

Cell, Volume 184

Supplemental information

**Splice site m⁶A methylation prevents binding
of U2AF35 to inhibit RNA splicing**

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Table S1. List of all deep-sequencing libraries created in this study. Related to STAR Methods and Figures 1-4.

Data is available from Gene Expression Omnibus (GEO: GSE146873).

sample	experiment	description	reads	sequencing type
RR723	m6A profiling on RNA mix from mouse, worm and BmN4-SID1	INPUT-Total RNA-1	78748292	single-end
RR724	m6A profiling on RNA mix from mouse, worm and BmN4-SID1	INPUT-Total RNA-2	109227705	single-end
RR725	m6A profiling on RNA mix from mouse, worm and BmN4-SID1	INPUT-Total RNA-3	98509826	single-end
RR726	m6A profiling on RNA mix from mouse, worm and BmN4-SID1	INPUT-PolyA+ RNA-1	111319107	single-end
RR727	m6A profiling on RNA mix from mouse, worm and BmN4-SID1	INPUT-PolyA+ RNA-2	111369816	single-end
RR728	m6A profiling on RNA mix from mouse, worm and BmN4-SID1	INPUT-PolyA+ RNA-3	104925272	single-end
RR729	m6A profiling on RNA mix from mouse, worm and BmN4-SID1	m6A IP-Total RNA-1	97238279	single-end
RR730	m6A profiling on RNA mix from mouse, worm and BmN4-SID1	m6A IP-Total RNA-2	116365247	single-end
RR731	m6A profiling on RNA mix from mouse, worm and BmN4-SID1	m6A IP-Total RNA-3	103682866	single-end
RR732	m6A profiling on RNA mix from mouse, worm and BmN4-SID1	m6A IP-PolyA+ RNA-1	99423158	single-end
RR733	m6A profiling on RNA mix from mouse, worm and BmN4-SID1	m6A IP-PolyA+ RNA-2	90657183	single-end
RR734	m6A profiling on RNA mix from mouse, worm and BmN4-SID1	m6A IP-PolyA+ RNA-3	105299920	single-end
RR618	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	input_totalRNA_WT-1	107952378	pair-end
RR619	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	input_totalRNA_WT-2	104276535	pair-end
RR620	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	input_totalRNA_WT-3	99043875	pair-end
RR621	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	m6A_IP_totalRNA_WT-1	88177640	pair-end
RR622	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	m6A_IP_totalRNA_WT-2	92603501	pair-end
RR623	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	m6A_IP_totalRNA_WT-3	80301018	pair-end
RR624	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	input_polyA_2_WT-1	51187060	pair-end
RR625	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	input_polyA_2_WT-2	52291052	pair-end
RR626	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	input_polyA_2_WT-3	33117898	pair-end
RR627	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	input_polyA_2_KO-1	39691391	pair-end
RR628	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	input_polyA_2_KO-2	35240657	pair-end
RR629	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	input_polyA_2_KO-3	39991008	pair-end
RR630	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	m6A_IP_polyA_2_WT-1	12022240	pair-end
RR631	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	m6A_IP_polyA_2_WT-2	36551759	pair-end
RR632	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	m6A_IP_polyA_2_WT-3	25683360	pair-end
RR633	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	m6A_IP_polyA_2_KO-1	54841480	pair-end
RR634	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	m6A_IP_polyA_2_KO-2	44893258	pair-end
RR635	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	m6A_IP_polyA_2_KO-3	43057847	pair-end
RR600	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	input_polyA_1_WT-1	22391643	pair-end
RR601	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	input_polyA_1_WT-2	23096755	pair-end
RR602	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	input_polyA_1_WT-3	19042425	pair-end
RR603	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	m6A_IP_polyA_1_WT-1	18362889	pair-end
RR604	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	m6A_IP_polyA_1_WT-2	18425770	pair-end
RR605	m6A profiling of the worm Mett-10 KO and WT on NA22 plates	m6A_IP_polyA_1_WT-3	18620691	pair-end
RR892	m6A profiling of the worm Mett-10 KO and WT on OP50 plates	input_polyA_WT-1	44602975	single-end
RR893	m6A profiling of the worm Mett-10 KO and WT on OP50 plates	input_polyA_WT-2	57428958	single-end
RR894	m6A profiling of the worm Mett-10 KO and WT on OP50 plates	input_polyA_WT-3	63145019	single-end
RR895	m6A profiling of the worm Mett-10 KO and WT on OP50 plates	input_polyA_KO-1	56220445	single-end
RR896	m6A profiling of the worm Mett-10 KO and WT on OP50 plates	input_polyA_KO-2	46443279	single-end
RR897	m6A profiling of the worm Mett-10 KO and WT on OP50 plates	input_polyA_KO-3	42188533	single-end
RR898	m6A profiling of the worm Mett-10 KO and WT on OP50 plates	m6A_IP_polyA_WT-1	11536036	single-end
RR899	m6A profiling of the worm Mett-10 KO and WT on OP50 plates	m6A_IP_polyA_WT-2	11339449	single-end
RR900	m6A profiling of the worm Mett-10 KO and WT on OP50 plates	m6A_IP_polyA_WT-3	11065165	single-end
RR901	m6A profiling of the worm Mett-10 KO and WT on OP50 plates	m6A_IP_polyA_KO-1	14331371	single-end
RR902	m6A profiling of the worm Mett-10 KO and WT on OP50 plates	m6A_IP_polyA_KO-2	13228517	single-end
RR903	m6A profiling of the worm Mett-10 KO and WT on OP50 plates	m6A_IP_polyA_KO-3	12318564	single-end

Table S3. DNA primers and RNA oligonucleotides used in this study. Related to STAR Methods and Figures 1-6.

Name	Sequence	Name in the study/Comments
Worm mutants		
oKDMM42	GGTGATTGTTGTTCCGAGTGC	Reverse primer for detecting and sequencing of intron 2 deletion in <i>sams-3</i> . If edit is present, it creates 473 bp with oKDMM43
oKDMM43	GTGACCAGGTAAGTAACCAACG	Forward primer for detecting and sequencing of intron 2 deletion in <i>sams-3</i> . If edit is present, it creates 473 bp with oKDMM42
oKDMM41	GACTCCAGCAGCGATTTCAG	Forward primer for detecting and sequencing of intron 2 deletion in <i>sams-4</i> . If edit is present, it creates 433 bp with oKDMM44
oKDMM44	ACGTTATCTCCGAAGCGTAG	Reverse primer for detecting and sequencing of intron 2 deletion in <i>sams-4</i> . If edit is present, it creates 433 bp with oKDMM41
oKDMM12	GCAACGTGTCGCTAAAGAGG	Forward primer for detecting and sequencing of intron 2 deletion in <i>sams-5</i> . If edit is present, it creates 526 bp with oKDMM39
oKDMM39	TCCGCTGCTTACCTTTTCGAG	Reverse primer for detecting and sequencing of intron 2 deletion in <i>sams-5</i> . If edit is present, it creates 526 bp with oKDMM12
oKDMM17	CCGTTCATCCCAACTCCATC	Forward primer to detect and sequence C-terminal HA tag in <i>sams-3</i> . If edit is present, it creates 554 bp band with oKDMM17
oKDMM18	ATGAACCAACCGCTGAGAAC	Reverse primer to detect and sequence C-terminal HA tag in <i>sams-3</i> . If edit is present, it creates 554 bp band with oKDMM17 to be sequenced
oFsa0131	TGTGGTGTGGCAGAGTAG	Forward primer to detect and sequence deletion of <i>mett-10</i> . If edit is present, it creates around 260 bp band with oFsa0195
oFsa0195	ATGTCCATGCCAACATCCAGC	Reverse primer to detect and sequence deletion of <i>mett-10</i> . If edit is present, it creates around 260 bp band with oFsa0131
oKDMM5	AAACTTGATTGTACAATGCTGAG	sgRNAs for C-terminal HA tagging of <i>sams-3</i>
oKDMM6	TCTTGTGACACATTGTACAATCAA	
oKDMM7	CGATCTCAACCGAAATGGAATTGCTCATGGAGGAGGATCAATGGGAGGATACCCATATGATGTTCCAGATTACGCTGGCAGTTAACGATTGTACAATGCTGATTCAATTTGTTG	Repair template for the C-terminal tagging of <i>sams-3</i>
oKDMM19	AAACTTCTGTAATCAAAGTAACC	sgRNA for removing intron 2 of <i>sams-3</i> , <i>sams-4</i> and <i>sams-5</i>
oKDMM20	TCTTGGTTACTTTGATTACAGAAA	
oKDMM21	AAACTTGTAAACAGGTAAGAAACC	
oKDMM22	TCTTGGTTTCTTACCTGTTACAA	sgRNA for removing intron 2 of <i>sams-4</i>
oKDMM23	AAACCTGAATCACTCACCACAAGCAC	
oKDMM24	TCTTGTGCTTGTGGTGAGTGATTACAGG	
oKDMM25	AAACCAAGCAACCTTAGCGTGAGC	sgRNA for removing intron 2 of <i>sams-4</i>
oKDMM26	TCTTGTCTACGCTAAGTTGCTTG	
oKDMM27	TCTTGTCTACGCAAAAGTTGCTATG	
oKDMM28	AAACATGCAACCTTTGCGTGAG	sgRNA for removing intron 2 of <i>sams-3</i>
oKDMM29	TCTTGAAGGTTGCTATGTTGTAAG	
oKDMM30	AAACCTTACCACATGCAACCTTTC	
oKDMM31	AAACACAGTTTCTGTAAAACCTTAC	sgRNA for removing intron 2 of <i>sams-5</i>
oKDMM32	TCTTGTAAAGTTTACGAAACTGT	
oKDMM33	AAACCAAGCAACCTTGGCGTGAGC	
oKDMM34	TCTTGTCTACGCCAAAGTTGCTTG	sgRNA for removing intron 2 of <i>sams-5</i>
oKDMM35	CGACAGCTTTCGAGGTGATCTCACCGCACAAACATGATCATACCCGTTTGTAGTCACTGTTTCAACAGCAACCTTAGCGTGAGGGTCTTGAGCCAGATGAGCG	
oKDMM36	CGCTGTTCTTGATGCTCATTTGGCTCAAGATCCTCACGCAAAAGTTGCTATGAAACAGTGAATAAACCGGGTATGATCATGTTGTGGGTGAGATCACCTC	
oKDMM37	CAGCTTTGAGGTGATCTCACCGCACAAACATGATCATACCCGTTTGGTCACTGTTTACAAAGCAACCTTGGCGTGAGGATCCTGAGCCAAGTGAAGCATC	Repair template for removing intron 2 in <i>sams-5</i>
sams-3 artificial constructs		
DH298	ACGAAGTGTTCACCTT	Forward primer for <i>sams-3</i> FL amplification
DH299	CTCAATAAATGATTTTTTATAAG	Reverse primer for <i>sams-3</i> FL amplification
DH300	CCCTAGAACACCGTCTGTTACATCAAGAACAGCGTCCGAGAT	Primer to introduce specific sequences into exon2
DH301	TGAACGACCGTGTCTAGGAGCGCAAAGTTGCATGTG	Primer to introduce specific sequences into exon2
DH302	TACGCATCAAAAGTAGGCTGTGGACGAGAACCTGTGATGTC	Primer to introduce specific sequences into exon3
DH303	ACAGCCTACTTTGAGTGCGTAATACGATGATTCCTCGAAG	Primer to introduce specific sequences into exon3
DH304	CTTATAAAAATCAATTTATTGAGCCTGCGAGCCTGGCATGC	Forward primer for pUC19 fragment amplification
DH305	AAGGTTGAACACTTCGTTGTTGTTCTGGAAATTGAGA	Reverse primer for pUC19 fragment amplification
MM320	GATTACAGACTTGGTGACTAAAACGGGTATG	Forward primer for METT-10 consensus motif mutation
MM321	TTAGTACCAAGTCTGTAATCAAAGTAACCG	Reverse primer for METT-10 consensus motif mutation
HeLa splicing constructs		
MM415	ATGGCTAGCCACCAGAGTGTTCACCTTACAAC	Forward primer for <i>sams-3</i> FL cloning into phRL-TK vector
MM416	CATGCGGCCGCTCTAGAACTCAATAAATGATTTTTTATAAGGTC	Forward primer for <i>sams-3</i> FL cloning into phRL-TK vector
Splicing		
MM378	GGTGAACGTGGATGAAGTTGGTGGTGGGCCCCGGGAGGTTGGTATCAAGGTTACAAGACA GGTTTAAGGAGACCAATAGAAACTGGGCATGTGGAGACAGAGAAGACTCTGGCCCTCGAGGT TCTGATAGGCACTGACTCTCTGCTATTGGTCTATTTCCACCCTTAGGCTGCTGGTG GTCACCTTGGACCCAGAGGTTCTTGGAGATATCCGTACACCATCAGGGTACGAGCTAGC CCATGGCGTACACCATCAGGTTAGACTAGTAGATCTCTACACCATCAGGGTACGGAATTC	Human B-globin with T7 promoter
MM379	TAATACGACTCACTATAGGTTGAACGTTGATGAAGTTG	Forward primer to amplify 3' fragment of B-globin
MM460	/52MOErG//i2MOErG/GAAAAATAGACCAATAGGCAG	Reverse primer to amplify 3' fragment of B-globin
MM_RNA_59	/5phos/ACCCATAGGCTGCTGGTGGTCTACCTTGGACCCAGAGGTTCTTTGAG	Unmethylated oligo for B-globin pre-mRNA ligation

MM_RNA_60	/5phos/ACCCCTm6AGGCTGCTGGTGGTCTACCCCTGGACCCAGAGGTCTTTTGAG	Splice site methylated oligo for B-globin pre-mRNA ligation
MM_RNA_61	/5phos/ACCCCTAGGCTGCTGGTGGTCTm6ACCCCTGGACCCAGAGGTCTTTTGAG	Exon methylated oligo for B-globin pre-mRNA ligation
MM453	CTGGGTCCAAGGGTAGACCACCAGCAGCCTAAGGGTGGGAAAAATAGACCAATAGGCAGA	Splint oligo for B-globin ligation
MINX_FL	CCACTCTGGATCGGAAACCCGTCGGCCTCCGAACGGTAAAGAGCCTAGCATGTAGAAGTGGT TACCTGCAGCCCAAGCTTGTCTGCAGCTGTAGGGCCAGTAGTCCAGGGTTTCCTGTGATGATG TCATACTTACTCTGCCCTTTTTTCCACAGCTCGCGGTGAGGACGACAAACTCTTCGGG GTCTTCCAGTGGGG	MINX pre-mRNA sequence
MM_RNA_85	/5phos/cacagctcgcggttgaggacaaactcttcgcggtctttccagtgg	Unmethylated oligo for MINX pre-mRNA ligation
MM_RNA_86	/5phos/cacm6Agctcgcggttgaggacaaactcttcgcggtctttccagtgg	Splice site methylated oligo for MINX pre-mRNA ligation
MM_RNA_87	/5phos/cacagctcgcggttgagg/in6Me-rA/caaactcttcgcggtctttccagtgg	Exon methylated oligo for MINX pre-mRNA ligation
MM578	gagtttctcctcaaccgagctgtggaaaaaaaagg	Splint oligo for MINX ligation
MM617	TAATACGACTACTATAGGGCCACTCTGGATCGGAAACCC	Forward primer to amplify 3' fragment of MINX
MM582	/52MOErG//i2MOErA/aaaaaaaggacaggaTaagtatgac	Reverse primer to amplify 3' fragment of MINX
MM583	/52MOErG//i2MOErT/gtgttaaaaggacaggaTaagtatg	Reverse primer to amplify 3' fragment of the weak polypyrimidine tract MINX
MM585	gagtttctcctcaaccgagctgtggtgtgtaaaagg	Splint oligo for the weak polypyrimidine tract MINX ligation
sams-3 RT-PCR		
MM395	CTCGGACGCTGTTCTTGTATG	PCR for intron retention, endogenous sams-3
MM396	AACCTGGTAGTCGACGACAG	PCR for intron retention, endogenous sams-3
MM363	TGTGAACGACCCGTGTCTTAGG	PCR for intron retention in mini-gene constructs
MM364	CGTATTACGCACTCAAGTAGGC	PCR for intron retention in mini-gene constructs
Mett116 knock-in mice		
tracerRNA		
CD.Cas9.PGDV2419.AB RNA	CTCAAAGGAACCACTACGCG GUUUUAGAGCUAUGCU	gRNA for cat-dead and RNA-binding mutant <i>Mett116</i> mouse
MM233	TCATCTCCCTAGTGGTGAAGTGCCTGCAAGACACTCTGATGGATGCGCTTAAAGAAGAG TCTGAGATAGTCTATGACTTCTGTATGTCAACCCCTCCGGCTTCGCCAACCATTGGAAGC CAAGGTACAGTACCTTTAAAGTTACCAATGCTTAGCTAGCTTTTACATCATTGCAGAGATA TCAACAAAAGGCAG	ssDNA template for homology recombination for F187G modification
MM232	TCATCTCCCTAGTGGTGAAGTGCCTGCAAGACACTCTGATGGATGCGCTTAAAGAAGAG TCTGAGATAGTCTATGACTTCTGTATGTCAACCCCTCCGGCTTCGCCAACCATTGGAAGC CAAGGTACAGTACCTTTAAAGTTACCAATGCTTAGCTAGCTTTTACATCATTGCAGAGATA AGAACAAAAGGCAG	ssDNA template for homology recombination for 185AA-PP186 modification
MM342	TCTCCATTGTGCGAGGCTCTG	Forward primer for F187G genotyping
MM343	CTTCCAAATGGTTGGCGAAGC	Reverse primer for F187G genotyping
MM348	CGTCTCCATTGTGCGAGGTC	Forward primer for PP185-186AA genotyping
MM349	ATTGGTTGGCAAAAATGCGGC	Reverse primer for PP185-186AA genotyping
MM340	AACTTGATGCGCTCCATTG	Forward primer to amplify the whole catalytic site region for sequencing
MM341	TGGTAACCTTTAAAGTACTGTACC	Reverse primer to amplify the whole catalytic site region for sequencing
Mett116 conditional KO		
MM101	aaagatttgcttggcggtttcc	Forward primer to detect loxP insertion in the <i>Mett116</i> locus
MM102	cccaggaagtggcactatcaag	Reverse primer to detect loxP insertion in the <i>Mett116</i> locus
oIMR7643	CACGTGCAGCCGTTTAAAGCCGCT	Forward primer for <i>Ddx4-cre</i> genotyping
iIMR7644	TTCCATTCTAAACAACCCCTGAA	Reverse primer for <i>Ddx4-cre</i> genotyping
MM314	AAATTCAAATGGCATTGGG	Forward primer for <i>Mett116</i> deletion genotyping
MM315	CCGAATCCTCATCTATTACATTG	Reverse primer for <i>Mett116</i> deletion genotyping
In vitro methylation		
		Name in the study/Comments
MM_RNA_5	CCCCCCCUGAGGUACAGAGAAGGGGGGG	Mouse 3'UTR ; 29nt
MM_RNA_6	UGUUGGCGUAGGUACAGAGAAGCCUUA	Mouse 3'UTR mut ; 29nt
MM_RNA_31	ACAACGGUUACUUUGAUUACAGAAACGGUGACUAAAACGG	RNA-0; 40nt
MM_RNA_32	GGUUAUUUGAUUACAGAAACGGUGACUAA	RNA-1 ; 30nt
MM_RNA_34	GGUUAUUUGAUUACAGAAACGGUGACUAA	RNA-2 ; 30nt
MM_RNA_33	GGUUAUUUGAUUACAGAAACGGUGACUAA	RNA-3 ; 30nt
MM_RNA_35	GGUUAUUUGAUUACAGAAACGGUGACUAA	RNA-4 ; 30nt
MM_RNA_36	GGUUAUUUGAUUACAGAAACGGUGACUAA	RNA-5 ; 30nt
MM_RNA_37	GGUUAUUUGAUUACAGAAACGGUGACUAA	RNA-6 ; 30nt
MM_RNA_43	GGUUAUUUGAUUACAGAAACGGUGACUAA	RNA-7 ; 30nt
MM_RNA_38	CCCCCCCUCAGAAACCCCGCCC	RNA-8 ; 25nt
MM_RNA_39	CCCCCCCUCAGAAACGGGGGGG	RNA-9 ; 25nt
MM_RNA_100	GGUUAUUUGAUUACAGAAACUCUAUUGGAA	RNA-10 ; 30nt
MM_RNA_101	UCAGUGGUUGAUUACAGAAACUCUAUUGGAA	RNA-11 ; 30nt
MM_RNA_120	GGUUAUUUGAUUACAGAAACGGUGUGAA	RNA-12 ; 30nt
MM_RNA_121	GCAUAUUUGAUUACAGAAACGGUGUGAA	RNA-13 ; 30nt
MM_RNA_122	GGUUAUUUGAUUACAGAAACGGUGUGAA	RNA-14 ; 30nt
MM_RNA_123	GCAUUGUUUGAUUACAGAAACGGUGUGAA	RNA-15 ; 30nt
MM_RNA_124	CCCCCUUUGAUUACAGAAACGGGGGGAA	RNA-16 ; 30nt
MM_RNA_44	AAACUUUUUUUUUUAAGAAACUGUUGCUAA	Mouse ; 30nt
MM_RNA_45	AAACUUUUUUUUUUAAGAAACUGUUGCUAA	Mouse mut ; 30nt
MM_RNA_46	UUUUUUUUUUUUAAGAAACUUAACUAA	Silkworm ; 30nt
MM_RNA_47	UUUUUUUUUUUUAAGAAACUUAACUAA	Silkworm mut ; 30nt
MM_RNA_48	CAUAAUUUUUUUAAGAAACGUCGCCAA	Fly ; 30nt
MM_RNA_49	CAUAAUUUUUUUAAGAAACGUCGCCAA	Fly mut ; 30nt
MM_RNA_67	UAUUUUUUUUUUUUAAGAAACUUAACUAA	RNA-67/Muc11 ; 40nt
MM_RNA_68	AGAGUGGUUUUUUUUAAGAAACUUAACUAA	RNA-68/Spag1 ; 40nt
MM_RNA_69	AAUCUUUUUUUUUUUUAAGAAACUUAACUAA	RNA-69/Pla2r1 ; 40nt
MM_RNA_70	UUUCUGGAAUUUUUUUAAGAAACUUAACUAA	RNA-70/Gyg ; 40nt
MM_RNA_71	GCAUUGGUGGGUCUUUUUAAGAAACUUAACUAA	RNA-71/Des ; 40nt
MM_RNA_72	AUGCAAAACUUUUUUUAAGAAACUUAACUAA	RNA-72/Helt ; 40nt
MM_RNA_73	ACUCUUUUUUUUUUUUUAAGAAACUUAACUAA	RNA-73/Pecam ; 40nt
MM_RNA_74	AUUUUUUUUUUUUUUUAAGAAACUUAACUAA	RNA-74/Gm48535 ; 40nt
MM_RNA_75	CUUUUGGGCUUUUUUUUAAGAAACUUAACUAA	RNA-75/Gm15810 ; 40nt
MM_RNA_76	GAUGCUUUUUUUUUUUUAAGAAACUUAACUAA	RNA-76/Tjp2 ; 40nt
MM_RNA_80	UAGAAUUUUUUUUUUUUUAAGAAACUUAACUAA	Sorbs1 ; 45nt
MM_RNA_81	UAAUUGUUUUUUUUUUUUUAAGAAACUUAACUAA	Lrppc ; 40nt

RP RNA 19	GCGUCUUUACGGUGCUUAAAACAAAACAAAACAAAACAAA	40 nt RNA marker
RP RNA 1	TGACATGAACACAGGTGCTCAGATAGCTTT	30 nt RNA marker
RP RNA 3	UGACAUGAACACAGGUCUCAGAUAGCU	28 nt RNA marker
RP RNA 18	AGCACCGUAAAGACGC	16 nt RNA marker
ITC		
KM RNA 10	CUAGG	ITC experiment; 5 nt
KM RNA 11	CUm6AGG	ITC experiment; 5 nt
SCARLET		
MM437	GGAGAGACAACCTAAAGAGACTTAAAAGATTAATTTAAAATTTATCAAAAAGAGTATTGACT TAAAGTCTAACCTATAGGATACTTACAGCCATCGCCGGTCTGTGAGTTAATAG	Universal DNA oligo for splint ligation
MM438	TGATCATACCCGTTTTAGTCACCGTTTCTCTATTAACCTCACAGGACCGCGATGGCTG	sams-3 splint oligo
MM698	mCmGmUmUmUmCmU GTAA mUmCmAmAmAmGmU	sams-3 chimera
MM614	CCTTGCGCAGGGCCATGCTAATCTTCTCTCTATTAACCTCACAGGACCGCGATGGCTG	U6snRNA splint oligo
MM702	mCmUmUmCmUmCmU GTAT mUmGmUmUmCmC	U6 snRNA chimera
MM616	CCACTTTTATATCTATAGCGCGCTGTCTATTAACCTCACAGGACCGCGATGGCTG	Positive control splint oligo
MM615	mGmCmGmUmUmGmU TCAG mAmGmUmCmUmAmA	Positive control chimera
MM RNA 98	UUAGACUCUGAACACGCGCGCUAUGAGAUUAAAAAGUGG	Positive control oligo - unmethylated
MM RNA 99	UUAGACUCUGAm6ACAACGCGCGCUAUGAUUAAAAAGUGG	Positive control oligo - methylated
MM RNA 96	GTTACAACGGTTACTTTGATTACAGAAACGGTGACTAAAACGGGT	sams-3 control oligo - unmethylated
MM RNA 97	GTTACAACGGTTACTTTGATTACm6AGAAACGGTGACTAAAACGGGT	sams-3 control oligo - methylated

Table S4. Composition of nutrient-low and nutrient-high plates used for *C. elegans* culture. Related to Figure 1-4

Nutrient-low media

NGM (nematode growth medium)	2 litres
Agar	35 g
Peptone	5 g
Phosphate Buffer pH 6,0 + NaCl	50 ml phosphate buffer + NaCl
MgSO4 1 M	2 ml
CaCl2 1 M	2 ml
Cholesterol in ETOH (5 mg/ml)	2 ml
Buffer NGM Phosphate + NaCl 40X	2 litres
1 M Phosphate Buffer pH:6.0	72 g K2HPO4
	216 g KH2PO4
2 M NaCl	240 g NaCl

Nutrient-high media

Pepton-rich plates	2 litres
Agar	50 g
Peptone	40 g
Phosphate Buffer pH: 6,0 + NaCl	50 ml phosphate buffer + NaCl
MgSO4 1M	2 ml
Cholesterol in ETOH (5 mg/ml)	2 ml
Buffer Pepton Rich Phosphate + NaCl 40X	2 litres
1 M Phosphate Buffer	40 g K2HPO4
	240 g KH2PO4
820 mM NaCl	96 g NaCl

Table S5: List of worm strains used in this study. Related to Figure 1-4.

Strain	Genotype	Source	Comments
N2	wild type	CGC	wild type strain
VC1743	<i>mett-10 (ok2204) III</i>	CGC	<i>Mett-10</i> deletion
FAS198	<i>sams-3 (uge125) IV</i>	This study	<i>sams-3</i> intron 2 deletion
FAS199	<i>sams-4 (uge126) IV</i>	This study	<i>sams-4</i> intron 2 deletion
FAS200	<i>sams-3 (uge127) IV; sams-4 (uge126) IV</i>	This study	<i>sams-3</i> intron 2 deletion and <i>sams-4</i> intron 2 deletion
FAS201	<i>sams-4 (uge126) IV; sams-5 (uge128) IV</i>	This study	<i>sams-4</i> intron 2 deletion and <i>sams-5</i> intron 2 deletion
FAS202	<i>sams-3 (uge129) IV; sams-4 (uge126) IV; sams-5 (uge128) IV</i>	This study	<i>sams3</i> intron 2 deletion, <i>sams-4</i> intron 2 deletion and <i>sams-5</i> intron 2 deletion
FAS203	<i>sams-3 ((uge130) [sams-3::HA]) IV</i>	This study	HA-tagged <i>sams-3</i>
FAS204	<i>sams-3 (uge131) IV; sams-3 ((uge130) [sams-3::HA]) IV</i>	This study	HA-tagged <i>sams-3</i> with intron 2 deleted
FAS206	<i>sams-3 ((uge130) [sams-3::HA]) IV; sams-1 (uge132) [OLLAS::sams-1] X; mett-10 (ok2204) III</i>	This study	HA-tagged <i>sams-3</i> with <i>mett-10</i> deletion NOTE: This strain has <i>sams-1</i> tagged with OLLAS in the background, which was not used in this study