

Additional File 1 for:

The *C. elegans* 3'UTRome V2: an updated genomic resource to study 3'UTR biology

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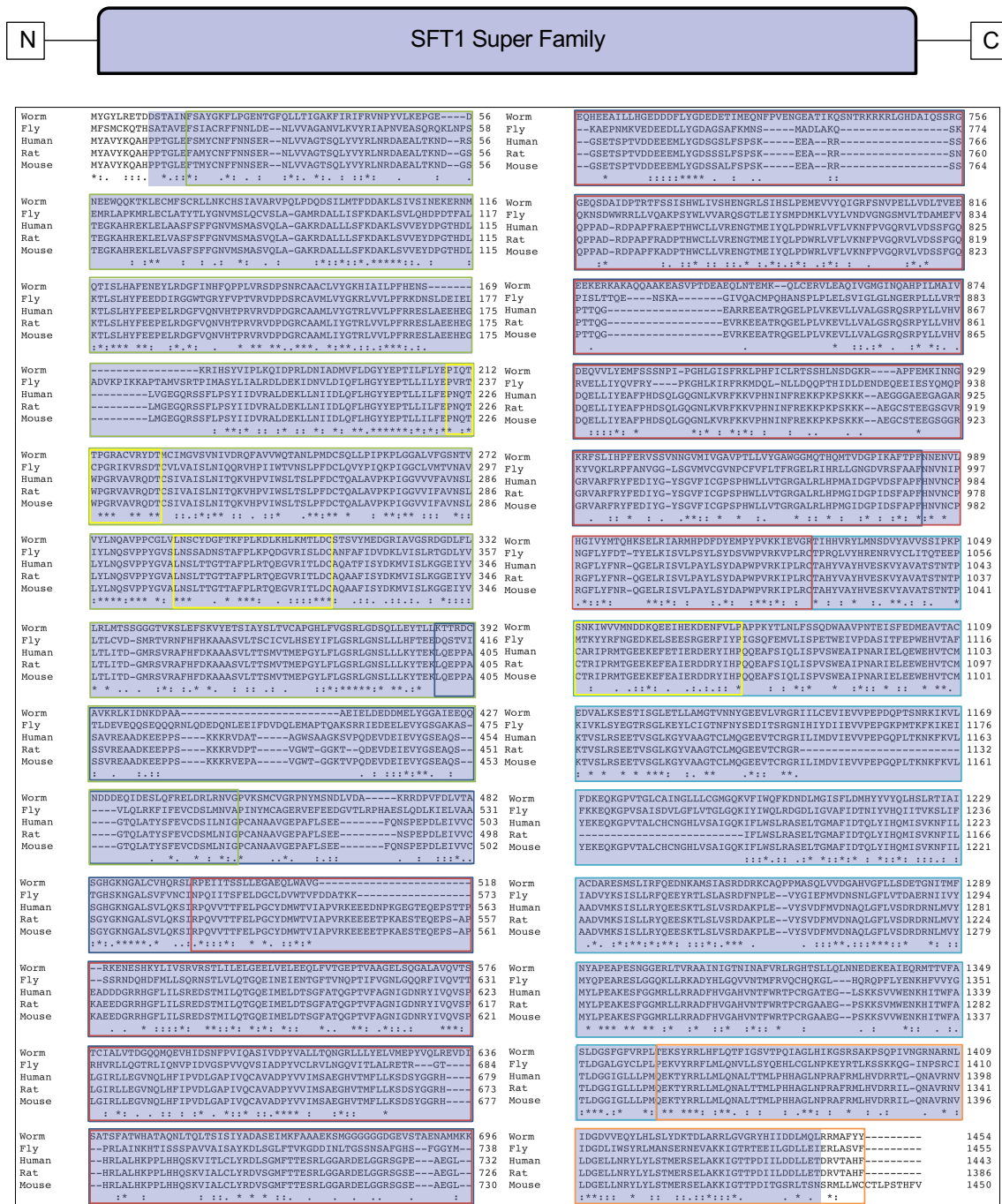
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CPSF complex

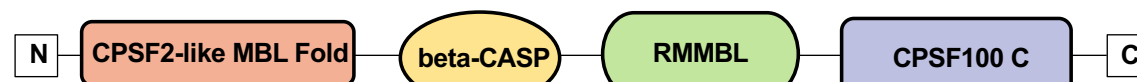
cpsf-1 (CPSF160)



Supplemental Fig. S1: Protein alignment of members of the CPC complex in five organisms. Amino acid sequence alignment for the members of the CPC from five organisms produced with Clustal Omega Multiple Sequence Alignment. Conserved domains produced with the Batch Conserved Domain Search on NCBI are represented by the highlighted regions of each figure. Known domains determined from previously published literature are outlined.

CPSF Complex

cpsf-2 (CPSF-100)



Worm	MTSIIKLVKFSAGKDEGLCYLLQVDDGYILLDCGWDERFLQVFEELKFFPKISAVLI	60	Worm	KASFFKTKKSFMPFYIEEKVKDDYGEVIKPEDYTVISIKDLR-----KGQNKD	528
Fly	MTSIIKLVKFSAGKDEGLCYLLQVDDGYILLDCGWDERFLQVFEELKFFPKISAVLI	60	Fly	HSGFFKSNKRHMVFPYHEEKVKDEYGEIINLDYRADIATGYEFPMEEQNKEMVKE	505
Human	MTSIIKLVKFSAGKDEGLCYLLQVDDGYILLDCGWDERFLQVFEELKFFPKISAVLI	60	Human	KGSFFKQAKKSYMPFAPAEERIKWDEYGEIIPKEDFLVPELQATE-----EKS	500
Mouse	MTSIIKLVKFSAGKDEGLCYLLQVDDGYILLDCGWDERFLQVFEELKFFPKISAVLI	60	Mouse	KGSFFKQAKKSYMPFAPAEERIKWDEYGEIIPKEDFLVPELQATE-----EKS	500
Rat	MTSIIKLVKFSAGKDEGLCYLLQVDDGYILLDCGWDERFLQVFEELKFFPKISAVLI	60	Rat	KGSFFKQAKKSYMPFAPAEERIKWDEYGEIIPKEDFLVPELQATE-----EKS	500
Worm	SHDPDLHLGGLPYLVKGLGNCPIYATIPVFKGMQFMYDLYVSHLDVNEFEHYLDDVD	120	Worm	EPVVKKREEEVEEYVNDVHEMPTCVFEFNKRVESVCEPIEYEGISDGESETKLLA	588
Fly	SHDPDLHLGGLPYLVKGLGNCPIYATIPVFKGMQFMYDLYVSHLDVNEFEHYLDDVD	120	Fly	EPGIGAEQQAQNGIIVNDVLEKPKTLISQRTIEIKARVYIDYEGRSDDGSIKIKIN	554
Human	SHDPDLHLGGLPYLVKGLGNCPIYATIPVFKGMQFMYDLYVSHLDVNEFEHYLDDVD	120	Human	ESGL-----TNGEPMDDQLSDVPTKCVSATESIEIKARVYIDYEGRSDDGSIKIKIN	554
Mouse	SHDPDLHLGGLPYLVKGLGNCPIYATIPVFKGMQFMYDLYVSHLDVNEFEHYLDDVD	120	Mouse	ESGL-----TNGEPMDDQLSDVPTKCVSATESIEIKARVYIDYEGRSDDGSIKIKIN	554
Rat	SHDPDLHLGGLPYLVKGLGNCPIYATIPVFKGMQFMYDLYVSHLDVNEFEHYLDDVD	120	Rat	ESGL-----TNGEPMDDQLSDVPTKCVSATESIEIKARVYIDYEGRSDDGSIKIKIN	554
Worm	TAPEKVEQVYQNTVTKGDD--SGVHTALPAGHMLGGSIRICRVGTGDIYVYVDFNHKK	179	Worm	GILLPQIIVVHGSRDDTRDLVAVFADSGEDTTLKAPAGALVADVASEFTYQVALSDAI	648
Fly	TAPEKVEQVYQNTVTKGDD--SGVHTALPAGHMLGGSIRICRVGTGDIYVYVDFNHKK	180	Fly	QLRPRRVIHCTAGETQVAVRHCQNG---ARVPTPKGRIIDVTSFETHIYQVRLTEGL	623
Human	TAPEKVEQVYQNTVTKGDD--SGVHTALPAGHMLGGSIRICRVGTGDIYVYVDFNHKK	180	Human	QMKPRLIIVHGPPEASDLAECCRAFGGDKIVYMPKPLHETVDATSETHIYQVRLKDSI	614
Mouse	TAPEKVEQVYQNTVTKGDD--SGVHTALPAGHMLGGSIRICRVGTGDIYVYVDFNHKK	180	Mouse	QMKPRLIIVHGPPEASDLAECCRAFGGDKIVYMPKPLHETVDATSETHIYQVRLKDSI	614
Rat	TAPEKVEQVYQNTVTKGDD--SGVHTALPAGHMLGGSIRICRVGTGDIYVYVDFNHKK	180	Rat	QMKPRLIIVHGPPEASDLAECCRAFGGDKIVYMPKPLHETVDATSETHIYQVRLKDSI	614
Worm	ERHLNGCSDFNFRPHLLITGAHHISLPQRRKRDDELVTKILLTVRQGDCHVILDTA	239	Worm	LADIQFKEVSEGNLAWIDARVMEK--EADNMLAVTSNLLDKNREEDVNDQENGAT	707
Fly	ERHLNGCSDFNFRPHLLITGAHHISLPQRRKRDDELVTKILLTVRQGDCHVILDTA	240	Fly	VSLQFQKQK--DARVANVGLRQVRAEAMVTVVY---VQEGTLLDLETLADDE	659
Human	EIHLNGCSLEMLSRPSSLITDSFNATVQPRRQRDELLTNVLETLRGGDGNLVAFTA	240	Human	VSSLPQCKAK--DAELAWIDGVLDVMSRVKVTGVLEEGELK	654
Mouse	EIHLNGCSLEMLSRPSSLITDSFNATVQPRRQRDELLTNVLETLRGGDGNLVAFTA	240	Mouse	VSSLPQCKAK--DAELAWIDGVLDVMSRVKVTGVLEEGELK	654
Rat	EIHLNGCSLEMLSRPSSLITDSFNATVQPRRQRDELLTNVLETLRGGDGNLVAFTA	240	Rat	VSSLPQCKAK--DAELAWIDGVLDVMSRVKVTGVLEEGELK	654
Worm	GRVLELAHLLDQLWNSADAGLSTYNLVMHSHVASVVFQAKSOLEWNEKLFKYDSSAR	291	Worm	EGEGNAEPMEIGENGSOESLAISESGVEVNGHTNDRSRKTKGIRKGNLIDPLPKRL	767
Fly	GRVLELAHLLDQLWNSADAGLSTYNLVMHSHVASVVFQAKSOLEWNEKLFKYDSSAR	291	Fly	-----DQDAS-----FQDAS-----VQEGTLLDLETLADDE	680
Human	GRVLELAHLLDQLWNSADAGLSTYNLVMHSHVASVVFQAKSOLEWNEKLFKYDSSAR	291	Human	DDGEDEKQVDPADSSSAMAAQK---AMKSL--FGDE--KELGEEETIPLPELPHPE	707
Mouse	GRVLELAHLLDQLWNSADAGLSTYNLVMHSHVASVVFQAKSOLEWNEKLFKYDSSAR	291	Mouse	DDGEDEKQVDPADSSSAMAAQK---AMKSL--FGDE--KELGEEETIPLPELPHPE	707
Rat	GRVLELAHLLDQLWNSADAGLSTYNLVMHSHVASVVFQAKSOLEWNEKLFKYDSSAR	291	Rat	DDGEDEKQVDPADSSSAMAAQK---AMKSL--FGDE--KELGEEETIPLPELPHPE	707
Worm	YNPFTLKHVTLCHSHOEMLRVR--SPKVLCSQDMESEGRLEFLDWCSDPRNGVILTA	351	Worm	TIHQAVFVNDPKLSDFKNLLTDKGYKAEFLSGTLLINGGNCISIRNNDTVGFQMEGATK	827
Fly	YNPFTLKHVTLCHSHOEMLRVR--SPKVLCSQDMESEGRLEFLDWCSDPRNGVILTA	351	Fly	IPHNSVLINEHLSDFKQTLMRNNINSEFSGVGLWCSNGTALALRVDAKVMGECISE	740
Human	NNPFPQKHLCHLSDSLARVP--SPKVLASQDLECFGRSRLIQWQDQPKNSIILTYR	351	Human	VPHQSVFPMNPRLSDFKQVLLREGIQAEFVGGVLCVQNG--VAVRTTEGRIGLECCLO	766
Mouse	NNPFPQKHLCHLSDSLARVP--SPKVLASQDLECFGRSRLIQWQDQPKNSIILTYR	351	Mouse	VPHQSVFPMNPRLSDFKQVLLREGIQAEFVGGVLCVQNG--VAVRTTEGRIGLECCLO	766
Rat	NNPFPQKHLCHLSDSLARVP--SPKVLASQDLECFGRSRLIQWQDQPKNSIILTYR	351	Rat	VPHQSVFPMNPRLSDFKQVLLREGIQAEFVGGVLCVQNG--VAVRTTEGRIGLECCLO	766
Worm	PASFTLAALKVMAERANDGVLKHEDRLISLVVKKRVALEGEELLEYKRRKAERDAETR	411	Worm	DYKLRRLRYDQFAVL-- 843	
Fly	TSPGTLARLIDNP-----PGKQIELDVRVRRVLEGALEEVLTQTQEKLNPLIV	401	Fly	EYKIRRELLYQYAVI-- 756	
Human	TPGTLARLIDNP-----SERKTEELRRVRLKGELEEVLEKELKKAARK	401	Human	DFYRIRDLLEYQYAVI-- 784	
Mouse	TPGTLARLIDNP-----SERKTEELRRVRLKGELEEVLEKELKKAARK	401	Mouse	DFYRIRDLLEYQYAVI-- 782	
Rat	TPGTLARLIDNP-----SERKTEELRRVRLKGELEEVLEKELKKAARK	401	Rat	DFYRIRDLLEYQYAVI-- 782	
Worm	LRMERARRQAQANESDSDS--DDDDIAAPVPRHSEKDFRSPDGENAHTFDIMAKWDNQ	477			
Fly	-----K--PDVEEESSESEDDI--EM-----SVITGKHDIVVRPEGRH	445			
Human	LEQS--KE--ADISSDESDEEDIDQP-----SAHKTKHLDMKMGEGSR	449			
Mouse	LEQS--KE--ADISSDESDEEDIDQP-----SAHKTKHLDMKMGEGSR	449			
Rat	LEQS--KE--ADISSDESDEEDIDQP-----SAHKTKHLDMKMGEGSR	449			

Metallo-beta-lactamase domain (Mandel et al., 2006)
Beta-CASP domain (Mandel et al., 2006)

cpsf-3 (CPSF-73)

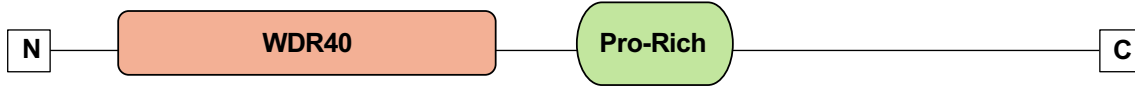


Worm	-----MEEGDNDSLCTFLGSGQVGRSCHLELYKGRVMLDCGVHGLHGVDALP	53	Worm	IIAGYCVBGTAKHLISEPEEITVLSGKELPMRMDVYVFSATIDYQOQSEFIRALKPF	412
Human	-----MSAIPAESDQLLIRPLGAGQVGRSCILIEFKGRKIMLDCGHPGLEGDHALP	54	Human	IIAGYCVBGTAKHLISEPEEITVMSGQKPLRMDVYVFSATIDYQOQSEFIRALKPF	413
Mouse	-----MSAIPAESDQLLIRPLGAGQVGRSCILIEFKGRKIMLDCGHPGLEGDHALP	54	Mouse	IIAGYCVBGTAKHLISEPEEITVMSGQKPLRMDVYVFSATIDYQOQSEFIRALKPF	412
Fly	MTQATQDARMDEESDQLIRPLGAGQVGRSCILIEFKGRKIMLDCGHPGLEGDHALP	60	Fly	IIAGYCVBGTAKHLISEPEEITVMSGQKPLRMDVYVFSATIDYQOQSEFIRALKPF	418
Worm	FVDVPEIENIDLLITLHFDLDCGALPWLQKTSFKGRGTFMTHATKAIYRWLLSDYKVS	113	Worm	HLVLVHGEQNEMLRKAALIREYEDNDEVHIEVHNPNTEAVTNFRKELAKVWGLAD	472
Human	YIDLIDPAEIDLLITLHFDLDCGALPWLQKTSFKGRGTFMTHATKAIYRWLLSDYKVS	114	Human	HLVLVHGEQNEMLRKAALIREYEDNDEVHIEVHNPNTEAVTNFRKELAKVWGLAD	472
Mouse	YIDLIDPAEIDLLITLHFDLDCGALPWLQKTSFKGRGTFMTHATKAIYRWLLSDYKVS	114	Mouse	HLVLVHGEQNEMLRKAALIREYEDNDEVHIEVHNPNTEAVTNFRKELAKVWGLAD	472
Rat	YIDLIDPAEIDLLITLHFDLDCGALPWLQKTSFKGRGTFMTHATKAIYRWLLSDYKVS	114	Rat	HLVLVHGEQNEMLRKAALIREYEDNDEVHIEVHNPNTEAVTNFRKELAKVWGLAD	472
Fly	YVDLIDAEIDLLITLHFDLDCGALPWLQKTSFKGRGTFMTHATKAIYRWLLSDYKVS	120	Fly	HLVLVHGEQNEMLRKAALIREYEDNDEVHIEVHNPNTEAVTNFRKELAKVWGLAD	478
Worm	KYGGPRNQLVTEDELEKSMKAIETIDFREQVENVIRFPWYVAGVILGACQFMIETAGV	173	Worm	RVEPNNETISGLVKNRNFYSIMVPEELGSLVSLRISLSELRMSVHYSGSKLLIFNLQ	532
Human	NISA--DMMLVTEDELEKSMKAIETIDFREQVENVIRFPWYVAGVILGACQFMIETAGV	172	Human	KKPEQQRVSGILVKNRNFYHLSPCDLSNVTDLAMSTVQQAIPYTGFFLLYQYQK	532
Mouse	NISA--DMMLVTEDELEKSMKAIETIDFREQVENVIRFPWYVAGVILGACQFMIETAGV	172	Mouse	KKPEQQRVSGILVKNRNFYHLSPCDLSNVTDLAMSTVQQAIPYTGFFLLYQYQK	532
Fly	NIST--EQMLVTEDELEKSMKAIETIDFREQVENVIRFPWYVAGVILGACQFMIETAGV	178	Fly	KNEVSGKLSGLVKNRNFYHLSPCDLSNVTDLAMSTVQQAIPYTGFFLLYQYQK	538
Worm	RVLVTDQFSQDRHLMAAEIPNPKPDLIIESTYVTHHEKREERARFCMTVHDIVNR	233	Worm	IMDDACLINQIKLKEISKGSVQTAITVQKQVNTVYGNHVVVWVMSNPNVYDADS	592
Human	KLLYTDQFSQDRHLMAAEIPNPKPDLIIESTYVTHHEKREERARFCMTVHDIVNR	232	Human	LRGDEVELEIQE-----KPAKVF---KNTITVQEGMVLKLANPSNDYADT	579
Mouse	KLLYTDQFSQDRHLMAAEIPNPKPDLIIESTYVTHHEKREERARFCMTVHDIVNR	232	Mouse	LRGDEVELEIQE-----KPAKVF---KNTITVQEGMVLKLANPSNDYADT	579
Rat	KLLYTDQFSQDRHLMAAEIPNPKPDLIIESTYVTHHEKREERARFCMTVHDIVNR	232	Rat	LRGDEVELEIQE-----KPAKVF---KNTITVQEGMVLKLANPSNDYADT	579
Fly	KILYTDQFSQDRHLMAAEIPNPKPDLIIESTYVTHHEKREERARFCMTVHDIVNR	238	Fly	IGAGCEV--LEA-----EKRLVY---GCIELVTEQKILVMEQATVHNVYADA	584
Worm	SGRCLIPVAFAGQAEQLLIDVWQHPHLDIPYIYASSLAKKCMVYQYVYVANNNDK	293	Worm	VVAALHQAQNPVDPKYL---SNSSFPQNTAIEGMVKHICGDDVYSIMSERGLLAQF	648
Human	SGRCLIPVAFAGQAEQLLIDVWQHPHLDIPYIYASSLAKKCMVYQYVYVANNNDK	292	Human	VTVVILEVQSNPKIRKGAQVQVSKLEMHVYSKRLLEMLDQIFGECVSV--KDDSVLST	638
Mouse	SGRCLIPVAFAGQAEQLLIDVWQHPHLDIPYIYASSLAKKCMVYQYVYVANNNDK	292	Mouse	VTVVILEVQSNPKIRKGAQVQVSKLEMHVYSKRLLEMLDQIFGECVSV--KDDSVLST	638
Fly	SGRCLIPVAFAGQAEQLLIDVWQHPHLDIPYIYASSLAKKCMVYQYVYVANNNDK	298	Fly	VLAICMQSLGGTNGKATQK---KESDRPRELIEITLQDFGDCNPKMFGDLP	642
Worm	IRKQIANNPFFVKHISNLKSMDFHFDIGPSVVMASPGMIQNGLSRELFSWCTDKRNGV	353	Worm	EEDGRRLVGESSDQFVMMGDDPMDPTSHLLQNLTEKMRQVITTTNEVIDMEC	707
Human	IRKQIANNPFFVKHISNLKSMDFHFDIGPSVVMASPGMIQNGLSRELFSWCTDKRNGV	352	Human	V--DGKTANINLETR--TVECEGSEDDLESREVELAARQYALVTPH-----	684
Mouse	IRKQIANNPFFVKHISNLKSMDFHFDIGPSVVMASPGMIQNGLSRELFSWCTDKRNGV	352	Mouse	V--DGKTANINLETR--AVECEGSEDDLESREVELAARQYALVTPH-----	684
Rat	IRKQIANNPFFVKHISNLKSMDFHFDIGPSVVMASPGMIQNGLSRELFSWCTDKRNGV	352	Rat	V--DGKTANINLETR--AVECEGSEDDLESREVELAARQYALVTPH-----	684
Fly	IRKQIANNPFFVKHISNLKSMDFHFDIGPSVVMASPGMIQNGLSRELFSWCTDKRNGV	358	Fly	V--SGKRAINLETR--AISCADDV---LRQMLTTVQKHLQTLVYAL-----	685

Metallo-beta-lactamase domain (Mandel et al., 2006) Ligands to Zn1 (Mandel et al., 2006)
Beta-CASP domain (Mandel et al., 2006) Ligands to Zn2 (Mandel et al., 2006)
Bridging ligand to Zinc atoms (Mandel et al., 2006) General acid for catalysis (Mandel et al., 2006)

CPSF Complex

pfs-2 (WDR33)

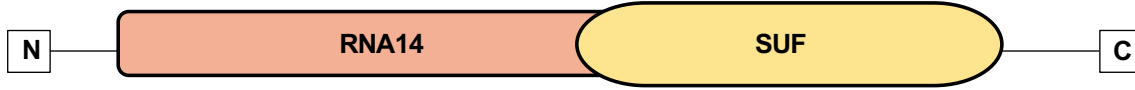


Species	Protein	Accession	Start	End	Species	Protein	Accession	Start	End
Worm	MTAVSNLAFMNMGGMRGNMNPVTLTIQPS-TSSNMQRPMNN-...HHPH-...	51	Worm	-----GGNGGWORPPQGSYGGQQPPQ-...SYGGQGL-...QGSYAS-...	673				
Fly	-----MVSQPPQLLTPALSAATMFTSLPPNMGQHYRHHPHGSM-...	44	Fly	DRDRERARERERDQSGRPNWASNAWNSNG-...NFGNGN-...GSMGNS-...NGAESF-...	760				
Human	-----MATEIGS-PPRFHMPRFQHQAP-...	22	Human	PGQMORHPGPH-GPLGPGQPGPGQSSGPGQGHMGPGQPGPGQGHIGPGQPGPGQHLGFP-...	732				
Mouse	-----MATEIGS-PPRFHMPRFQHQAP-...	22	Mouse	PGQMORHPGPH-GPLGPGQPGPGQSSGPGQGHMGPGQPGPGQGHIGPGQPGPGQHLGFP-...	731				
Rat	-----MATEIGS-PPRFHMPRFQHQAP-...	22	Rat	PGQMORHPGPH-GPLGPGQPGPGQSSGPGQGHMGPGQPGPGQGHIGPGQPGPGQHLGFP-...	731				
Worm	-----NRFQREHVPDMVGGDGRRLRKNVANVRHVYDVTVLNHCENRLWQ-...	99	Worm	-----QQ-PPRQIQHIP-...SDIDYRTAPSSNGSTGCDVDRMTVMP-...	712				
Fly	KHGYNQKFPFPGQRFPCMSQD--DFDGKRLRKS--VNRKTYDYNASIIKALENRYLQ-...	100	Fly	-----NDRDRGGGQRNRRIINNSGPNCGGGGGGGG-...GGGNNRGNRNNRY-...	807				
Human	-----RLFYKRFDFQQQAMQL--TFDGKMRKA--VNRKTYDYNASVIKYLENRYQ-...	73	Human	GPPTGQMGQPGPRGMQ--GPPHPIQG--G-PGSGIQGGVSGPLMGLNPRGMQGP-...	787				
Mouse	-----RLFYKRFDFQQQAMQL--TFDGKMRKA--VNRKTYDYNASVIKYLENRYQ-...	73	Mouse	GPPTGQMGQPGPRGMQ--GPPHPIQG--G-PASQIQG--...PLMGLNPRGMQGP-...	781				
Rat	-----RLFYKRFDFQQQAMQL--TFDGKMRKA--VNRKTYDYNASVIKYLENRYQ-...	73	Rat	GPPTGQMGQPGPRGMQ--GPPHPIQG--G-PTSQIQG--...PLMGLNPRGMQGP-...	781				
Worm	YKQ-RILQPDILYQAVPADSTTPVDCLIKFIRIRANMKVKCPVYSCWSPGK-...	158	Worm	-----NQPP-...	718				
Fly	RDYDRDLAQDSYVHPLMPSAYLNPNSNAVTRFVKATNKRKCFPLTAVTEGRR-...	160	Fly	PGPRENQGPAPQGMIMGHPQEMRGPPLGGLLHGHPQEMRGPQETRMGQPPPGQSMGL-...	807				
Human	RQDRDMRAIQPDAGYVNDLVPFVIGMLANPNMAVTRFVRSSTNKVKCPVYVVRVTEGRR-...	133	Human	PGPRENQGPAPQGMIMGHPQEMRGPPLGGLLHGHPQEMRGPQETRMGQPPPGQSMGL-...	847				
Mouse	RQDRDMRAIQPDAGYVNDLVPFVIGMLANPNMAVTRFVRSSTNKVKCPVYVVRVTEGRR-...	133	Mouse	PGPRENQGPAPQGMIMGHPQEMRGPPLGGLLHGHPQEMRGPQETRMGQPPPGQSMGL-...	841				
Rat	RQDRDMRAIQPDAGYVNDLVPFVIGMLANPNMAVTRFVRSSTNKVKCPVYVVRVTEGRR-...	133	Rat	PGPRENQGPAPQGMIMGHPQEMRGPPLGGLLHGHPQEMRGPQETRMGQPPPGQSMGL-...	841				
Worm	LTGCGTGFELMNGTAFNFETLQAHDSAIRLKWASNEQWLLSAGQVYKYNQPMN-...	218	Worm	EPEHWRGPPVSHQOQSQO--HPPPI-NMQ-...RMDPRDRPRLSG-...RSD-...	762				
Fly	LVGASGSEFELMNGTAFNFETLQAHDSVIRVMVSHSNDVMVGGVYKYNQSMN-...	220	Fly	FPQELRGSFGSQGQPGQSLGPPPGQMGQPPPGQGNPARGPHSGQIPFPQOQK-...	807				
Human	LVGASGSEFELMNGTAFNFETLQAHDSVIRVMVSHSNDVMVGGVYKYNQSMN-...	193	Human	FPQELRGSFGSQGQPGQSLGPPPGQMGQPPPGQGNPARGPHSGQIPFPQOQK-...	907				
Mouse	LVGASGSEFELMNGTAFNFETLQAHDSVIRVMVSHSNDVMVGGVYKYNQSMN-...	193	Mouse	FPQELRGSFGSQGQPGQSLGPPPGQMGQPPPGQGNPARGPHSGQIPFPQOQK-...	901				
Rat	LVGASGSEFELMNGTAFNFETLQAHDSVIRVMVSHSNDVMVGGVYKYNQSMN-...	193	Rat	FPQELRGSFGSQGQPGQSLGPPPGQMGQPPPGQGNPARGPHSGQIPFPQOQK-...	901				
Worm	NAMFSAHNDGAIIRGLAFATDVKFAASDDGTRVWQFARVTEERVLRSHGAEVRCID-...	278	Worm	QL-...SPSGPPQQQSSAQGGKQWMPFAGEAGNQNGYAGHRGGV-...	809				
Fly	NVKMFOAHL-EAIRGASFPSTDSKVFSGSDDTLRVWDFRMRQERVLRHGADVKCVHM-...	279	Fly	PLLDGGRAPFNEQSGTGPPLIP-GLGQ--GAQRIPPLNFGQGP-...-...	953				
Human	NVKMFOAHL-EAIRGASFPSTDNKFAFCSDDGTVRWFDFRMRQERVLRHGADVKCVHM-...	252	Human	PLLDGGRAPFNEQSGTGPPLIP-GLGQ--GAQRIPPLNFGQGP-...-...	947				
Mouse	NVKMFOAHL-EAIRGASFPSTDNKFAFCSDDGTVRWFDFRMRQERVLRHGADVKCVHM-...	252	Mouse	PLLDGGRAPFNEQSGTGPPLIP-GLGQ--GAQRIPPLNFGQGP-...-...	947				
Rat	NVKMFOAHL-EAIRGASFPSTDNKFAFCSDDGTVRWFDFRMRQERVLRHGADVKCVHM-...	252	Rat	PLLDGGRAPFNEQSGTGPPLIP-GLGQ--GAQRIPPLNFGQGP-...-...	947				
Worm	HPTKGLIATGSRDTPQVFKWDPKSGSLATLQHEKSSVMVAEKNKGNWLLTGRDRHLV-...	338	Worm	GGRGRGQOPY-...	820				
Fly	HPQGMIVSGSKDQOPIKWDPKSGSIALALALHAHKSVMVLDKWNNDGNWLLTASRDHL-...	339	Fly	PNKGDGSGPPNHHMGPMSERRHEQSGGPEHGERGPFPGQDQCRGPPDRRGGHPDFPDD-...	1013				
Human	HPTKGLVSGSKDQOPIKWDPKTQSLATLHAHKNVMEVKLNLNGWLLTASRDHL-...	312	Human	PNKGDTRGPPNHHMGPMSERRHEQSGGPEHGERGPFPGQDQCRGPPDRRGGHPDFPDD-...	1007				
Mouse	HPTKGLVSGSKDQOPIKWDPKTQSLATLHAHKNVMEVKLNLNGWLLTASRDHL-...	312	Mouse	PNKGDTRGPPNHHMGPMSERRHEQSGGPEHGERGPFPGQDQCRGPPDRRGGHPDFPDD-...	1007				
Rat	HPTKGLVSGSKDQOPIKWDPKTQSLATLHAHKNVMEVKLNLNGWLLTASRDHL-...	312	Rat	PNKGDTRGPPNHHMGPMSERRHEQSGGPEHGERGPFPGQDQCRGPPDRRGGHPDFPDD-...	1007				
Worm	KMYDIRMK-EMRYRAHKKEVISLAWHPIHEGLFVSGGDSGIYVWVDEKEREIGLLE-...	397	Worm	SRPDDFHPDKRFGRHLREFEGRGGPLPQEKWRGGGPPFPDHPRENEGDGRGAAR-...	1073				
Fly	KLFDIRNLKEELQVFRGKKEATAVAVHVEHGLFASGSDGSLFVHWVGEVEGVMEM-...	372	Fly	SRPDDFHPDKRFGRHLREFEGRGGPLPQEKWRGGGPPFPDHPRENEGDGRGAAR-...	1066				
Human	KLFDIRNLKEELQVFRGKKEATAVAVHVEHGLFASGSDGSLFVHWVGEVEGVMEM-...	372	Human	SRPDDFHPDKRFGRHLREFEGRGGPLPQEKWRGGGPPFPDHPRENEGDGRGAAR-...	1067				
Mouse	KLFDIRNLKEELQVFRGKKEATAVAVHVEHGLFASGSDGSLFVHWVGEVEGVMEM-...	372	Mouse	SRPDDFHPDKRFGRHLREFEGRGGPLPQEKWRGGGPPFPDHPRENEGDGRGAAR-...	1067				
Rat	KLFDIRNLKEELQVFRGKKEATAVAVHVEHGLFASGSDGSLFVHWVGEVEGVMEM-...	372	Rat	SRPDDFHPDKRFGRHLREFEGRGGPLPQEKWRGGGPPFPDHPRENEGDGRGAAR-...	1067				
Worm	AHDQIWSMKWHLGLHILATGSDNDNTKFWARNRPGDVTEDIFGLSNTNMG-HDKERE-...	456	Worm	PGWEGRRPDERFRPDPRFRGRREESFRGAPPRIHGRAPPRGRDNGFPDDEGPE-...	1133				
Fly	AHDQIWSLAWHLGLHILCSDNDHTSKFWTRNRPGLMDRKYNLTLPASLALDECEY-...	459	Fly	PGWEGRRPDERFRPDPRFRGRREESFRGAPPRIHGRAPPRGRDNGFPDDEGPE-...	1126				
Human	AHEGMIWSLAWHLGLHILCSDNDHTSKFWTRNRPGLMDRKYNLTLPGHSE--DGYEY-...	430	Human	PGWEGRRPDERFRPDPRFRGRREESFRGAPPRIHGRAPPRGRDNGFPDDEGPE-...	1126				
Mouse	AHEGMIWSLAWHLGLHILCSDNDHTSKFWTRNRPGLMDRKYNLTLPGHSE--DGYEY-...	430	Mouse	PGWEGRRPDERFRPDPRFRGRREESFRGAPPRIHGRAPPRGRDNGFPDDEGPE-...	1126				
Rat	AHEGMIWSLAWHLGLHILCSDNDHTSKFWTRNRPGLMDRKYNLTLPGHSE--DGYEY-...	430	Rat	PGWEGRRPDERFRPDPRFRGRREESFRGAPPRIHGRAPPRGRDNGFPDDEGPE-...	1127				
Worm	PRMAPPKSIETQETRYDPTFIPGMLDEHLYEQLNRDHNMM--TDDSTLLVDP-DLTRQ-...	513	Worm	-----	820				
Fly	-----DALIFQMGPEORVEETESL-...-TADGKIPSLDLDPS-...	494	Fly	-----	807				
Human	DDL-----EPNSLAVIPGMGIPQQLKAMEQEQMGKDESSEIEMTIPGLDWGME-...	479	Human	-----	820				
Mouse	DDL-----EPNSLAVIPGMGIPQQLKAMEQEQMGKDESSEIEMTIPGLDWGME-...	479	Mouse	-----	807				
Rat	DDL-----EPNSLAVIPGMGIPQQLKAMEQEQMGKDESSEIEMTIPGLDWGME-...	479	Rat	-----	820				
Worm	NFAPMIGAKRLLKQPKAKAQRQFERMWNNSKIGGASGD--FTTMGGGLREDAGEE-...	569	Worm	-----	820				
Fly	KAIN--DRDREKVPYSKIPRNFQVNWAGPRADDPSV--L-SHEELAAEAEDKDTN-...	548	Fly	-----	807				
Human	EVMQDKQKVPQKVPYAKIPAQFQAWMKNKVPAPAPNEVLDNRKEDIKLEEKKTQA-...	539	Human	-----	820				
Mouse	EVMQDKQKVPQKVPYAKIPAQFQAWMKNKVPAPAPNEVLDNRKEDIKLEEKKTQA-...	539	Mouse	-----	807				
Rat	EVMQDKQKVPQKVPYAKIPAQFQAWMKNKVPAPAPNEVLDNRKEDIKLEEKKTQA-...	539	Rat	-----	820				
Worm	-----AQFGSKSFLGPTTGGSLGPP-...	591	Worm	-----	820				
Fly	GLNHQIASENTMGLIAGMLGLDPTIVGLVYVNRIRVHDSRLMAIIRQAGEFLNK-...	608	Fly	-----	807				
Human	EIEQ-----EMA-----TLQYTNQLL-EQKIERLAQKQV-QIOPPPSSGTPLLG-...	585	Human	-----	1252				
Mouse	EIEQ-----EMA-----TLQYTNQLL-EQKIERLAQKQV-QIOPPPSSGTPLLG-...	585	Mouse	-----	1246				
Rat	EIEQ-----EMA-----TLQYTNQLL-EQKIERLAQKQV-QIOPPPSSGTPLLG-...	585	Rat	-----	1247				
Worm	-----RHOQPPMSG-----PGQYGPGRM-...	635	Worm	-----	820				
Fly	MOCKFPQLQSLAAKQAPNTEFVEPPLEQRD-...-DREREG-...	706	Fly	-----	807				
Human	-----PQPPHOGGGGPGQMGQPGQPGQGLPRPDHMG-...	673	Human	-----	1336				
Mouse	-----PQPPHOGGGGPGQMGQPGQPGQGLPRPDHMG-...	672	Mouse	-----	1330				
Rat	-----PQPPHOGGGGPGQMGQPGQPGQGLPRPDHMG-...	672	Rat	-----	1331				

Legend:
 N-terminal domain, contacts CPSF-160 and CPSF-30 (Clerici et al., 2017)
 WD40 repeats, contact U3 and A6 of PAS (Clerici et al., 2017)

CstF Complex

suf-1 (CstF77)



Worm	-----MSGLSRNPFERRIETNFVDVDAWNLRLREHQSRPIDQERDFYESLVR	47	Worm	YNCKRDEVAIRVFKLGLKYYENEPEFGLAYADFLSNLNDNTRVFERILTSSKLPAD	467
Fly	MSSARDLIKVDIEWGMLRVAQQVLELRFYDIESWSVMIREACTRPIHEVRSLSVESLVN	60	Fly	YYCSKDKBIAFRIFELGLKRFGGSPYVMCYIDVLSHLNEDNTRVLFERVLSSGGLSPH	480
Human	-----AAEYVPEVKVKAEEKLEENFYDLDAWSILIREAQNOPIDKARKTYERLVA	50	Human	YYCSKDKSVAFKIFELGLKRYGDIPEVLYAIDVLSHLNEDNTRVLFERVLSSGGLPPE	470
Rat	---MSGDAAEQAAEYVPEVKVKAEEKLEENFYDLDAWSILIREAQNOPIDKARKTYERLVA	59	Rat	YYCSKDKSVAFKIFELGLKRYGDIPEVLYAIDVLSHLNEDNTRVLFERVLSSGGLPPE	479
Mouse	---GGAAEQAAEYVPEVKVKAEEKLEENFYDLDAWSILIREAQNOPIDKARKTYERLVA	57	Mouse	YYCSKDKSVAFKIFELGLKRYGDIPEVLYAIDVLSHLNEDNTRVLFERVLSSGGLPPE	477
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Worm	QFPNSGRYKWAYIEHELRSKNFENVEKLFSCRIVSVLNIDLKWCYIHYVPETKQGRDQYR	107	Worm	KSIRIWRDRFLDFESCVDGLASILKVEKRRRTAYEEAQDQTMNHSMLVIDRYKFMDLMPG	527
Fly	VFPTTARYWKLYIEMEMBSRYRVEKLFQRCLVKILNIDLKWLTYVKTSGLSLTHK	120	Fly	KSVEVNRFLFESNIGLSSIVKVERRRSAVFENLKEYE-GKETAQLVDRYKFLDLYPC	539
Human	QFPSSGRFWKLYIEAEIKAKNYDKVEKLFQRCLMKVLHIDLKWCYLSYVRETKGKLPYSYK	110	Human	KSGETIWARFLAFESNIGLSSILKVEKRRPTAFR--EYEE-GKETALLVDRYKFMDLYPC	527
Rat	QFPSSGRFWKLYIEAEIKAKNYDKVEKLFQRCLMKVLHIDLKWCYLSYVRETKGKLPYSYK	119	Rat	KSGETIWARFLAFESNIGLSSILKVEKRRPTAFR--EYEE-GKETALLVDRYKFMDLYPC	536
Mouse	QFPSSGRFWKLYIEAEIKAKNYDKVEKLFQRCLMKVLHIDLKWCYLSYVRETKGKLPYSYK	117	Mouse	KSGETIWARFLAFESNIGLSSILKVEKRRPTAFR--EYEE-GKETALLVDRYKFMDLYPC	534
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Worm	EEMAKAVDFALEKVMQVAYSIFTEYIAFLKRVAVQVAENQRITAVRKIYQKALATP	167	Worm	SGEQLKLCYGNALKTESI--ACPSFVSGKNVPTHGQQAASAINGAGGHADVARYGFPF	585
Fly	EKMAQAVDFALEKICMDLHFSFIQWDYIVFLRGEVAVGNVAENQKITAVRRVYQKAVWTP	180	Fly	TSTELKSGIYAENVGIIILNKVQGA--QS-----QNTGEV-ETDSEATPPLPR	584
Human	EKMAQAVDFALDKIGMEIMSYQIWDYINFLKGEVAVGSAENQRITAVRRVYQKAVWTP	170	Human	SASELKALGYKDVSRAKLAAIIFPPVVPVAP-----SIVPVL-KDEVDRKPEYPK	574
Rat	EKMAQAVDFALDKIGMEIMSYQIWDYINFLKGEVAVGSAENQRITAVRRVYQKAVWTP	179	Rat	SASELKALGYKDVSRAKLAAIIFPPVVPVAP-----SIVPVL-KDEVDRKPEYPK	583
Mouse	EKMAQAVDFALDKIGMEIMSYQIWDYINFLKGEVAVGSAENQRITAVRRVYQKAVWTP	177	Mouse	SASELKALGYKDVSRAKLAAIIFPPVVPVAP-----SIVPVL-KDEVDRKPEYPK	581
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Worm	MHNLELIWVDYCYEKAINITLAEKLIARKEVQNRARVEKLDQMTGRGLNRQAVSVPF	227	Worm	PDISQMFKPRVNTASFPVPPGPPQVAHMLSLPPTFCIGPFINVELLGNMI	645
Fly	IVGIEQLWQYIAFEQININPISSEKMSLERSKDYMNARRVAKEYHTKGLNRNLPVAVP	240	Fly	PDFSQMIFKPRPCAHGAPLAGGVFPQPALAALCATLPPNSFRGPFVVELLFDIF	644
Human	MINIEQLWRDYNKYEEGINIHLAKKMIEDRSRDMNARRVAKEYETVMKGLDRNAPSVPF	230	Human	PDTQQMIFPQPRHLAPPLGHPVPGGVFPVPAVVMKLLPPIPCQGFVQVDELMEIF	634
Rat	MINIEQLWRDYNKYEEGINIHLAKKMIEDRSRDMNARRVAKEYETVMKGLDRNAPSVPF	239	Rat	PDTQQMIFPQPRHLAPPLGHPVPGGVFPVPAVVMKLLPPIPCQGFVQVDELMEIF	643
Mouse	MINIEQLWRDYNKYEEGINIHLAKKMIEDRSRDMNARRVAKEYETVMKGLDRNAPSVPF	237	Mouse	PDTQQMIFPQPRHLAPPLGHPVPGGVFPVPAVVMKLLPPIPCQGFVQVDELMEIF	641
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Worm	KGTATEFKQVLEWKNLIWETKINPLQTEYEQHARRVYVTEQSLCLCYGYPDIWYBAAM	287	Worm	NNMOLFNVSYPKSEDNMLGFMLEQDKKDMVQLLATTSDPSAVVRS-SALS--DLKRRK	702
Fly	TLTKEEVKQVLEWKRNIETEKSNLRTEDQLITKRVMFATQCLLVLHHPAVVHQASG	300	Fly	MRLNLPDSAPQWCDNELSKFDLAKSVHIV-DP-STYTCVQHSVAVPDRRRLLPG	702
Human	QNTPOEAQQVDMWKKYIQWKSNNLRTEDQLITKRVMFAYEQCLLVLGHHPDIWYEAAG	290	Human	RRCKIPMTVEAVRITGG--APELA-----V-EG---NGPVES-NAVITKAVKRPNE	680
Rat	QNTPOEAQQVDMWKKYIQWKSNNLRTEDQLITKRVMFAYEQCLLVLGHHPDIWYEAAG	299	Rat	RRCKIPMTVEAVRITGG--APELA-----V-EG---NGPVES-NAVITKAVKRPNE	689
Mouse	QNTPOEAQQVDMWKKYIQWKSNNLRTEDQLITKRVMFAYEQCLLVLGHHPDIWYEAAG	297	Mouse	RRCKIPMTVEAVRITGG--APELA-----V-EG---NGPVES-NAVITKAVKRPNE	687
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Worm	FLQEAHTLDEKGDVMAQVLEKLETISLYERAITGLMKESKLLFYAYADPQEEHQFEAV	347	Worm	DSDEDEYSHLGAIVIGSLGSRDAYKRRMKNKNE--- 735	
Fly	FLDTSARVLETKEGDVAQAKIFADECANILERSINGVLRNLLFYAYADFEGRKLYEKV	360	Fly	GDSDEDE---LQTAVP--PSHDIYRLQLKRFKSN 733	
Human	YLEQSSKLLAERGMNNAKLFSDAANIYERAI STLKKNMLLYFAYADYEESRMKYEKV	350	Human	DSDEDEE---KGAVVP--PVHDIYRARQQRIR--- 708	
Rat	YLEQSSKLLAERGMNNAKLFSDAANIYERAI STLKKNMLLYFAYADYEESRMKYEKV	359	Rat	DSDEDEE---KGAVVP--PVHDIYRARQQRIR--- 717	
Mouse	YLEQSSKLLAERGMNNAKLFSDAANIYERAI STLKKNMLLYFAYADYEESRMKYEKV	357	Mouse	DSDEDEE---KGAVVP--PVHDIYRARQQRIR--- 715	
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Worm	RNIYDRLLGIEHINPLFYIQLMRFIRRSEGNARLVFKRAREDRRTGYQVFAAALLP	407			
Fly	RTVFNKLLQLPDIIDPLFYVQIMKFAARAEIKSARSIKFKAREDRSRHIFVAALMH	420			
Human	HSIYNRLAIEDIDPLFYIYQIMKFAARAEIKSGRMIFKFKAREDRTRHHVYVTAALMH	410			
Rat	HSIYNRLAIEDIDPLFYIYQIMKFAARAEIKSGRMIFKFKAREDRTRHHVYVTAALMH	419			
Mouse	HSIYNRLAIEDIDPLFYIYQIMKFAARAEIKSGRMIFKFKAREDRTRHHVYVTAALMH	417			
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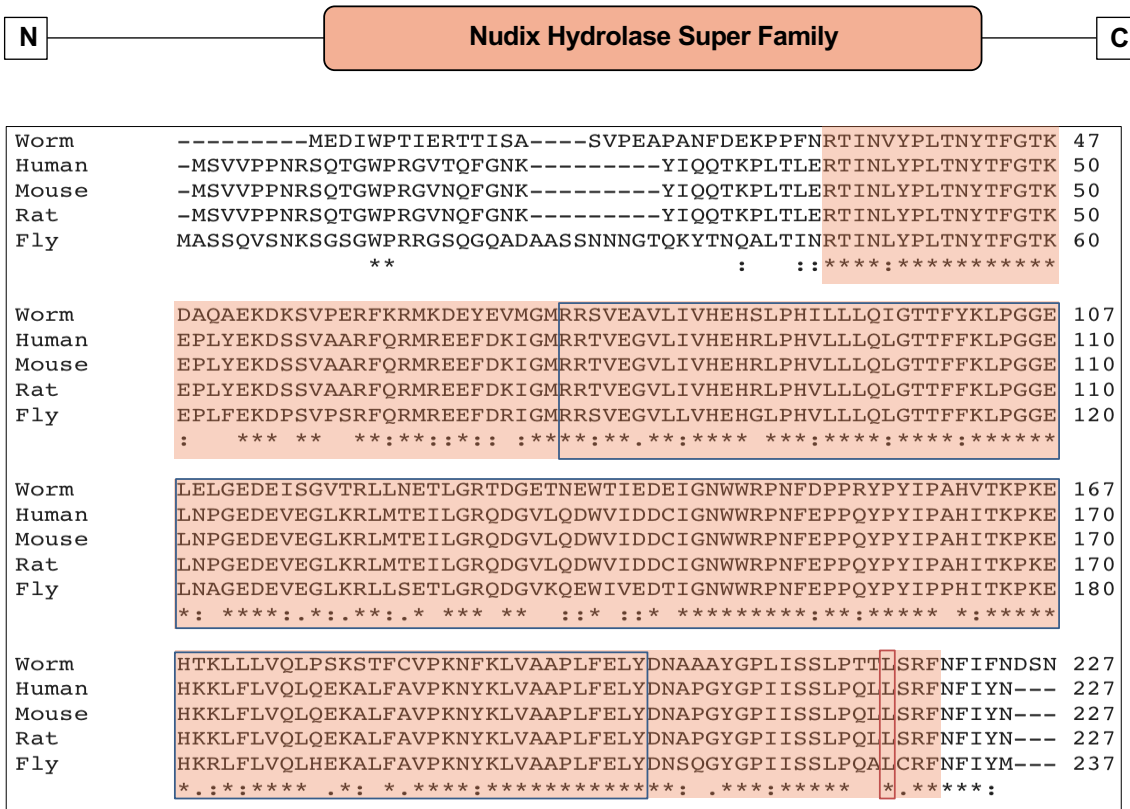
Proline-rich segment that facilitates interactions with CstF-64 and CstF-55 (Bai et al., 2007)

HAT-N Domain (Bai et al., 2007)

HAT-C Domain that interacts with CPSF-160 (Bai et al., 2007)

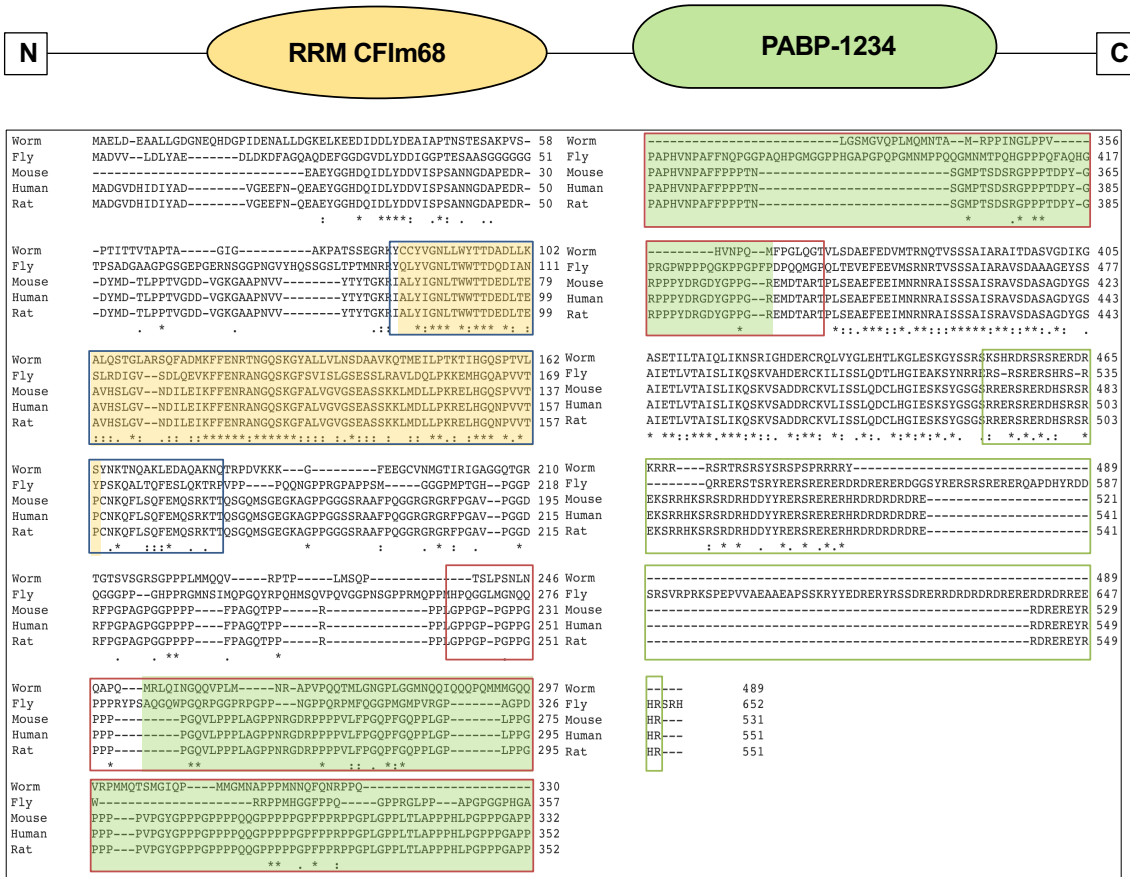
CFin Complex

cfim-1 (CFim25)



Nudix domain (Yang et al., 2011) CFim68 and CFim59 tethering site (Zhu et al., 2017)

cfim-2 (CFim68)



RRM domain (Yang et al., 2011, Martin et al., 2010) RS/RD/RE region (Yang et al., 2011)

Pro/Gly-rich region (Yang et al., 2011)

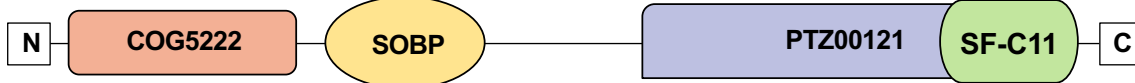
clpf-1 (CLP1)



Worm	-----MSEENVOEFVLKEDCELRFAAGDD-SDVCLLVKGYAEIPGTELLNKKYTFPA	53	Worm	VDGEGYKIVKAASAFEVDVVVLDHERLVSDELKELPEFVRLTHVPSKGGVEQRTGQIR	293
Fly	-----MSBDGKDYLTLESDELRFIEQKDAKVLVSLVSGFAELPGTELKVKKQVEFGV	54	Fly	VKGGYAHLLHAAKAYGACAIPLVDQERLYNELRDVPHGVHVVLLPKSGGVVERSKELR	288
Human	MGEESNDKKHPTKFELERETFLRFEVEASQ-SVQLELLTGMAEIPGTELTRNKKFTFDA	59	Human	VKGGYQALVHAASAFEVDVVVLDQERLYNELRDLPHFVRTVLLPKSGGVVERSKDFR	293
Rat	MSEESNDKKHPTKFELERETFLRFEVEASQ-SVQLELLTGMAEIPGTELTRNKKFTFDA	59	Rat	VKGGYQALVHAASAFEVDVVVLDQERLYNELRDLPHFVRTVLLPKSGGVVERSKDFR	293
Mouse	MSEESNDKKHPTKFELERETFLRFEVEASQ-SVQLELLTGMAEIPGTELTRNKKFTFDA	59	Mouse	VKGGYQALVHAASAFEVDVVVLDQERLYNELRDLPHFVRTVLLPKSGGVVERSKDFR	293
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Worm	KSRVAATPKGATIELVGTESAYVAESTPMVYILNIHAAMEVRRKREDAAGSNKKR	113	Worm	SKMRGENVHRYFVCTRANLYPTFDVSFDVTLCKIGAEQLPDSCLPFGMEVNHETKL	353
Fly	GAKVAIFTYQCVLHVSGKMDVCIYISKETPMQVYVNCCHAALQFRMEARH-----KDHV	108	Fly	HEARDQRIKEYFVGNTRAPPYPSFEVVFQDLRLYKIGAPLPDSCMPIGKAEKDNRKV	348
Human	GAKVAFTWHGCSVLQSGRTEVAYVSKDTPMLLYLNTHTALEQMRRAK-----EEHR	113	Human	RECRDERIREYFYGF-RGCFYPAFNVKFSDVKIYKVGAPTIIPDSCLPLGMSQEDNQLKL	352
Rat	GAKVAFTWHGCSVLQSGRTEVAYVSKDTPMLLYLNTHTALEQMRRAK-----EEHR	113	Rat	RECRDERIREYFYGF-RGCFYPAFNVKFSDVKIYKVGAPTIIPDSCLPLGMSQEDNQLKL	352
Mouse	GAKVAFTWHGCSVLQSGRTEVAYVSKDTPMLLYLNTHTALEQMRRAK-----EEHR	113	Mouse	RECRDERIREYFYGF-RGCFYPAFNVKFSDVKIYKVGAPTIIPDSCLPLGMSQEDNQLKL	352
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Worm	GPRLLLVGPIDVGKTVSRILCNYSVRQGRTEFVVELDVGGQNSVSPGTVAAVLVQKTD	173	Worm	VIMEPSADIKHHLAFSRSTKADENVLKSVPVGFCLVTEVDLEKRTMSILCPQRT-IP-S	411
Fly	GPVAMVVGPMVDGKSTLCRILLNYAVRGRRLYADLDVGGQSAISGVSATILLIERPAN	168	Fly	VAVTTPPALIHVLLALSPAESVEDDVGTVAGFCVTEVDMERQAVMLLSPQRPRLPPN	408
Human	GPRVMVVGPTDVGKSTVCRLLLNAYVRLGRRTYVELDVGGQSSVIPCTMGALYIERPAD	173	Human	VPVTPGRDMVHLLSVSTAEGTEENLETSVAGFIVVTSVDLEHQVFTVLSFAPRPLPKN	412
Rat	GPRVMVVGPTDVGKSTVCRLLLNAYVRLGRRTYVELDVGGQSSVIPCTMGALYIERPAD	173	Rat	VPVTPGRDMVHLLSVSTAEGTEENLETSVAGFIVVTSVDLEHQVFTVLSFAPRPLPKN	412
Mouse	GPRVMVVGPTDVGKSTVCRLLLNAYVRLGRRTYVELDVGGQSSVIPCTMGALYIERPAD	173	Mouse	VPVTPGRDMVHLLSVSTAEGTEENLETSVAGFIVVTSVDLEHQVFTVLSFAPRPLPKN	412
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Worm	VIDGFERNQPIVFNFGHTSFSANLSLYALFKEMATTLNAQIQENDEAKIGGMIINTCGW	233	Worm	KVLVFSIDITHLDDQEKRR	428
Fly	VEEGFAKTAFLVYHFGHKSFGNSVLYLAVSRKMAEVTLQSLNSKRTKSSGIIINTCGW	228	Fly	ALLLWSELQFMDK	423
Human	VEEGFSIQALVYHFGSTTPGTMIKLYKITSRLADVFNQRCVNRRAVSQGVINTCGW	233	Human	FLLI-MDIRFMDK	425
Rat	VEEGFSIQALVYHFGSTTPGTMIKLYKITSRLADVFNQRCVNRRAVSQGVINTCGW	233	Rat	FLLI-MDIRFMDK	425
Mouse	VEEGFSIQALVYHFGSTTPGTMIKLYKITSRLADVFNQRCVNRRAVSQGVINTCGW	233	Mouse	FLLI-MDIRFMDK	425
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- N-terminal domain (Dikfidan et al., 2014)
- Polynucleotide kinase domain (Dikfidan et al., 2014)
- C-terminal domain (Dikfidan et al., 2014)
- Residues that crosslink to Pcf-11 (Schäfer et al., 2018)

rbpl-1 (RBBP6)

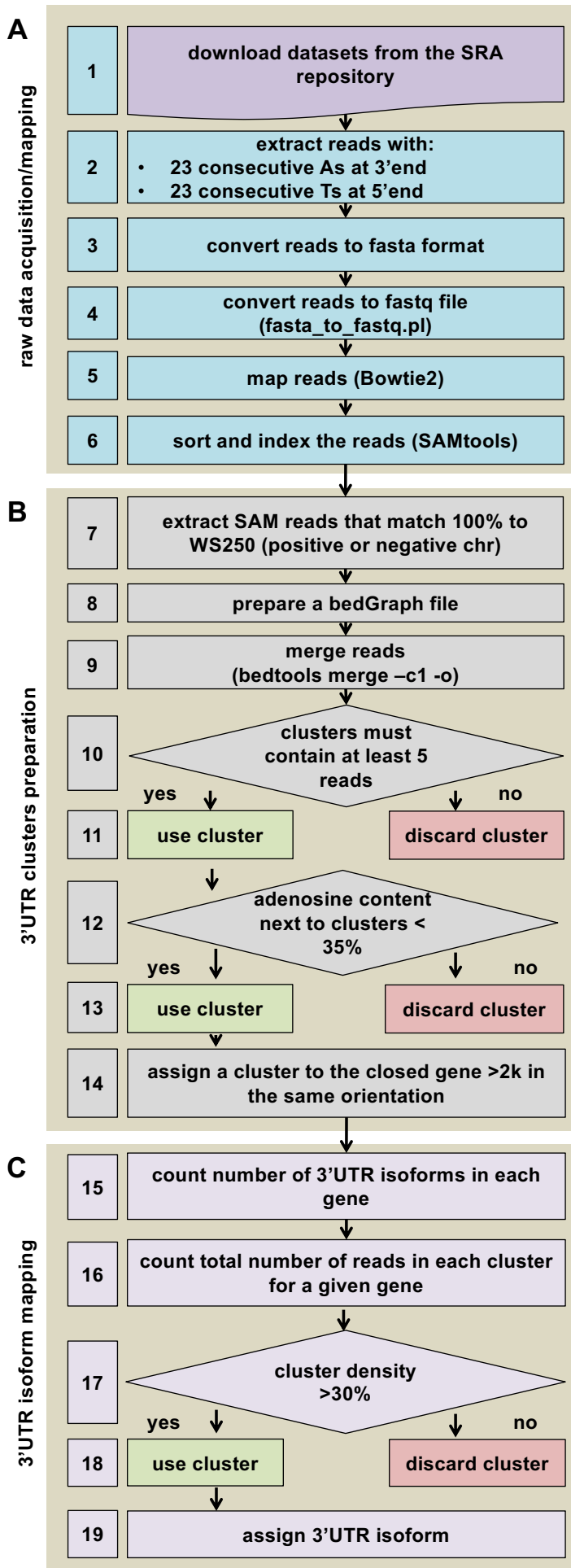


Worm	MSSIHYKFAELDYKTLQFDGLHTRGQLVREICAKENL-KLEIFELQNAHTKTYTS	59	Worm	SSTINTADEDDSSKMKKHKSKKNNKHKHREEDGDEERKRRKHKHKHKKSKKEK	810
Fly	-MSVHYKFKSLNPTFTFDGLHISVGLKREIVQGRKGLIIDFLQITNAQSKREYK	59	Fly	SSK-----GDSK-----ARGDNR-----HEAPRRHRSRSISEPK	738
Human	MSCVHYKFSKSLNPTFTFDGLHISLCLDKLQKIMGREKL-KAADCDLQITNAQKREYD	59	Human	NKDNPKSKKEESEN-----AFDGGK-----GN-KHKHRRKRGKEE--	944
Rat	MSCVHYKFSKSLNPTFTFDGLHISLCLDKLQKIMGREKL-KAADSDLQITNAQKREYD	59	Rat	NPKDNPKSKKEESEN-----VFDGGK-----GN-KHKHRRKRGKEE--	930
Mouse	MSCVHYKFSKSLNPTFTFDGLHISLCLDKLQKIMGREKL-KAADSDLQITNAQKREYD	59	Mouse	NKDNPKSKKEESEN-----VFDGGK-----GN-KHKHRRKRGKEE--	945
Worm	D-ELIPRNSIIVQFRPKDAKRVQVAGVGNVQLDATSFLDSSIHSSAE	114	Worm	RDE--DEDDLTEKKEK-----KERKYODK-----DEDSNRKE-----PR	845
Fly	DFPLIPKNTLITSRIPAHFKK--GWE--PPAAENAFSA-----APAKQDNFN	105	Fly	PNSNYSRLTTPPAKITTP-----KMTAQLROR	766
Human	DNALIPKNSVIVRRIPGVGVSKSTYV--ISRTPEAMATKADDSASISLAQLTKT	117	Human	-----SEGLFPELLETSSKRSRFTGVEENKTDLVLPVSRDPAVPRDEMDAEIFTK	999
Rat	DNALIPKNSVIVRRIPGVGVSKSTYV--ISRTPEVMGTAKADDSASISLAQLTKT	117	Rat	-----SEFLPELLETSSKRSRSGIDETKTDALVLPVSRDPAVPRDEMDAEIFTK	985
Mouse	DNALIPKNSVIVRRIPGVGVSKSTYV--ISRTPEVMGTAKADDSASISLAQLTKT	117	Mouse	-----SEFLPELLETSSKRSRSGIDETKTDLVLPVSRDPAVPRDEMDAEIFTK	1000
Worm	----FENDEAEKRLHHRDQSTRAYDQSNFRRRQPGIMTGPPTTNCNCSQGHWYK	170	Worm	SLDDEKVELDKNFA--DKKEKKGKWEDEEIPEDRKEELPKESDRDRDRDRHDE	902
Fly	MDLSKMGQTEEDIQAMMGSQVTDVDPKTYHRKLGQSQVGEVPSYCNCKKSGHWYK	165	Fly	E-----SSPK-----TPKSHDDYLAKARIM-----ASQFV	794
Human	ANLAEANASEEDKIKAMMSQGHGYDPINYMK--KPLGPPPSVYTCFCGKPGHYIK	173	Human	SVEKDKRERDKPKAGDKTKRKNDSGSAVSKENIKVPAKQPEKVDGERERSRSEPT	1059
Rat	ANLAEANASEEDKIKAMMSQGHGYDPINYMK--KTLVGPPPSVYTCFCGKPGHYIK	159	Rat	SVEKDKRERDKPKVKSDDTKRKSOGGATAKENVLKPSGQDKVDGERERSRSEPT	1045
Mouse	ANLAEANASEEDKIKAMMSQGHGYDPINYMK--KTLVGPPPSVYTCFCGKPGHYIK	174	Mouse	SVSDKREKDKPKVKSDDTKRKSOGGATAKENVLKPSGQDKVDGERERSRSEPT	1065
Worm	CPMLNT-----KRTTISQELMETTV-DPDDAMHPSGVIPIMHWKARQETLA	220	Worm	DDRKERRHERDSQKIDQDRKREKRDRETAJD-SDKLQAPTKVREKDRKDRKDYE	961
Fly	CFPVGQKQDQ--EVRKNTGIPRSFRDKPDAEN-----ESADVLP	204	Fly	NDTME-----TIVGKFNKA-----KSLDKDRK-----KKKD	823
Human	CPTNODKNEFEGRIKKSQIPIRSMFMEVQDPMKGMALNTGKVAIPITIDAEAYIAGK	233	Human	KKAEEPTKDTNTPSSSSQDEKICTPTPKRAHSAKHEQKPKVKEEYV-----KRDYS	1115
Rat	CPTNODKNEFEGRIKKSQIPIRSMFMEVQDPMKGMALNTGKVAIPITIDAEAYIAGK	219	Rat	KKAEEATKDVSPSSS-QDKEVCTCTPKRAHSAKHEQKPKVKEEYV-----KRDYS	1100
Mouse	CPTNODKNEFEGRIKKSQIPIRSMFMEVQDPMKGMALNTGKVAIPITIDAEAYIAGK	234	Mouse	KKAEEATKDVSPSSS-QDKEVCTCTPKRAHSAKHEQKPKVKEEYV-----KRDYS	1116
Worm	RK--NEDGSSPAQTSRKYPELLCPTCQSLFKFAIIVTSCCGNSYCAICLEARLDDPP	277	Worm	RDREKRDYKKEKES-----KRKEEDRNEKEQREKEVEKEKEDK-----EKRR	1008
Fly	-----AYQNGEIPEDLTCGICRQIVDVAIMICSSSFCDCVRLTLESEED	251	Fly	KDVS-KLTKTEKAKKPKNEKPKLNGEKEKREKREKREKREKREKREKREKREKREK	871
Human	EKPPFPEPSSSEEDDPIPELLLCLCKIDMTDAVIPCPCNSYDCICIRTALESSE	293	Human	KDVS-KLTKTEKAKKPKNEKPKLNGEKEKREKREKREKREKREKREKREKREKREK	1174
Rat	EKPPFPEPSSSEEDDPIPELLLCLCKIDMTDAVIPCPCNSYDCICIRTALESSE	279	Rat	KDVS-KLTKTEKAKKPKNEKPKLNGEKEKREKREKREKREKREKREKREKREKREK	1156
Mouse	EKPPFPEPSSSEEDDPIPELLLCLCKIDMTDAVIPCPCNSYDCICIRTALESSE	294	Mouse	KDVS-KLTKTEKAKKPKNEKPKLNGEKEKREKREKREKREKREKREKREKREKREK	1174
Worm	QKCPGADGCKDITISIPINKTLADAAJLWLSATCGAPDTPQVDFEFPQ-----RIR	331	Worm	IVKESKPKRKSVERHMQKADSTSSSSRRTTAPSLEKPKVSTVA-SKSPFTNIRV---	1064
Fly	SCPCDCK-EKMCSPGSLINPRFLRNSVNAFKNETGYNKSAAKPAVKNREKPKVEKVEK	310	Fly	VLN--PRA-----QSPSIEINAA	889
Human	HTCPTCH-QNDVSDALIANKLRQAVNFKNETGYTKRLKQIPLPPPPVPPPPPIQR	352	Human	IVK--PSPKRMEPDT-----KMDRTEPKKISL-SAPAKIKILNRE	1214
Rat	HTCPTCH-QNDVSDALIANKLRQAVNFKNETGYTKRLKQIPLPPPPVPPPPPIQR	338	Rat	IVK--PSPKRMEGQV-----KLERTEPKKASSTTPAKIKILNRE	1197
Mouse	HTCPTCH-QNDVSDALIANKLRQAVNFKNETGYTKRLKQIPLPPPPVPPPPPIQR	353	Mouse	IVK--PSPKRMEGQV-----KLERTEPKKASSTTPAKIKILNRE	1215
Worm	----IGLK-----APSSSQOITPSCISPGST-----LWOOQ	359	Worm	----QL-----ROYSSSST	1073
Fly	-----KPVAEV-EPEETE-----KPEKO-KESETNGSNPKS-----ESPEPA	348	Fly	TKGKIGNSTENSTKPESEKLESTSSKVKQEVKGVKRVKRTVTEGSSSLVDVTSST	1274
Human	NLQPLMRSPISROQDPLMIVTSSAHTPSISLSTNSQSSALPVPNGSPSAPAVPDI	412	Human	TKGKIGNAENSTKPESEKLESTSSKIKQEVKGVKARRVAGTEGSSSLVDVTSST	1257
Rat	NLQPLMRSPISROQDPLMIVTSSAHTPSISLSTNSQSSALPVPNGSPSAPAVPDI	398	Rat	TKGKIGNAENSTKPESEKLESTSSKIKQEVKGVKARRVAGTEGSSSLVDVTSST	1275
Mouse	NLQPLMRSPISROQDPLMIVTSSAHTPSISLSTNSQSSALPVPNGSPSAPAVPDI	413	Mouse	TKGKIGNAENSTKPESEKLESTSSKIKQEVKGVKARRVAGTEGSSSLVDVTSST	1275
Worm	T-----TLTYS-SGCTSL-----	371	Worm	KQEDEERSKDRRKKDETDVESIGKEKESKSRKVPKESVDVVKHSTKIKFDI---	1127
Fly	TEPS--QKEKDYSDVEDNITIKMPQPAADS-----	379	Fly	--SPT-----HNATENVNPKSHSILTVGAASDDNLGPKSKLSEANSVNLKWEIDENILG	942
Human	TATVSVHSEKSDGQFRDSDNKLPAALASEHSKGTSSIAITALMEEKYQVPLVTP	472	Human	GGSPV-----RKSEKTDTRKVTIKTMEYNDNTAPAEVIMIQVQSGKWDKDFESE	1329
Rat	TATVSVHSEKSDGQFRDSDNKLPAALASEHSKGTSSIAITALMEEKYQVPLVTP	458	Rat	GGSPV-----RKSEKTDTRKVTIKTMEYNDNTAPAEVIMIQVQSGKWDKDFESE	1312
Mouse	TATVSVHSEKSDGQFRDSDNKLPAALASEHSKGTSSIAITALMEEKYQVPLVTP	473	Mouse	GGSPV-----RKSEKTDTRKVTIKTMEYNDNTAPAEVIMIQVQSGKWDKDFESE	1330
Worm	-----SAQPS-----	376	Worm	LDSSK--KAAGADQPSSETSVDLRAENAFKATAMALRFPQ-----VTL	1127
Fly	-----TVFVSRKSPSYSHRSSE-----SHRRDSDYVSD	408	Fly	E-EDVKSTQPISSVGVKPVASIKNVSTKPSNIVKVPKESPEKIQKFDVSHIIOHE	1388
Human	SLLGQSLHGLQIPLTTPGVRIINARAGGRRGVEHNSKLGYSVPPQIIRGERSCYRS	532	Human	EEDVKTQPIOSVQKPSIINKVTTKPSATVKTKEKESPEKIQKFDVSHIIOHE	1372
Rat	SLLGQSLHGLQIPLTTPGVRIINARAGGRRGVEHNSKLGYSVPPQIIRGERSCYRS	518	Rat	EEDVKTQPIOSVQKPSIINKVTTKPSATVKTKEKESPEKIQKFDVSHIIOHE	1389
Mouse	SLLGQSLHGLQIPLTTPGVRIINARAGGRRGVEHNSKLGYSVPPQIIRGERSCYRS	533	Mouse	EEDVKTQPIOSVQKPSIINKVTTKPSATVKTKEKESPEKIQKFDVSHIIOHE	1389
Worm	-----NVNPSIPGIPLASQVPSH-----VQDVSLLPPLQROE	408	Worm	-----NSK-----DNSKDRSVRSDDRSSPRRNSN-----RSVDRKLTGK-----ISN	1128
Fly	HDHKKQ--RPS--KESVNRDRLSLLPGLTFLPSYQGHMAESEARRSAYKPY--MQ	462	Fly	VSKNSGASSEKGTKDDYSLVENKPN--EKRNKSTQPEKESKRRKDRKTRKDSV	1046
Human	NRGRHRSERSORTQGPSLPTATVFFVFPVPP-----PLYPPPHLTL	573	Human	LRSKGSVSEKGRADKDHASAKEDNP--DKRRTIQDPEKSTVDRLSQGHFKMLOS	1430
Rat	NRGRHRSERSORTQGPSLPTATVFFVFPVPP-----PLYPPPHLTL	559	Rat	LRSKGSVSEKGRADKDHASAKEDNP--DKRRTIQDPEKSTVDRLSQGHFKMLOS	1447
Mouse	NRGRHRSERSORTQGPSLPTATVFFVFPVPP-----PLYPPPHLTL	574	Mouse	LRSKGSVSEKGRADKDHASAKEDNP--DKRRTIQDPEKSTVDRLSQGHFKMLOS	1447
Worm	LPFGIPGLPQGLPPGQVGLSATVLPQHGMLNYGM-----PLFSAGFPVAVSVRPS	464	Worm	-----DRSRDRSKGRRAARSDDANRGRSDRH-----GSRKRNRL--SRDRAEPE	1128
Fly	MORGPPPHMMS-----HHMAYNFGNFMNMGQRPPLSVYQNGSVHMRAPYSAGGGMNM	519	Fly	SKAERTSDKHS-----TRASNKDFTPNRKDDYDREYSSSKRDEKRELTRKDSVPR	1078
Human	LPFGVFPV-----QFSQF--PPGQPPAGYSV-----PPGPF--PAPA	609	Human	SKETRTEKES-----VRSNKNDFTPGRDKKVDYSDRYSVSKRDEKRELTRKDSVPR	1503
Rat	LPFGVFPV-----QFSQF--PPGQPPAGYSV-----PPGPF--PAPA	595	Rat	SKETRTEKES-----VRSNKNDFTPGRDKKVDYSDRYSVSKRDEKRELTRKDSVPR	1487
Mouse	LPFGVFPV-----QFSQF--PPGQPPAGYSV-----PPGPF--PAPA	610	Mouse	SKETRTEKES-----VRSNKNDFTPGRDKKVDYSDRYSVSKRDEKRELTRKDSVPR	1504
Worm	AISDEWN-----AFLQNKDRNSRR--DHKDRTR-----	491	Worm	-----KROERSYK-----RSSPEDDKLIRKQESQSKHG-----KHDC	1128
Fly	NMSQFQSNLAIYQVAAKVGGSDIDPLEAFN--RIMKEKE--RKKVDRFR-----	569	Fly	NKDSASQGNKPREKRDLPKGTGDSKKSNSPSRDRKHDKATYTRKRNKETSVD	1563
Human	NLSTPWSVSGVTAHNSITPTQAPPLSR--EFFYRORLKEEKKSKLDEFTNDFAK	667	Human	SKDSLSQKSKLREKDLPKQTE--LAKNSNSPDRKPKHDKAAYTRKRNKETSVD	1546
Rat	NLSTPWSVSGVTAHNSITPTQAPPLSR--EFFYRORLKEEKKSKLDEFTNDFAK	653	Rat	SKDSLSQKSKLREKDLPKQTE--LAKNSNSPDRKPKHDKAAYTRKRNKETSVD	1546
Mouse	NLSTPWSVSGVTAHNSITPTQAPPLSR--EFFYRORLKEEKKSKLDEFTNDFAK	668	Mouse	SKDSLSQKSKLREKDLPKQTE--LAKNSNSPDRKPKHDKAAYTRKRNKETSVD	1563
Worm	-----RKRDRSRRRRRSSSSSSSSSS--DEDERK-----RKRREK--ESSKRRSV	538	Worm	-----KRSRYSK-----RSSPEDDKLIRKQESQSKHG-----KHDC	1128
Fly	-----SSDRSRSDRGRHRFSRPH--EKDNRDRKDRP-----	605	Fly	NKDSASQGNKPREKRDLPKGTGDSKKSNSPSRDRKHDKATYTRKRNKETSVD	1563
Human	ELMEYKIKQKRRRFRSRSKSPYSGSYRSSTYSKRSRSGTRSRYSRFSRSHRSY	713	Human	NKDKREKHVLE--RNKESGSKNLLIYLPFPQVEKELTQGDISTKVPKPOLSHS	1622
Rat	ELMEYKIKQKRRRFRSRSKSPYSGSYRSSTYSKRSRSGTRSRYSRFSRSHRSY	713	Rat	NGKEREKHAASRNKESGSKLPSIPNPPDMKELAAQVKSAAVKPKPOLSHS	1606
Mouse	ELMEYKIKQKRRRFRSRSKSPYSGSYRSSTYSKRSRSGTRSRYSRFSRSHRSY	728	Mouse	NSGKERKHAASRNKESGSKLPSIPNPPDMKELAAQVKSAAVKPKPOLSHS	1622
Worm	EK--ERFRADREHRRDRDRDRDRDRDRDRDRDRDRDRDRDRDRDRDRDRDRDR	596	Worm	-----SSSSSLVQYDNTI-----QKE-----GAS	1128
Fly	-----RSRERKREHRYRHHRHRSRQPNDSG-----	633	Fly	RLSSDLTRETDEAAPPDYNESDESNSVVKEEAVASISDKLKEKTEKASLTVAT	1662
Human	SRSPPYPRGRGK-----SNRYSRSHSGYHRSRSPYRYSRSHRSRSHAFRQGSPT	782	Human	RLSSDLTRETDEAAPPDYNESDESNSVVKEEAVASISDKLKEKTEKASLTVAT	1682
Rat	SRSPPYPRGRGK-----SNRYSRSHSGYHRSRSPYRYSRSHRSRSHAFRQGSPT	768	Rat	RLSSDLTRETDEAAPPDYNESDESNSVVKEEAVASISDKLKEKTEKASLTVAT	1682
Mouse	SRSPPYPRGRGK-----SNRYSRSHSGYHRSRSPYRYSRSHRSRSHAFRQGSPT	783	Mouse	RLSSDLTRETDEAAPPDYNESDESNSVVKEEAVASISDKLKEKTEKASLTVAT	1682
Worm	RDDVRRKERREKREEDDQKTKDAESKDEDEIDIGIIEAYGNVQA-----	643	Worm	-----SDNGMEHRKQR-----DKLKHHSK--YSSTDLSKSKRDKPKSKKSKL	1128
Fly	-----KSPFG--RKRSGH-----RRSASP--KPYG--KSDYRD-----	661	Fly	VQVGISRNQSHSSPSVSRSHSPSGQTRSHSSSSASASQDSKSKKSKKSKKSKKSKK	1224
Human	KRNVPQG--ETEREYF-----NRYREV--PPYD--MKAYGRSVDPRDFEKERYEW	830	Human	SQPADRSOSQSSPSVSRSHSPSGQTRSHSSSSASASQDSKSKKSKKSKKSKKSKK	1742
Rat	KRNVPQG--ETEREYF-----NRYREV--PPYD--IKAYGRSVDPRDFEKERYEW	816	Rat	SQPADRSOSQSSPSVSRSHSPSGQTRSHSSSSASASQDSKSKKSKKSKKSKKSKK	1726
Mouse	KRNVPQG--ETEREYF-----NRYREV--PPYD--IKAYGRSVDPRDFEKERYEW	831	Mouse	SQPADRSOSQSSPSVSRSHSPSGQTRSHSSSSASASQDSKSKKSKKSKKSKKSKK	1742
Worm	-----QTDGDAQVAENAGNDESTSPKESVSKPDETHEEADDEEVPDEEM--	692	Worm	-----KSKSKK-----	1128
Fly	-----KPY--NKP-----SAPKTEAVEPPGPELQLTDED-----	691	Fly	KKKSKK-----	1231
Human	EKRYEWEKYYKGYVAG-----AQPRSANRENFSPEFLPLNIRNSPFRGRRE	881	Human	KHKHKHAGTEVELEKSKQKHKHKKSKKKNKDEKKEKEDKQKVSVTV	1792
Rat	EKRYEWEKYYKGYVAG-----AQPRSANRENFSPEFLPLNIRNSPFRGRRE	867	Rat	KHKHKHAGVQGVKSKQRHKHKKSKKKNKDE--KEDDQKVSVTV	1774
Mouse	EKRYEWEKYYKGYVAG-----AQPRSANRENFSPEFLPLNIRNSPFRGRRE	882	Mouse	KHKHKHAGVQGVKSKQRHKHKKSKKKNKDE--KEDDQKVSVTV	1790
Worm	--DTEVVDRKSDIPVYQAMETSEAEVAETKESVVEDEEENHEDVEDHKKESQ	750			
Fly	QTRKKEPT-----SER--	908			
Human	DYVGGQSHRNRNIGSNVPEK-----LSARDGH	908			
Rat	DYVAGQSHRNRNIGSNVPEK-----ISTRDSH	894			
Mouse	DYAGQSHRNRNIGSNVPEK-----LSTRDSH	909			

- Domain With No Name (DWN), ubiquitin-like (Pugh et al., 2006)
- RING finger domain (Chibi et al., 2008, Lee et al., 2014)
- Proline-rich domain (Pugh et al., 2006)
- SR domain (Pugh et al., 2006)
- Rb-binding domain (Pugh et al., 2006)
- Zinc knuckle (Lee et al., 2014)
- p53-binding domain (Pugh et al., 2006)

Name	Experiment #	Eggs/Hatched	Lethality (%)
<i>cpsf-1</i> (<i>CPSF160</i>)	1	163/11	93.7
	2	238/5	97.9
	3	149/1	99.3
<i>cpsf-2</i> (<i>CPSF100</i>)	1	68/37	64.8
	2	178/28	86.4
	3	221/25	89.8
<i>cpsf-4</i> (<i>CPSF30</i>)	1	323/5	98.5
	2	699/17	97.6
	3	204/3	98.6
<i>cpf-1</i> (<i>CstF-50</i>)	1	251/76	76.8
	2	200/64	75.8
	3	185/25	88.1
<i>cpf-2</i> (<i>CstF-64</i>)	1	446/54	89.2
	2	138/14	90.8
	3	61/3	95.3
<i>cfim-1</i> (<i>CFIm25</i>)	1	249/23	91.5
	2	196/20	90.7
	3	154/2	98.7
<i>cfim-2</i> (<i>CFIm68</i>)	1	137/1	99.3
	2	282/27	91.3
	3	260/32	89.0
<i>lrp-2</i> (<i>CFIm59</i>)	1	311/116	72.8
	2	281/97	74.3
	3	222/93	70.5
<i>symk-1</i> (<i>Symplekin</i>)	1	62/4	93.9
	2	19/4	82.6
	3	114/5	95.8
<i>rbpl-1</i> (<i>RBBP6</i>)	1	293/0	100
	2	344/0	100
	3	116/0	100
<i>pcf-11</i> (<i>CPF11</i>)	1	141/5	96.6
	2	105/0	100
	3	172/5	97.2
<i>clpf-1</i> (<i>CLP1</i>)	1	286/23	92.6
	2	289/18	94.1
	3	208/17	92.4
<i>pkc-3</i> (<i>negative control</i>)	1	5/0	100
	2	8/0	100
	3	18/1	94.7
	4	51/1	98.1
	5	3/0	100
	6	22/0	100
	7	53/0	100
	8	6/0	100
	9	13/0	100
	10	19/0	100
	11	5/0	100
	12	4/0	100

Supplemental Fig. S2: Results of the RNAi experiments of the *C. elegans* CPC: Twelve genes for the members of the *C. elegans* CPC were knocked-down using RNAi. Clones/rows are color-coded as from Figure 1. The human orthologs of each gene are shown in parenthesis in the first column. For each RNAi experiment we use 15 worms, and the number of eggs unhatched vs hatched at the end of the experiment were counted. The percent lethality was consistently high across all tested clones. *pkc-3* RNAi was used as a negative RNAi control, since it is known to induce strong embryonic lethality.



Supplemental Fig. S3: Bioinformatic Pipeline used in this study: The pipeline uses raw transcriptome datasets downloaded from the public repository SRA trace archive to extract and map 3'UTR end clusters to the closest protein-coding genes in the correct orientation. The pipeline is divided in three large steps: A) Acquisition/Mapping, B) 3'UTR cluster preparation and C) 3'UTR isoforms mapping.

In the acquisition/mapping step, we used custom made Perl scripts to extract reads with 23 consecutive As at the 3' end or 23 consecutive Ts at the 5' end, and then mapped these filtered reads to the WS250 version of the *C. elegans* genome (Bowtie2).

We then sorted and indexed the reads for visualization purposes.

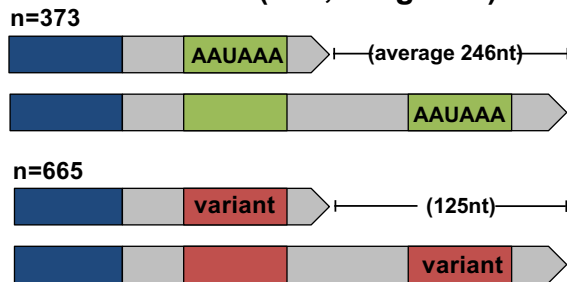
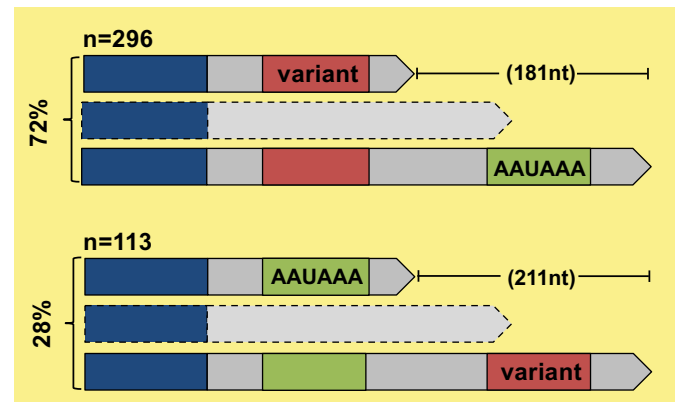
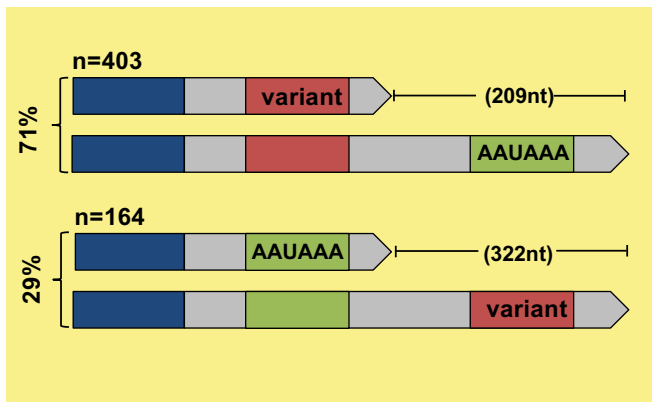
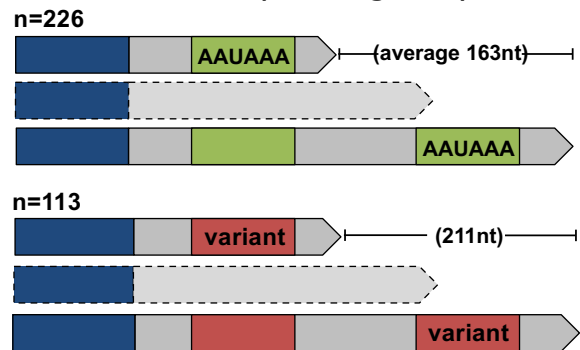
In the 3'UTR cluster preparation step we extracted SAM reads with 100% match to the WS250, and used them to prepare a new bedGraph file (BEDTools).

We then merged the reads and discarded the clusters with less than 5 reads. Restrictive parameters for cluster identification and 3'UTR end mapping included the discard of clusters with an Adenosine content of <35% downstream of its end.

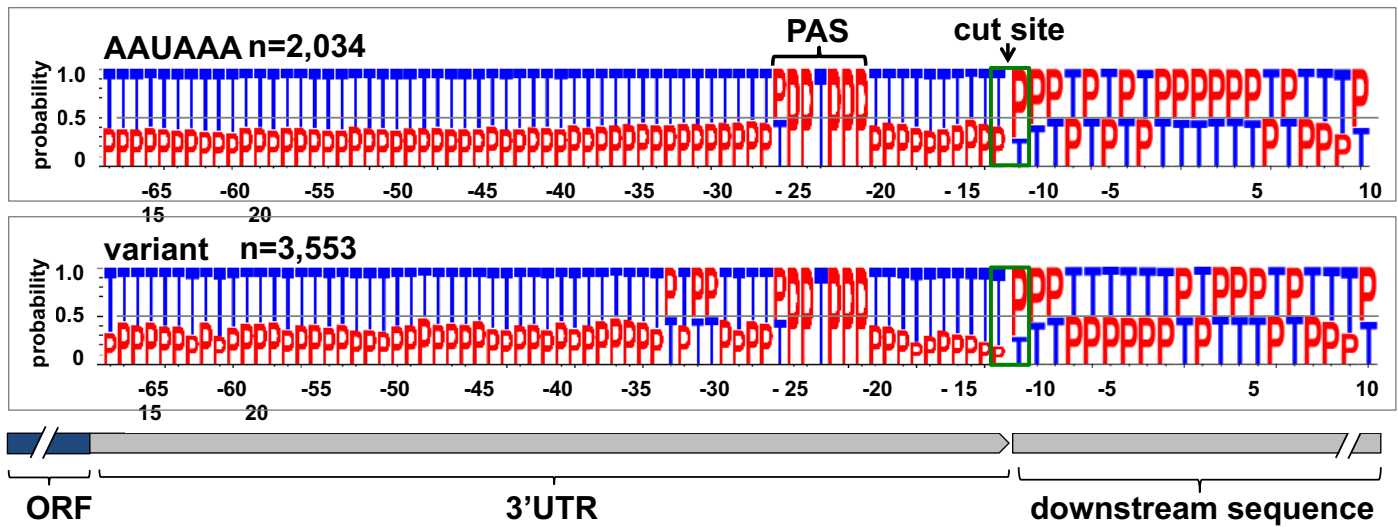
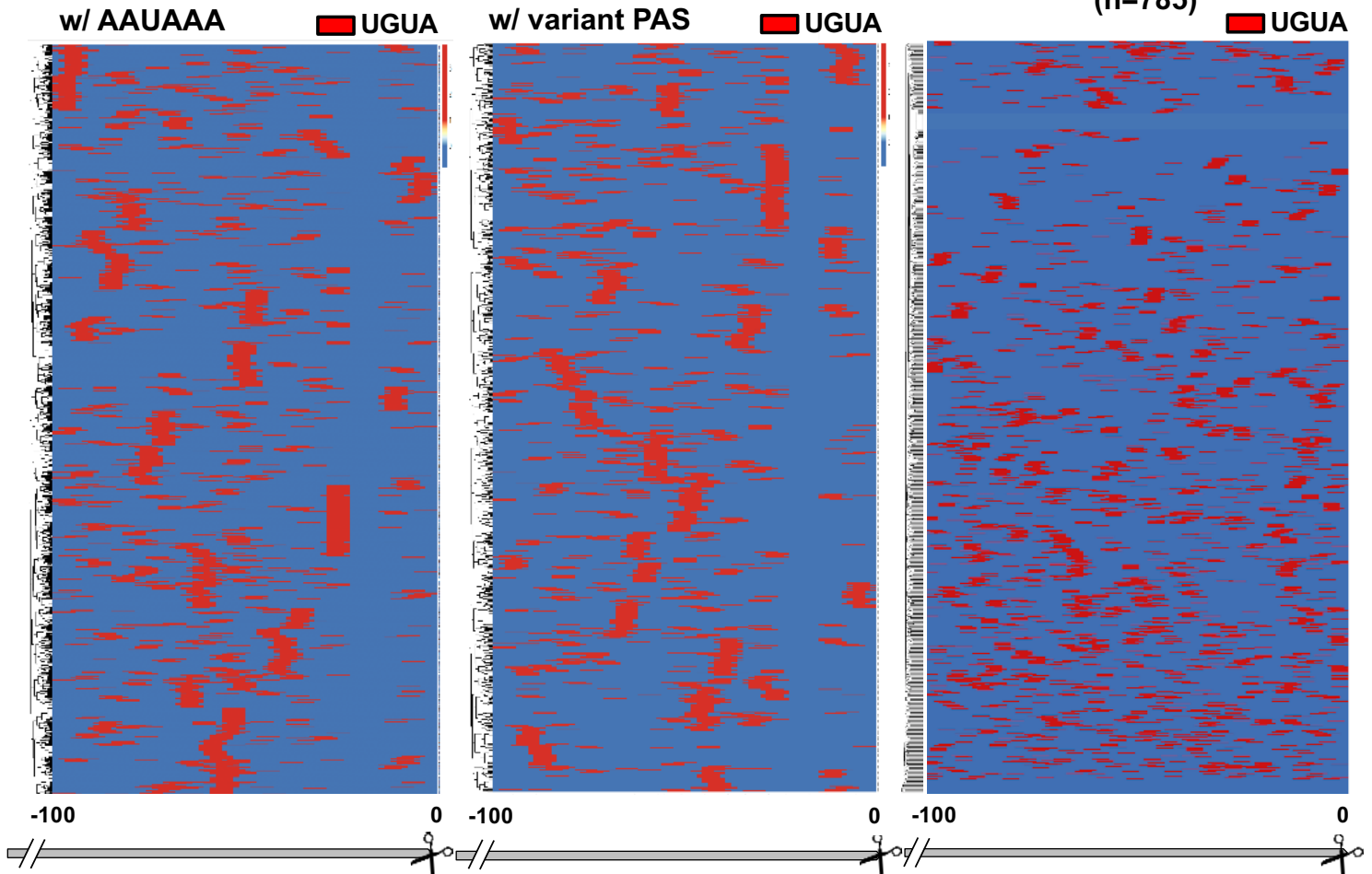
Clusters were assigned to a mapped 3'UTR end and attached to the closest gene with 2,000nt in the same orientation.

At the completion of these steps we performed the 3'UTR isoform mapping step, which consists of the counting and assignment the total number of 3'UTR isoforms to a given gene.

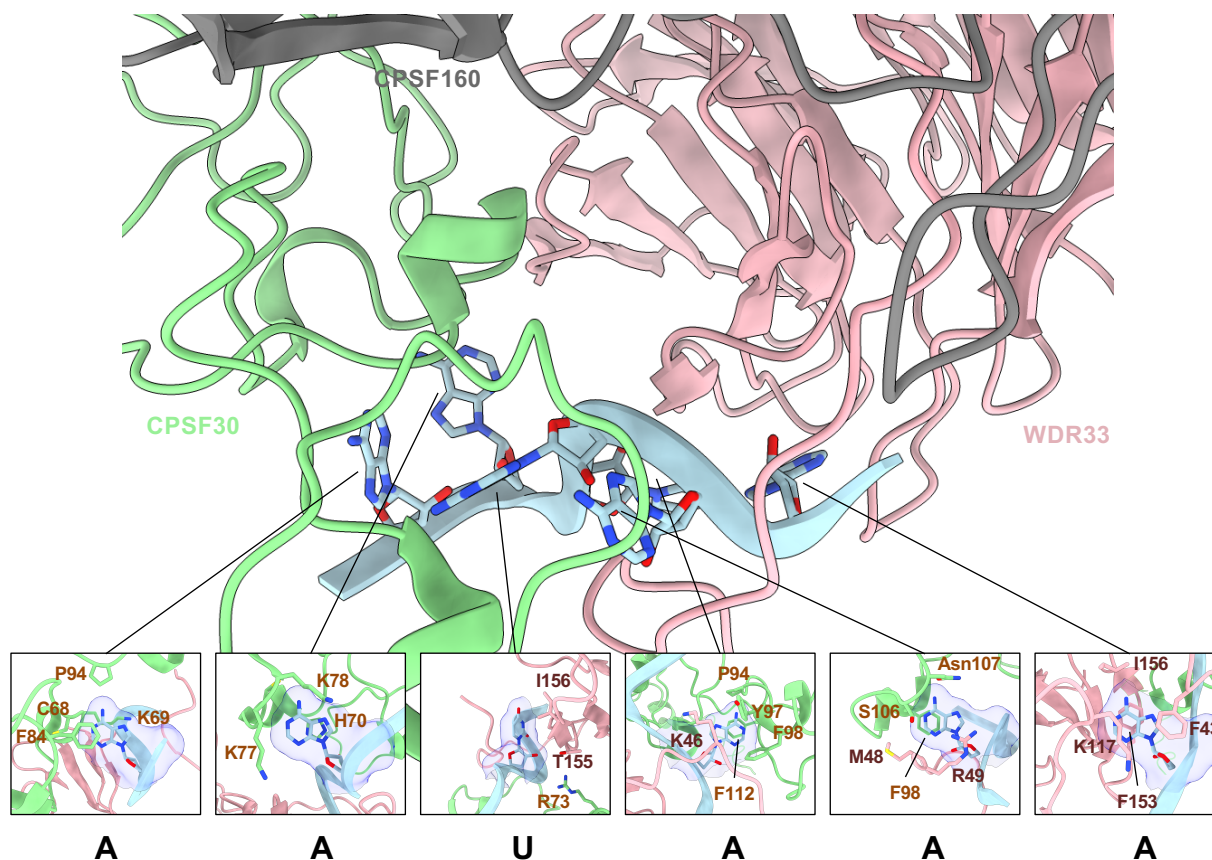
We discarded clusters with a density of less than 30% of the total number of reads.

A**PAS switch in genes with two 3'UTR isoforms with at least 10nt differences (n=4,750 genes)****B****PAS switch in genes with three or more 3'UTR isoforms with at least 10nt differences (n=766 genes)**

Supplemental Fig. S4: PAS site usage in genes with multiple 3'UTR isoforms. A) In genes with only two 3'UTR isoforms with a difference of at least 10nt between isoforms, 373 pairs of isoforms had canonical PAS elements in both isoforms with an average of 246nt difference between isoforms while 665 pairs had variant PAS elements in both isoforms with an average of 125nt difference between them. In isoform pairs where the type of PAS element switches, 71% have a shorter isoform with a variant PAS element and a longer isoform with a canonical PAS element with an average of 209nt between them while the remaining 29% have a canonical PAS element on the shorter isoform and a variant PAS element on the longer isoform with an average of 322nt between them. B) In genes with three or more 3'UTR isoforms, genes where the longest and the shortest isoform both have canonical PAS elements have an average of 163nt between them while genes where the longest and the shortest isoforms both have variant PAS elements have an average of 211nt between them. 72% of genes switch from a variant PAS elements in the short isoform to a canonical PAS element in the long isoform, with an average of 181nt between them. 28% of genes have canonical PAS elements in the short isoforms and variant PAS elements in the long 3'UTR isoform, with an average of 211nt between the two.

A**Genes with 1 3'UTR isoform (stringent – cluster ≥ 100 reads)****B****Genes with 1 3'UTR isoform****Genes with 2 3'UTR isoforms (only distal) (n=785)**

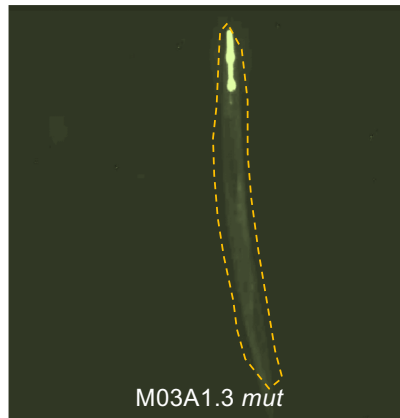
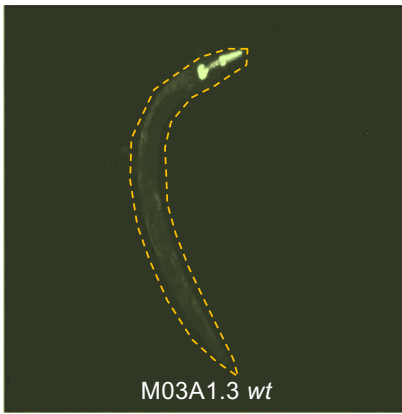
Supplemental Fig. S5: Detection of the 'UGUA' element in *C. elegans* 3'UTRs. A) Logo plot of genomic region within the cut site in genes with only one 3'UTR isoform and with canonical or variant PAS element. There are not immediate elements visible. (T) = Pyrimidine, (P) = Purine. B) Identification of the 'UGUA' motif (red) within 100nt upstream of the cleavage site in genes with one or two 3'UTR isoforms.



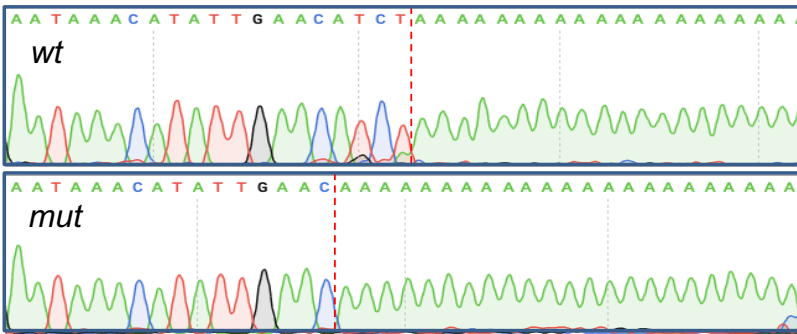
Supplemental Fig. S6: Nucleotide binding site of the human CPSF160-WDR33-CPSF30 complex. Ribbon representation of the cryo-EM structure of human CPSF160-WDR33-CPSF30 complex (PDB code: 6DNF) (Sun et al., 2018). The nucleotides of the bound RNA fragment do not show a specific interaction with either CPSF30 or WDR33. The interactions are mostly established by π - π ring stacking. Color gray shows the CPSF160, pink for WDR33, and light green for CPSF30. Sticks represent the RNA molecules bound with CPSF30 and WDR33. Surfaces in the insets are for individual nucleotides.

A M03A1.3 wt 3'UTR

TGAAAGGACCTGCAGTGTTTTGGGCGATTGGAGTATTCTTCTGCATTGCT
 GTTGC GTTGTCACTTCTTGTGTCGTC AATGGATATAAAAAATGTA TAA TTATT
 AATGGAATTTTGGAAATCTCATCTAATTTTATTGATTTTATTGAATACGGGT
 AGTTTCTGATAATTACTTTGCATTGTAAAAAACAAACTTTGTATGAATA
 AACATATTGAACATCT **AA**GTGCTTGC GTTTTTTTTAAACTCAACTTTGGTT
 GGCATATCTTGGCTCTCTTTAGTTTTTATTAAAAAATGTCAACTACAGA

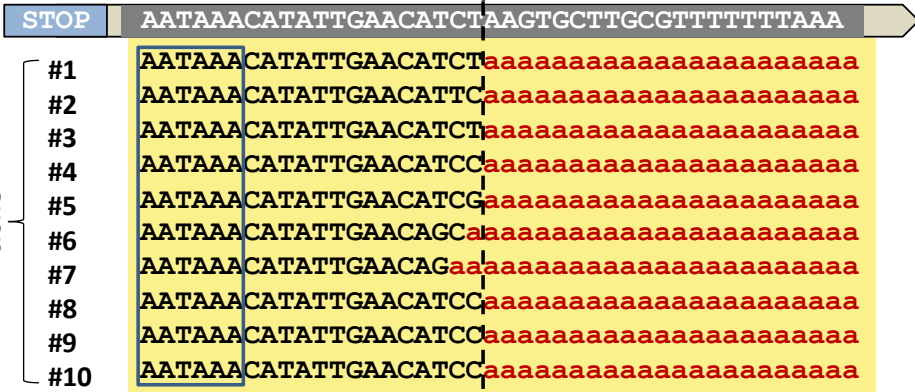


B



C

M03A1.3 wt 3'UTR



M03A1.3 mut 3'UTR

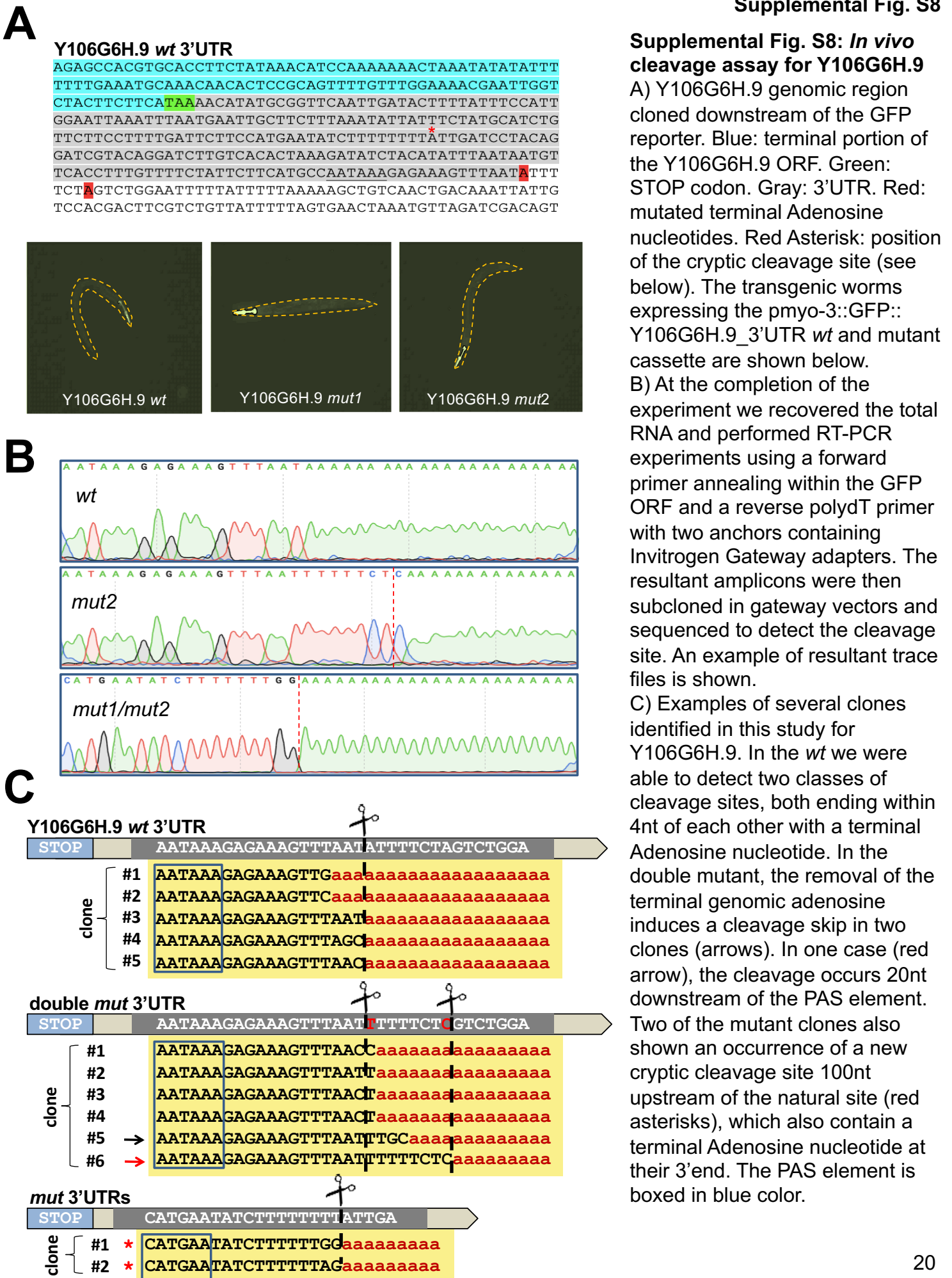


Supplemental Fig. S7: In vivo cleavage assay for M03A1.3

A) M03A1.3 genomic region cloned downstream of the GFP reporter. Blue: terminal portion of the M03A1.3 ORF. Green: STOP codon. Gray: 3'UTR. Red: mutated terminal Adenosine nucleotides. The transgenic worms expressing the pmyo-3::GFP::M03A1.3_3'UTR wt and mutant cassette are shown below.

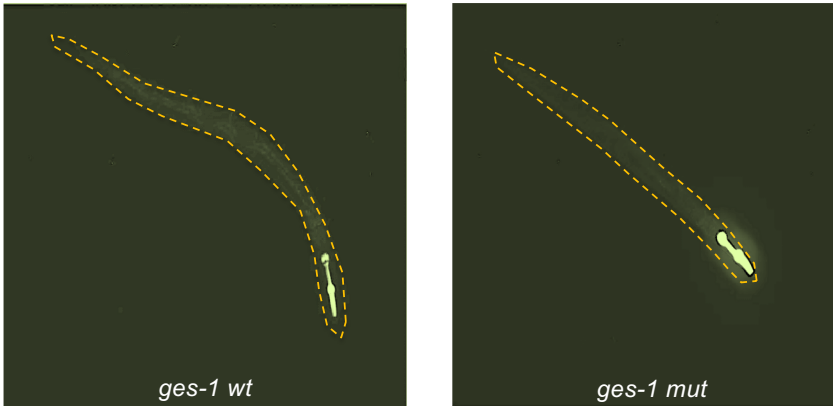
B) At the completion of the experiment, we recovered the total RNA and performed RT-PCR experiments using a forward primer annealing within the GFP ORF and a reverse polydT primer with two anchors containing Invitrogen Gateway adapters. The resultant amplicons were then subcloned in gateway vectors and sequenced to detect the cleavage site. An example of resultant trace files is shown.

C) Examples of 10 clones identified in this study for M03A1.3. The removal of the terminal genomic Adenosine nucleotide induces a cleavage site 3nt upstream of the canonical cleavage site in three clones (arrows), which also contain a terminal Adenosine nucleotide. The PAS element is boxed in blue color.



A *ges-1* wt 3'UTR

TCCAACTAATAGTGCCATGCATTTCGTCAAACAAGGACGAGCTGTAAAAAT
 GCAATAAATTTATGTATTTAATTGATTTTCGAATAAATATACTTTTGCTAC
 AAAATCTTCGGCAAATGCTCATGCTCGATTTCTCCCGCCAATTGAGCACC
 TGTCAATTTATCTTGTCAATTTTCTGTACAAACACTTCTTGCCCCGACCA



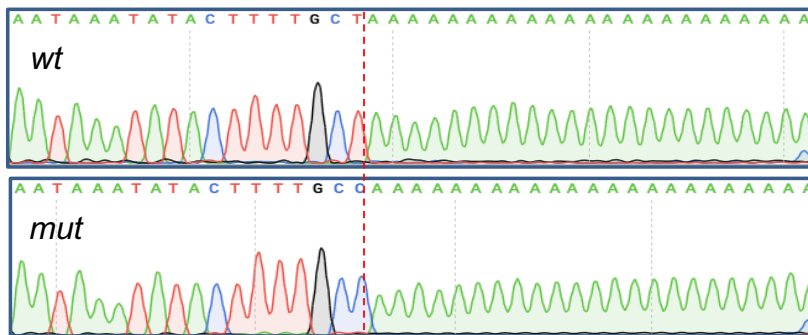
Supplemental Fig. S9: *In vivo* cleavage assay for *ges-1*

A) *ges-1* genomic region cloned downstream of the GFP reporter. Blue: terminal portion of the *ges-1* ORF. Green: STOP codon. Gray: 3'UTR. Red: mutated terminal Adenosine nucleotides. The transgenic worms expressing the *pmyo-3::GFP::ges-1_3'UTR wt* and mutant cassette are shown below.

B) At the completion of the experiment we recovered the total RNA and performed RT-PCR experiments using a forward primer annealing within the GFP ORF and a reverse polydT primer with two anchors containing Initrogen Gateway adapters. The resultant amplicons were then subcloned in gateway vectors and sequenced to detect the cleavage site. An example of resultant trace files is shown.

C) Examples of 10 clones identified in this study for *ges-1*. The removal of the terminal genomic Adenosine nucleotide does not alter the cleavage site but makes it more variable. The PAS element is boxed in blue color.

B



C

