++IYTYSGLFCVWINP	
MHC B	64	EVTLLKELVQEMNPPKFEKTEDMSNLSFLNDASVLHNLRSRYAAMLIYTYSGLFCVWINP	123
MHC A	129	YKRLPIYSESVIKHFMGKRRNEMPPHLFAVSDEAYRNMVQDKENQSMELITGESGAGKTEN	188
		YKRLPIY++S + FMGKR+ EMPPHLFAVSDEAYRNM+QD ENQSMELITGESGAGKTEN	
MHC B	124	YKRLPIYTDSCARFMGKRKTEMPPHLFAVSDEAYRMLQDHENQSMELITGESGAGKTEN	183
MHC A	189	TKKVISYFAIVGATQAASGKEAKDGKGGTLEEQIVQTNPVLEAFGNAKTVRNNSRFRG	248
		TKKVI YFA VGA+Q G E KK TLE+QIVQTNPVLEAFGNAKTVRNNSRFRG	
MHC B	184	TKKVICYFAAVGASQQEGGAEVDPNKKKVTLEDQIVQTNPVLEAFGNAKTVRNNSRFRG	243
MHC A	249	KFIRTHFSGSGLAGGDIEHYLLEKSRVVRQAPGERCYHIFYQIMSGNDPSLRGKLLSN	308
		KFIR HF+ G+LA DIEHYLLEKSRV+RQAPGERCYHIFYQI S P L+ +L L	
MHC B	244	KFIRIHFNKHGRLASCDIEHYLLEKSRVIRQAPGERCYHIFYQIYSDFRPELKKELLLDL	303
MHC A	309	DITYYHFCSQAELTIEGMDDKEEMRLTQEAFDIMGFEDNETMDLYRSTAGIMHMGEMKFK	368
		I Y F +QAEL I+G+DD EE +LT EAFDI+ F E D YR + MHMG MKFK	
MHC B	304	PIKDYWFVAQAELIIDGIDDVEEFQLTDEAFDILNFSAVEKQDCYRLMSAHMHMGNMKFK	363
MHC A	369	QRPREEQAEPDGEEDALNAAAMLGIAEEFLKALTKPRVRVGTEWVNKGQNLEQVNWAVS	428
		QRPREEQAEPDG ++A A+ M GI EEFLKALTKPRV+VGTEWV+KGQN EQVNWAV	
MHC B	364	QRPREEQAEPDGTDEAEKASNMYGIGCEEFLKALTKPRVKVGTEWVSKGQNCEQVNWAVG	423

MHC A	429	GLAKAIYARMFKWIITRCNKTLDAKEIERKHFIVGLDIAGFEIFDLNSFEQLWINFVNER	488
		+AK +Y+R+F W++ +CN TLD K I+R +FIGVLDIAGFEIFD NSFEQLWINFVNE+	
MHC B	424	AMAKGLYSRVFNWLVKKCNLTLDQKGIDRDYFIGVLDIAGFEIFDFNSFEQLWINFVNEK	483
MHC A	489	LQQFFNHMHMFVLEQEEYKREGIAWTFIDFGLDLQACIELIEKPLGIISILDEECIVPKAT	548
		LQQFFNHMHMFVLEQEEY REGI W FIDFGLDLQACIELIEKPLGIIS+LDEECIVPKAT	
MHC B	484	LQQFFNHMHMFVLEQEEYAREGIQWVFIDFGLDLQACIELIEKPLGIISMLDEECIVPKAT	543
MHC A	549	DMTYAQKLLDQHLGKHPNFQKPKPPKQGDHFAIVHYAGTVRYNATNFLEKNKDPLND	608
		D+T A KL+DQHLGKHPNF+KPKPPKQGDHFAIVHYAGTVRYN N+LEKNKDPLND	
MHC B	544	DLTLASKLVDQHLGKHPNFEKPKPPKQGEAHFAMRHYAGTVRYNCLNWLEKNKDPLND	603
MHC A	609	TAVALLKHSTDNSLMLDIWQDYQTQEEAAEAAGQTAGGKRGKSSSFATVSMIYRESLN	668
		T V+ +K S N L+++IWQDY TQEEAA AK G G K+GKS SF TVSM+YRESLN	
MHC B	604	TVVSAMKQSKGNDLLVEIWQDYTTQEEAAAKAKEGGGGGKKGKSGSFMTVSMIYRESLN	663
MHC A	669	NLMNMLYQTHPHFIRCIIPNEKKASGVIDSALVLNQLTCNGVLEGIRICRKGFPNRMLYP	728
		NLM ML +THPHFIRCIIPNEKK SG+ID+ALVLNQLTCNGVLEGIRICRKGFPNR L+P	
MHC B	664	NLMTMLNKTHPHFIRCIIPNEKKQSGMIDAALVLNQLTCNGVLEGIRICRKGFPNRTLHP	723
MHC A	729	DFKHRYAILAADAAC-ESDPKKASVGILDKISVDGNLTDEEFKVGETKIFFKAGVLAKLE	787
		DF RYAILAA AK + D KK + I+ K+ DG+L++E F++G TK+FFKAGVLA LE	
MHC B	724	DFVQRYAILAAKEAKSDDDKKCAEAIMSKLVNDGSLSEEMFRIGLTKVFFKAGVLAHLE	783
MHC A	788	DLRDEILSRIVTMFQSRIRSYLAKAEVRRRYEQQTGLLVQRNVRWCTLRTWEWFKLFG	847
		D+RDE L+ I+T FQS+IR +L + +RR EQ+ GLL+VQRNVR+WCTLRTWEWFKL+G	
MHC B	784	DIRDEKLATILTFQSQIRWHLGLKDRKRRMEQRAGLLIVQRNVRWCTLRTWEWFKLYG	843

MHC A 848 KVKPMLKAGKEQEAMGELAVKIQKLEEAQVQRGEIARSQLESQVADLVEEKNALFLSLETE 907
KVKPMLKAGKE E + ++ K++ LE+++ + E R +LE A LVEEK +LF +LE+

MHC B 844 KVKPMLKAGKEAEELEKINDKVKALEDSLAKKEEKLKEEESAKLVEEKTSLFTNLEST 903

MHC A 908 KANLADAEERNEKLNQLKATLESKLSIDITGQLEDMQERNEDLARQKKKTDQELSDTKKHV 967
K L+DAEER KL + +LS++ QL D ++R D+ R KKK + E+ KK +

MHC B 904 KTQLSDAEERLAKLEAQQKDASKQLSELNDQLADNEDRTADVQRAKKKIEAEVEALKKQI 963

MHC A 968 QDLELSLRKAEQEQSRDHNIRSLQDEMANQDEAVAKLNKEKKHQEESNRKLNEDLQSEE 1027
QDLE+SLRKAE EKQS+DH IRSLQDEM QDEA+AKLNKEKKHQEE NRKL EDLQSEE

MHC B 964 QDLEMSLRKAESEKQSKDHQIRSLQDEMQQDEATAKLNKEKKHQEEINRKLMEQLQSEE 1023

MHC A 1028 DKVNHLEKIRNKLEQQMDELEENIDREKRSRGDIEKAKRKVEGDLKVAQENIDEITKQKH 1087
DK NH K++ KLEQ +D+LE++++REKR+R D++K KRKVEG+LK+AQENIDE +Q+H

MHC B 1024 DKGHNQNKVKAKLEQTLDDLEDLEKRRARADLDKQKRKVEGELKIAQENIDESGRQRH 1083

MHC A 1088 DVETTLKRKEEDLHHTNAKLAENNSIIAKLQRLIKELTARNAELEELEAERNRQKSDR 1147
D+E LK+KE +LH +++L + ++++KLQR IK+ +R +ELEELE ER SR K+DR

MHC B 1084 DLENLKKKESELHSVSSRLEDEQALVSKLQRQIKDQSRRISELEELEENERQSRKADR 1143

MHC A 1148 SRSEAERELEELTERLEQQGATAAQLEANKKREAEIAKLRREKEEDSLNHETAISLRK 1207
++S+ +RELEEL E+L++QGGATAAQ+E NKKREAE+AKLRR+ EE ++NHE + LRK

MHC B 1144 AKSDLQRELEELGEKLDEQGGATAAQVEVNKKREAEAKLRRDLEEMNHNENQLGGLRK 1203

MHC A 1208 RHGDSVAELTEQLETQKLLKAKSEAEKSKLQRDLEESQHATDSEVRSRQDLEKALKTIEV 1267
+H D+VAELT+QL+ L K KAK E +K++ RD E+ D E + + EK K E+

MHC B 1204 KHTDAVAELTDQLDQLNKAKAKVEKDKAQAVRDAEDLAAQLDQETSGKLNNEKLAKQFEL 1263

MHC A 1268 QYSELQTKADEQSRQLQDFAALKNRLNNSDLNRSLEEMDNQLNSLHRLKSTLQSQLDE 1327
Q +ELQ+KADEQSRQLQDF +LK RL++EN DL R LE+ ++Q+N L RLKS L SQL+E

MHC B 1264 QLTELQSKADEQSRQLQDFTSLKGRLHSENGDLVRQLEDAESQVNQLTRLKSQLTSQLEE 1323

MHC A 1328 TRRNYDEESRERQALAATAKNLEHENTILREHLDEEAESKADLTRQISKLNAEIQQWKAR 1387
RR DEE+RERQ +AA AKN +HE L+E L+EE E K ++ RQ+SK NA+IQQWKAR

MHC B 1324 ARRTADEEARERQTVAAQAKNYQHEAEQLQESLEEEIEGKNEILRQLSKANADIQQWKAR 1383

MHC A 1388 FDSEGLNKLEEIEAAKKALQLKVQELTDTNEGLFAKIASQEKVRFKLMQDLDDAQSDVEK 1447
F+ EGL K +E+E AK+ K+ EL + + +K AS EK + +L+ DLDDAQ DVE+

MHC B 1384 FEGEGLLKADELEDAKRRQAQKINELQEALDAANSKNASLEKTKSRVLVGDLLDDAQVDVER 1443

MHC A 1448 AAAQVAFYEKHRRQFESIIAEWKKKTDLLSSELDAAQDRNQLSTDLEFKAKTANDELAEY 1507
A + EK ++ F+ II EW+KKTDDL++ELD AQRD R STDLEFKAK A +ELAE

MHC B 1444 ANGVASALEKKQKGFDKIIDEWRKKTDDLAAELDGAQRDLRNTSTDLEFKAKNAQEELAEV 1503

MHC A 1508 LDSTRRENKSLAQEVKDLTDQLGEGGRSVAELQKIVRKLEVEKEELQKALDEAEAALEAE 1567
++ RRENKSL+QE+KDLTDQLGEGGRSV E+QKI+R+LE+EKEELQ ALDEAEAALEAE

MHC B 1504 VEGLRRENKSLSQEIKDLTDQLGEGGRSVHEMQKIIRRLEIEKEELQHALDEAEAALEAE 1563

MHC A 1568 EAKVLRAQIEVSQIRSEIEKRIQEKEEEFENTRRNHQRALESMQATLEAETKQKEEALRI 1627
E+KVLRAQ+EVSQIRSEIEKRIQEKEEEFENTR+NH RALESMQA+LE E K K E LRI

MHC B 1564 ESKVLRAQVEVSQIRSEIEKRIQEKEEEFENTRKNHARALESMQASLETEAKGKAELLRI 1623

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KKKLE DIN+LEIALDHAN+A ADAQK +K+Y E V+ELQ Q+EEEQR + REQF +

MHC B 1624 KKKLEGDINELEIALDHANKANADAQKLNKRYQEQVRELQLQVEEEQRNGADTREQFFNA 1683

MHC A 1688 EKRNAILQSEKDELAQQAEAAERARRNAEAEICELREQNNDLNAHVSALTGQRRKLEGEL 1747
EKR +LQSEK+EL EAAERAR+ AE E + R+Q N+ NA VS+LT +RKLEGE+

MHC B 1684 EKRALLLQSEKEELLVANAEEARARKQAEYEAADARDQANEANAQVSSLSAKRKLEGEI 1743

MHC A 1748 LAAHAELEEIANELKNAVEQGGKASADAARLAEELRQEQEHSMHIERIRKGLELQIKEMQ 1807
A HA+L+E NE K A E+ +KA ADA RLAEELRQEQEHS H++R+RKGLE Q+KE+Q

MHC B 1744 QAIHADLDELNEYKAAEERSKKAIIADATRLAEELRQEQEHSQHVDRLRKGLEQQLKEIQ 1803

MHC A 1808 IRLDDAENAALKGGKKIIAQLEARIRAIQELDGEQRRHQDTEKNWRKAERRVKEVEFQV 1867
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MHC B 1804 VRLDEAEAAAALKGGKKVIAKLEQRVRELESELDGEQRRFQDANKNLGRADRRVRELQFQV 1863

MHC A 1868 VEEKKNEERLTELVDKLCCKLKIFKRQVEEAEVAASNLNKYKVLTAQFEQAEERADIAE 1927
E+KKN ERL +L+DKLQ KLK K+QVEEAE+ NL KYK LT Q E AEERAD AE

MHC B 1864 DEDKKNFERLQDLIDKLQKLTQKQVEEAEELANLNQKYKQLTHQLEDAEERADQAE 1923

MHC A 1928 NALSKMRNKIRASASMAPPDGFPMPVSSALIRSSSNAR 1967
N+LSKMR+K RASAS+AP + SAS+A+IRS S AR

MHC B 1924 NSLSKMRKSRASVAP----GLOSSAAVIRSPSRAR 1959

Phosphorylation Sites:

Underlined: sites predicted in Schriefer and Waterston, 1989

Highlighted: sites identified in this study by mass spectrometry

Yellow: specific to *unc-54(s74)*

Red: specific to wild type

Blue: common to wild type and *unc-54(s74)*

Figure S7

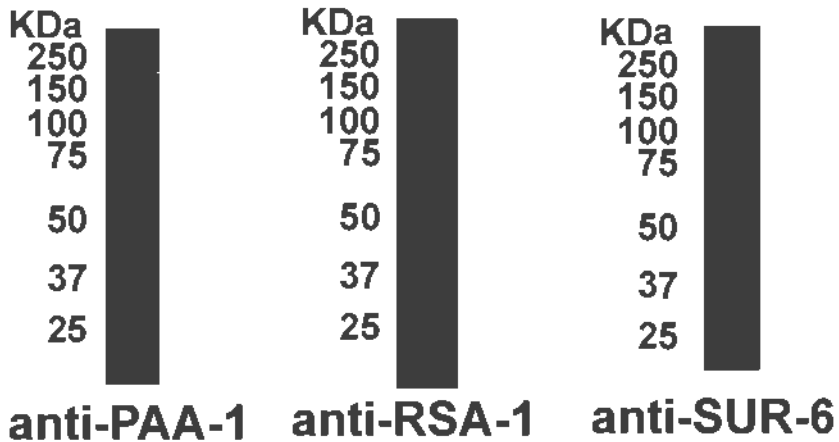


Table S1. Results of yeast 2-hybrid screens using 13 segments of UNC-89B.

Bait	Screening number	isolated clones (number of clones)
DH-PH	866200	SPD-2 (3), VET-1 (2), UNC-22 (5)
Ig4-7	1544200	no
KSP	525500	no
Ig8-13	1618100	no
Ig13-18	1803600	F22F4.1 (13)
Ig18-23	1463100	no
Ig23-28	2371000	no
Ig28-33	2478000	no
Ig33-38	6080000	no
Ig38-43	5325000	no
Ig43-48	9725000	no
Ig48-51-Fn1-Ig52	1240000	HIF-1 (95), HUM-6 (4), NHR-1 (5), T01B6.1 (2)
1/3IK-Ig53-Fn2	11174000	EPS-8 (2), GCK4 (7), KIN-18 (2), LIM-9 (12), LIN-13 (3), LIN-45 (3), PPTR-1 (4), PPTR-2 (2), T01B6.1 (3)

Table S2. New UNC-89 interactors summary

Protein	Isolated with	Character	SAGE (muscle)	Promoter fusion		RNAi phenotype	Localization of GFP-MHC A upon RNAi	Localization of anti-MHC A
				body wall muscle	pharyngeal muscle			
VET-1	DH-PH		ND	ND	ND		normal	ND
SPD-2	DH-PH	predicted coiled-coil domains	yes	no	no	Emb	abnormal (escaper)	slightly abnormal (ts mutant at 25° C)
UNC-22	DH-PH	twitchin	ND	yes*	yes*	Twitching	abnormal	ND
F22F4.1	Ig13-18		no	ND	ND		slightly abnormal	normal (RNAi)
HIF-1	Ig48-51-Fn1-Ig52	hypoxia response	yes	ND	ND		normal	ND
HUM-6	Ig48-51-Fn1-Ig52	myosin VII	yes	ND	ND		normal	ND
LIN-45	1/3IK-Ig53-Fn52	raf kinase	no	no	no	Emb	normal (escaper)	normal (mutants)
LIN-13	1/3IK-Ig53-Fn52	zinc finger	yes	yes	no	Larval lethal	normal	normal (mutants)
LIM-9**	1/3IK-Ig53-Fn52	FHL	yes	yes	yes		dim***	ND
T01B6.1	1/3IK-Ig53-Fn52	APC domain	no	ND	ND		abnormal/normal	normal (RNAi)
PPTR-1	1/3IK-Ig53-Fn52	PP2A regulatory	yes	yes	yes	Emb	abnormal (escaper)	abnormal (mutants)
PPTR-2	1/3IK-Ig53-Fn52	PP2A regulatory	yes	yes	no		normal	normal (mutants)
EPS-8	1/3IK-Ig53-Fn52	PTB, SH3, actin binding	yes	yes	yes	Emb	abnormal (escaper)	normal (L1 feeding RNAi)
KIN-18	1/3IK-Ig53-Fn52	protein kinase	no	no	yes		normal	ND
GCK-4	1/3IK-Ig53-Fn52	protein kinase	no	no	yes	Larval lethal	normal	ND

*: Matsunaga et al., 2017

** : Identified as UNC-89 interactor in Xiong et al., 2009

***: Meissner et al., 2009

Table S3. Phenotypes generated by *cash-1* RNAi.

Phenotype:	Unc¹	Vulval defects²	Sterile
# experiments	6	6	2
# worms	606	606	197
% with phenotype (average)	35%	38%	100%
S. D.	27%	25%	na
p value	0.011	0.004	na

¹Unc, uncoordinated.

²Vulval defects include protruded vulva and extruded vulva.

Table S4. Oligonucleotide primers used in this study

Name	Property	Sequence
BamHI-Ig53	UNC-89 Ig53, forward	GCGGGATCCAATGATGATGGAACCTTTGCC
Ig53-XhoI	UNC-89 Ig53, reverse	CGCCTCGAGTTAACGAGATGGAGTCTCTCCACT
BamH-Fn2	UNC-89 Fn2, forward	GCGGGATCCCGACTGATAAGTGGAGAGACT
Fn2-XhoI	UNC-89 Fn2, reverse	CGCCTCGAGTTAAATTTGCAACTTTGGTGCTCC
PPTR01	His tagged PPTR-1, forward	GCGGAATTC CATGGCGCTCATCAAAGATACTGCTGCA
PPTR02	His tagged PPTR-1, reverse	CGCGTCGACGGTACCTTATTTTTTTAGCCGGCGTCGTCG
PPTR03	His tagged PPTR-2, forward	GCGGAATTC CATGGCGAATATTGGCCGAACAAACACG
PPTR04	His tagged PPTR-2, reverse	CGCCCCGGGGTACCTCACTGTTTCGTCGGTGCTAGT
PPTR05	PPTR-1 antigen, forward	GCGCCCCGGGCAACGAGAAAAGGATCGTGAT
PPTR06	PPTR-1 antigen, reverse	CGCGTCGACTTATTTTTTTAGCCGGCGTCGTCG
PPTR07	PPTR-2 antigen, forward	GCGCCCCGGGACATTGAATGAAGAAAAGAA
PPTR08	PPTR-2 antigen, reverse	CGCGTCGACTCACTGTTTCGTCGGTGCTAGT
PPTR09	paa-1 RNAi, forward	GCGGTGACATGTCGGTTGTCGAAGAAGCC
PPTR10	paa-1 RNAi, reverse	CGCGTCGACCCTTGCAACGTTGAGCAGTG
PPTR11	let-92 RNAi, forward	GCGCTCGAGATGGCTGCTGCCCCACCATCT
PPTR12	let-92 RNAi, reverse	CGCCTCGAGCTACAGGAAGTAGTCAGGCGT

Table S5. *C. elegans* strains used in this study

strain name	genotype	type of mutation	mammalian homologue	biological phenotype**
JH2787	<i>pptr-1(tm3103)V</i>	genomic deletion	PP2A regulatory subunit (B') / B56	slow growth
MAS264	<i>pptr-1(abc19)V</i>	substitution (C95Y)	PP2A regulatory subunit (B') / B56	not yet characterized
MAS268	<i>pptr-2(ok1467)V</i>	genomic deletion	PP2A regulatory subunit (B') / B56	no phenotype
MAS294	<i>pptr-1(abc19) pptr-2(ok1467)V</i>	substitution (C95Y) and genomic deletion	PP2A regulatory subunit (B') / B56	not yet characterized
GB283	<i>unc-89(tm752)I</i>	genomic deletion	obscurin	uncoordinated movement
RW79	<i>unc-89(st79)I</i>	nonsense	obscurin	uncoordinated movement
EU1062	<i>sur-6(or550)I</i>	substitution (C302Y)	PP2A regulatory subunit (B)	temperature sensitive embryonic lethal
TH322*	<i>unc-13(e51) rsa-1(dd10) I/hT2 [bli-4(e937) let-?(q782) qls48] (I;III)</i>	substitution (Q340K in RSA-1a)	PP2A regulatory subunit (B'')	maternal effect embryonic lethal
TH323*	<i>unc-13(e51) rsa-1(dd13) I/hT2 [bli-4(e937) let-?(q782) qls48] (I;III)</i>	splice site	PP2A regulatory subunit (B'')	maternal effect embryonic lethal
BC347	<i>unc-54(s74)I</i>	substitution (R270C)	myosin heavy chain	uncoordinated movement
RW5008	<i>unc-54(s95)I</i>	substitution (G120R)	myosin heavy chain	uncoordinated movement
RW134	<i>unc-54(st134)I</i>	substitution (S119F)	myosin heavy chain	uncoordinated movement

*: balanced strain of *rsa-1*

** : as listed in Wormbase