

Supplemental materials: Sequences and Oligonucleotides

GenBank accession: DQ789401-DQ789568

Table S1: Novel C/D box snoRNAs, group I for *C. elegans*

Group I: *C. elegans* novel C/D-candidates

I.1 *C. elegans* novel C/D-candidates in INTRONS OF RPGs

name	NCBI	sequence	predicted targets
ComCe1	U41534 6843-6758 Rps-13	ttgatctgaggagtacttggtcgattccgataactac catatgatcatcaactgggctaccattttc aa gttga aaatggg	Gm1926/26S; guidebox D'(11nt) Gm452/26S; guidebox D (9nt)
ComCe2	Z69337 1239-1300 Rpl-3	gttctatgaagaaaagtctc aa attcglactgtatggc gactatattttatctgagaac	Gm75/5.8S; , guidebox D'(10nt)
ComCe3	U58760 3026-3096 Rpl-22.2	gcttttaaaat aa cagcctcatcaagtcgatagagtt cccgtctctatcgaagac cag gcttagggt	Gm61/U4 guidebox D'(9nt) Gm1265/26S; guidebox D'(10nt) Gm30/tRNAThr; guidebox D (10nt)
ComCe16	AF000196 3642-3589 Rpl-4	gacataa tt agatc ct ctattg aa tatttt aa attt caa act aa ctctgtgtt	Um 1025/26S; guidebox D'(11nt) Um3087/26S; guidebox D (11nt)
ComCe18	AC024780 13253-13195 Rps-4	gaatgaaggtcgggggcccgc g ggctcgt aa aaagtc cggctaa gg ttg ct taattc	Um 726/26S; guidebox D'(9nt) Um3301/26S; guidebox D'(9nt) Um 1345/26S; guidebox D (9nt) Um5/tRNAArg; guidebox D'(10nt)
ComCe19	AC006729 13141-13068 Rpl-7a	atttttatcagagtcagtacta aa agc aa gcttgagc ttgcactgagcatt act ctataggtgaagt	Um755/18S; guidebox D'(9nt) Um2133/26S; guidebox D'(9nt) Um 2821/26S; guidebox D'(9nt) Cm733/18S; guidebox D (9nt)

I.2 *C. elegans* novel C/D-candidates in INTRONS OTHER THAN RPGs

name	number of seq. clones	NCBI	sequence	predicted targets
Ce18	2	Z74041 20521-20595	gccgtgatgcttttcatg cc ctcaGCTG AGATCCCCTGATTAGAACC ACCCTTGAGGTTGT TT AA CTGAGGC(TA)	Cm2407/26S; guidebox D'(15nt) Um292/26S; guidebox D (10nt) Um 3136/26S; guidebox D (9nt)
Ce67	6	Z81042 7933-7867	ggg cg gtgaAATTGTTGCACAG ACC TT GTTCC TA TAGTTCA CTGAGGAAAATAG AA TCA TGA GC CT	Am1389/18S; guidebox D'(12 nt) Gm336/18S; guidebox D (11nt)
Ce86 (CeN35)	5	U64858 479-414	ggcccg tg gaaGACACGAATT AC CGTCTGATAACTAATGACG CTACCATGGCTGTAAAC CA GAGGCC(GA)	Um560/18S; guidebox D'(9nt)
Ce97	2	U29535 8107-7978	atctgcaatgaagaattg gc cag CG TC CTGA AA TCCGGCCGAGATGT	Cm57/U6; guidebox D'(12nt)

			GTGCCGATGGGCTTTCGGG AATCTGGATATCGGTTTCTG GATCGAAGAATTGGTTCAGA AAGATAGCACCCA CCGAGA CAGat	
Ce104.2		AL021481 16441-16370	TGAATTGACGAGTTGAATT GGGTTAGAGCAGGTGATG CTCGATGGAAAATGATCACA AATTAAGCTGATCA	Um538/26S; guidebox D'(10nt)
Ce110 (CeN42)	3	Z50795 17966-17908	tttgatgattacTAATAATTCGCTG TCTTTAGAGGACGCGGAGA TTGTGAGACTTGAAA(CAT)	Gm1259/26S; guidebox D'(10nt) Cm1010/18S; guidebox D(10nt)
Ce135 (CeN25-1)	9	Z68493 28489-28418	ttcttataatacTTCAGGGCTTA CTAAAGACCCAGTGTACAA TTTTTGCAGCCCTTCTTCT GAGGCAGG(GG)	Gm1067/26S; guidebox D'(11nt) Gm 35/U4; guidebox D'(10nt) Cm187/18S; guidebox D(10nt)
Ce151 (CeN129)	2	U64854 7896-7962	ctcgatgacgattaccfaactcagac ATACAAC TGGTGATAAAAA AATTTCTGTCTTAGAG(AC)	Cm 3060/26S; guidebox D'(10nt) Gm1373/18S; guidebox D(10nt) Gm1117/26S; guidebox D(11nt)
Ce169	1	U55854 23529-23456	cagtegaggaGGAAGTTTCCA TGCAACACTCTGAAGGATA GTGTGGATTATGGTTCACA ATTTACTGAGGCTG	Gm 1236/18S; guidebox D'(12nt)
Ce173.1 Ce173.2 Ce173.3 (CeN128)	3	Z49069 173.1 13736-13830 173.2 13832-13892 173.3 13907-13978	aatgatgactCAAAATAGCTATA TGAACCTTTTGTGACTCG ATAATAAGAGAAAATCTGAA AATTTTCAAGGTTTTTCTAG AGAATTCA CCGAATCTTTT GAAGTATCGGTGCACCAAG TGA AAAATAAAA TTGCGAC GCTTITAGTACGCTGAGA AAGTTTTTATCCAGTGTCTA AAGGCGCGGCGCAACATTT TTAAACTTCCGATGATTT GTGATTACTAAAAGGCGAA TCTGAGGCG(AA)	173-1: Gm396/26S; guidebox D'(10nt) Am96/5.8S; guidebox D(11nt) 173-2: Am90/18S; guidebox D(10nt) Am2287/26S; guidebox D(9nt) Am46/U5; guidebox D(9nt) 173-3: Gm 2720/26S; guidebox D'(12nt) Gm39/U5; guidebox D(11nt)
Ce234 (CeN47)	1	U88173 234.1 10657-10596 234.2 10592-10509	taaataaaGAATACCATCCCT GCTCTGCAGTCTGTGAGC AATCACTTGAGAACTCTGA TGAGGTATTGTAGCATCGG GTTACGGTAGCCGAGTCAG TTGATTCTCATCATGTGGCA CTTCGACGGTGAACAGTTA TGCCTCTGATA	234.1: Am 65/U6; guidebox D'(9nt) 234.2: Gm268/18S; guidebox D'(10nt) Cm209/26S; guidebox D(10nt)

Ce251	1	AF026210 25839-25723	gagcaatgaCGATTCTTGTACAG AGTCGTATCATCGAAGCGC ATAGTTTTTGGCTGTCGT AGAGCTGAAAATGTTTCGA CGGCGTGATCGATTGACTA ATCTTCTCTCTGAGCTC(TC)	Gm1879/26S; guidebox D'(11nt) Gm 2309/26S; guidebox D'(9nt) Am42/U6, guidebox D (12nt)
Ce254b (CeN23-2)	3	U11029 10175-10094	cccgatgATGAAGACCATAA ATGACGAATCCTAATAGCC CAATGGGTTTCATGCGGA TATGAGGCAATTGTCTGAG CGGG(C)	Cm2391/26S; guidebox D'(10nt) Am2384/26S; guidebox D (10nt)
Ce297 (CeN17)	2	Z49130 12059-12135	tcaccaatgatGC AATGGTTAAAT CAGacgagtctatttggctatcttcgagt tctcgaagaaatgccgctaagcgggtga aatgaggcaattgtcagggtga	Am2384/26S; guidebox D (11nt)
Ce298	1	Z81138 22031-21948	ctcgatgatgagaatcatcgaatcaga gagactcgtcagttccaacctcattgtga aaacAATCGATAGCTGAGCA G(A)	Am48/U6; guidebox D'(10nt) Um 1263/26S; guidebox D (11nt)
ComCe4		Z71181 21721-21645	taactggaagattcaataaaactttggag ttaccctgactctgtaccgatgacgaaaca cwaattgagtt	Am314/26S; guidebox D'(9nt) Am 628/26S; guidebox D (9nt)
ComCe10		U14635 33102-33029	gaatacataaattagtttccaccagaa gccaataattaccattgcgcaata acataatgaatattc	Um92/5.8S, guidebox D'(9nt) Um1825/26S, guidebox D'(9nt) Um910/26S, guidebox D'(9nt) Um 3111/26S, guidebox D (10nt)
ComCe20		AC006651 16008-16084	agaatctcgagaagcattctcactcgc tcgggtcgcttggaggacagacctgccga caattctgatttt	Um 416/26S; guidebox D'(9nt) Gm626/26S; guidebox D (10nt) GM1318/26S; guidebox D (9nt)
ComCe21		Z81042 9730-9627	aagctcaattcttctggttgcactcattc tcgtcttcgaaatccgagccgactggattac cacccttcacgcttccaatttctcaactggt ttt	Gm 1536/18S; guidebox D'(10nt) Gm368/26S, guidebox D (10nt)
ComCe23		U41108 18320-18406	gttttgatgttcccgatgaatctcctgaa cccaaccgagcttgggttacatttgcgga ggcaaggatctaaactgaaat	Cm2641/26S; guidebox D'(9nt) Am3242/26S; guidebox D (12nt)
BICe173.2 BICe173.3		U55856 173.2 21065-21003 173.3 20991-20920	tcttcaagtatcgggtcaccagtgaaaaa taaaatcgcgacgtttagcagctggaga gttttatccagtttctaaaggcgcgaagcaa catctcgaacttccgataatttgattacta aaaggcaactcagggc	173.2 Am90/18S; guidebox D (10nt) Am2287/26S; guidebox D (9nt) Am46/U5; guidebox D (9nt) 173-3: Gm445/26S; guidebox D'(10nt) Gm39/U5; guidebox D (11nt)
BICe298		Z81568 29237-29159	tgtagtgatgaaaatcatcgaatcaga ggcgcgtccgtctcggaccctattgtc catcatttctgaaca	Am48/U6, guidebox D'(10nt) Gm1358/26S; guidebox D (9nt)

***I.3 C. elegans* novel C/D-candidates in INTERGENIC REGIONS**

name	number of seq. clones	NCBI	sequence	predicted targets
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Ce55 (CeN61)	6	U88180 7151-7080	gtcgaatgacGAACCAAGAGTTAT CCTGTCTGATGATTGTG AGGACAAAAGACTATGGTA ACACTCCGAGAC(TA)	Gm 2927/26S; guidebox D' (12nt) Um 553/26S; guidebox D (9nt)
Ce59	7	Z99171 10202-10136	gtcaatgaagaGAAACACCGATC CCTCGTCTGACAAATTGCT GATAGATTGTACGTCAGTC GTAGAG(GT)	Um14/5.8S; guidebox D' (13nt) Am931/26S; guidebox D (11nt)
Ce94	3	Z79603 16340-16403	(GCGCC)AATAGGTTATCATZ CCTATTCCACITCAGGGGA ACTTCCCATGGCACCAA TTGACTGATATT(TT)	Gm1668/26S; guidebox D' (10nt) Gm46/tRNAAsn, guidebox D (9nt)
Ce96 (CeN25-2)	6	Z81491 29112-29209	attataaacgctctcaGGGCCTTGCA AAAGACCCA GTGAACAATT TTTGGAGAACCCTGTCCCTT CGAGGT CAGGGTAaatgttagt ttcagaat	Um2529/26S; guidebox D (11nt)
Ce98	6	Z48045 7798-7724	gcaatgatGT CATACTCAAATCT GTCACTCCTCAGACCATCC CTGGTGATAACACGGTTTT CCG CAGTCTGAGC(AGC)	Cm1196/18S; guidebox: D' (14nt) Cm367/18S; guidebox D (11nt)
Ce100	4	Z47074 15546-15632	caagagttgaTGACTTACTTAG GACACCTTTGGAGGGCCTC GCTCTGCTGAAAAGAAAAA TAGTACGCCCTAGTCTGAG CTCTtg	Um203/26S; guidebox D' (10nt) Cm2728 /26S; guidebox D' (9nt) Gm2731/26S; guidebox D (10nt) Am1222/26S; guidebox D (9nt)
Ce167	5	Z66516 28109-28170	gccgtgaTGATCAATTGAGCA TATCAITGACTGTTGGTGA GGTGATTTCAATTAGCTGAG GC(TT)	Am28/18S; guidebox D' (11nt) Um72/18S, guidebox D (9nt) Um1058/26S, guidebox D (9 nt)
Ce171 (CeN40)	7	AL032663 7898-7781	cggatgaTCGATGACTTGTGCA GTGGCCGAGGCGATCGGAT TGTGATGTCGCCTGAAAAG GCGGGACCCAACGTCGCGC CTTTCGCCAGAAGATGGAA ATATGCGCAACGTCTGAGC TG(A)	Um68/U1; guidebox D'-1 (9nt)
Ce211 (CeN5)	5	Z75111 1-65	tggcagtgatgATCACA AATCCG TGTTTCTGACAAGCGATTG ACGATAGAAAACCGCTGA GCCA	Am678/26S, guidebox D' (12nt)
Ce238	1	Z68342 34378-34307	gggtgatgattagattactcttctcgcgt ACCGACTGTTTCAGTGGTGG ATAAACCTTCTATGAGACTt	Um1566/26S; guidebox D' (13nt) Gm 1022/18S; guidebox D (9nt)
Ce240	2	Z81551 3789-3864	GAAAAATGATCCCGAAAAGG ATCTGAAAaatctcattattagatgagag cgtgagcaagatggcaatctgattttt	Um 800/18S; guidebox D' (10nt) Um1688/18S; guidebox D (9nt)
Ce254a (CeN23-1)	8	AL132949 74745-74666	(CGAAAAC)CCGCATATGAA GACCACTAAATGACCAATC CTAATAACCCAATGGGTTTC ATTGCGGATATGAGGCAIT TGCTGAGCGG(A)	Cm2391/26S; guidebox D' (10nt) Am2384/26S; guidebox D (10nt)
Ce282 (CeN52)	2	AC024753 25441-25375	aaagtcaccaTTCATAGTTCACA TCATTGCTAACGAGTGATG TGCTCCGCCAGGTGCTC ATTTt	Cm138/5.8S; guidebox D (9nt) Um1223/18S; guidebox D (9nt) Um3163/26S; guidebox D (9nt)

The number of clones describes their frequency in the sequenced cDNAs. The NCBI GenBank accession number and coordinates are given in column two or three. Gray = double stranded region, yellow = C' and C boxes, green = D' and D boxes, red = the complementary nt at the target site is methylated. Letters in parenthesis indicate that the cDNA is longer than the snoRNA sequence. Bold and underlined letters indicate the antisense elements, italic letters indicate G-U pairings corresponding to the target site. Capital letters represent cDNA sequences. The additional sequences completed by Wormbase or GenBank information are in lower case letters. Target sites are from rRNA, U-RNA or tRNA. Targets verified by the modification study of 26S rRNA (Higa et al. 2002) are shown in red letters. Letters in bold in predicted targets indicate that the same sequence is targeted by the *C. briggsae* snoRNA orthologs. RPGs = Ribosomal Protein Genes. Designations in parenthesis refer to Deng et al. 2006.

Table S2: Novel C/D box snoRNAs, group I for *C. briggsae*

Group I: *C. briggsae* novel C/D-candidates

I.1 *C. briggsae* novel C/D-candidates in INTRONS OF RPGs

name	Sanger	sequence	predicted targets
ComCb1	CAAC01000101 188952-188871	TGATCTGAGGAGTTACTCGGTG CGATTCCGATAGCTACCATATG ATCACCAACAGGGCTACCGGAT TTTCAAGTITGAATCT	Gm1927/26S; guidebox D'(11nt) Gm287/26S; guidebox D (10nt)
ComCb2	CAAC01000015 354218-354154	TAGTTCGATGAAGAGAA TGTCT GGAATTCGTA CTCTGTA TGGCG ACTAGTITTA TCTGAGA ACTA	Gm75/5.8S; guidebox D'(11nt) Am1052/26S; guidebox D (10nt)
ComCb3	CAAC01000012 170321-170390	ITTA GGCTAAAAGCCAGCCTA A TCTAGT CGATAG AGCACCCGT CTCTATCGCAATGACCAGGCTTA GGG	
ComCb18	CAAC01000028 271775-271715	AGAA TGAGGG TCGGGGGCCAC G GGGTTCGTA AAAGTCCGGCTA AGGTTC GTTGCTAA AATA	Um3302/26S, guidebox D'(9nt) Um1345/26S; guidebox D (9nt)

I.2 *C. briggsae* novel C/D-candidates in INTRONS OTHER THAN RPGs

name	Sanger	sequence	predicted targets
Cb18	CAAC01000141 405304-405377	GCCCATGATGGT TTCATGCGTGTTC AGCTGAGATCCCC TGATTAGAACC ACCCTTGAGGTTTGACTAACTGAG GC	Cm2408/26S, guidebox D'(13nt) Um3436/26S; guidebox D (9nt) Um1577/26S; guidebox D (9nt) Um276/26S, guidebox D (9nt)
Cb67	CAAC01000098 2090565-2090499	AGGCAATGAAAT TGTTCACAGAC CTGTACCTATTAGTTCAC TGAGGAT AAAAGCAATCATGAGCCT	Am1383/18S; guidebox D'(11nt) Gm1643/26S; guidebox D (9nt) Gm1451/26S; guidebox D (9nt) Gm2969/26S; guidebox D (9nt)
Cb86	CAAC01000364 10227-10162	GGCCCGTGAAGAAGTAAATCCG TCCGATAACCCATGACGCTATGAA GGCTGTA AAAACAGAGGCC	Um307/18S; guidebox D'(13nt) Am2682/26S; guidebox D (9nt) Gm1123/26S; guidebox D (9nt) Gm1135/18S; guidebox D (9nt)
Cb97	CAAC01000012 756446-756316	ATCTGTCGATGAAGAATTGTGCAG GGTCTGAAATCGGCCGAGATGT GTGCCGATGGGTCAATCGGGAATT CAGATATCGGTTCTGAAGCGAAG ATTGATTCAGAAAGATAGCACCCA CAGAGACAGAT	Cm57/U6; guidebox D'(13nt)
Cb104.2	CAAC01000274 42890-42969	TGATAATAGAATGGACGAGTTGAC GAGA ACTAGATGGGCGGTGTAGTT GGGAAGTGATCA CAGACTGGAATA TCTGATCG	
Cb151	CAAC01000098 630222-630289	CTCGATGATGATTCACCTACTCA CTCAGACATGATAACTGGTGATAA CTTCTTTC CCGTCTTAGAG	Cm3061/26S; guidebox D'(10nt) Gm2499/26S; guidebox D (13nt)
Cb169	CAAC01000012	CAGTCAAGGAGGAAGTTTCCATG	Gm1230/18S, guidebox D'(12nt)

	223247-223173	CACTCTGATGATAGTGTGGA TTATGGTTCACATGAAACTGAGG CTG	Gm639/26S; guidebox D (10nt)
Cb173.1 Cb173.3	CAAC01000012 Cb173.1 1897614-1897705 Cb173.3 1897777-1897885	GATGAGGACACAACCTAGTTATAT GAATTCCTTGAATCTCAACGTAG AGGAGCTCTGCATTTCAAAGAATT TCTTTGAGAAAACTGATTCGATT CTTCGTCTCGGCTTTCATAAGAAAA ATCAAACCTGCGACGCTTTAGTGGTG CTGAAGCAAACGCTATTTCAGTGTG TAAAGGCGCGACGCAACATCAGAA CTCTATTCGTTAGGCTAGTTGA GAACTGAAAATCAAACATATGAT TACTAAAAGGGAATCTGAGGCAT TGAA	173.1 Cm395/18S; guidebox D' (9nt) Um2655/26S; guidebox D (11nt) Cm144/U2; guidebox D (9nt) 173.3 Gm877/26S; guidebox D' (14nt) Gm1365/26S; guidebox D' (12nt) Gm40/U5, guidebox D (11nt)
Cb234.1 Cb234.2	CAAC01000068 Cb234.1 4251240-4251308 Cb234.2 4251155-4251236	TTAAATGAAGAATACCATCCITG CTCTGCATGGCCGTGAAACACAT ACACTTGAGAATTCTGAGTGAGGG TACTGTAGCATCGGGTACTGTACA CCAATCCAGACGATTCTCAGGTGGT TCGACGCCGGTGAACAGCTATGCG CTCTGATA	234.1 Am65/U6; guidebox D' (9nt) 234.2 Cm209/26S; guidebox D (10nt)
Cb251	CAAC01000031 220862-221003	TGAGCAATGACGATTTTCGATTAC AAAACGGTTTAGCATCAGGACACA AAGTGCTCGTCACTTTGTAACAGTT TCCAGTCGTCTTTGGCAGAAACC GTTTIGATGATGTGACCGAGCGAC TAATCTCTCTGAGACTCA	Am2348/26S; guidebox D' (10nt) Am992/18S; guidebox D' (9nt) Am42/U6, guidebox D (12nt)
Cb254b	CAAC01000041 28623-28706	ACCCGTGATGAAGACTACTAAAT GACGAATCTAAATAGCCCAATGGG TTTCATGCGGATATGAGGCAIT GTCTGAGCGGGT	Am2391/26S, guidebox D' (10nt) Am2385/26S; guidebox D' (10nt)
Cb297	CAAC01000005 387713-387825	TCACCGGTGATGTAATGGTCAAGTC AGACGAGTCTAAATTTGGCGATCGG TTCGAGTTCTTCGAAGACATCGCCG CCTAAAGCGGGGTGATAATGAGGC ATTTGCTGAGGGTA	Am2385/26S; guidebox D (11nt)
ComCb4	CAAC01000044 1358294-1358215	TAAACTGAAGATTCGATATGAACT CGCAAAGTTCCTGAAAATCTATT ACCAATGACGATCGCCCAATTA TGAGTTTA	Um129/U1; guidebox D' (10nt) Gm1583/26A; guidebox D (9nt)
BICb298	CAAC01000088 1176387-1176472	TTTCTGCAGTATGAGAATCATGC TAATCATGAGAGGCGCGTCCGTC TCAACCCCATGTTGTAGAAAATGA TATCTGAGCAGAGA	Am48/U6; guidebox D' (10nt) Cm501/26S; guidebox D (12nt)

I.3 C. briggsae novel C/D-candidates in INTERGENIC REGIONS

name	Sanger	sequence	predicted targets
Cb55	CAAC01000107 153464-153393	GTCAAATGACGATAGAAAGTTATC CTGTCTGATGATTGTGACGACAA ACAACATATGGTCACTCCGAGAC	Gm2928/26S; guidebox D' (12nt) Um553/26S; guidebox D (9nt)
Cb59	CAAC01000097 474811-474880	GCCTCAATGAAGATAAACACCGAT CCCTCGAGTGCATCTTGTGATA GTTGTACGCTCAGTCCGAGAGGT	Um14/5.8S; guidebox D' (12nt) Am931/26S; guidebox D (11nt)

Cb98	CAAC01000064 15200-15274	GCAATGATGTCATACTCA AATCTG TCA TCCTCAGA CGATCCCTGTTG ATAA TACGGTTT ACCGGAGTGCTG AGC	Cm1190/18S, guidebox: D'(14nt) Cm3385/26S; guidebox D (9nt) Cm906/26S; guidebox D'(1nt)
Cb100	CAAC01000012 2761377-2761461	AAGAGTTG TGATGACTTACTTAGG ACACCTTTGGAGGG TTTCGGTCCG CTGAAAAGAAAA ATAGT ACGCCIT AGTCTGA GCTCTT	Cm1544/26S; guidebox D'(9nt) Um84/5S; guidebox D'(9nt) Gm2732/26S; Guidebox D (10nt) Am1222/26S; Guidebox D (9nt)
Cb167	CAAC01000115 1003559-1003619	GCCGGGGAT GAGCAATTGAGCA IA TCACTGACTGTGGTGA GGT GACT AGATTCTGAGGC	Am28/18S, guidebox D'(11nt) Gm162/26S; guidebox D (10nt)
Cb171	CAAC01000093 66780-66902	AGCGAT TGATCGATTCTTTGTACAG TGTCCGAGGCTTTCTGGCCCGACGT GGCCTGAATAAGGCTGTAACCCAA CGTTTCGGGCCGTTAGGC AGAAGA TGGATGAAT TAGTGCATGTCTGA GCT	Um828/26S; guidebox D'(12nt) Um162/U2; guidebox (11nt) Um67/U1; guidebox D (9nt)
Cb211	CAAC01000012 785346-785410	TGGCAG TGATGATCACAATCCG IT GTTICTGA CAAGCGTT TGACGATA GAAAACCG CTGAGCCA	Am678/26S, guidebox D'(12nt)
Cb238	CAAC01000124 166458-166390	GTCGAT TGATTATATTCTACTGT TCACGTACCGA CTGTT CAGTGGCG GATACAACCTTCTATGAGAC	Um1567/26S; guidebox D'(13nt)
Cb254a	CAAC01000115 1203591-1203510	CCCGT CGATGAGACTACTAAATG ACGAATCCTAA TAAACCAATGGTT TTCAT TGCGGATATGAGGCATTTG TCTGAGCGGG	Am2392/26S; guidebox D'(10nt) Am2385/26S; guidebox D (10nt)
Cb282	CAAC01000016 1421666-1421598	CAAAG TCACCA TTCATAGT TCACAT CATGGCCTTACGAGTGATGT GTCTC CGCCA CGTG TCTCA TTTTG	Um1862/26S; guidebox D'(9nt) Cm138/5.8S, guidebox D (9nt) Um1217/18S, guidebox D (9nt) Um3164/26S; guidebox D (9nt)

I.4 C. briggsae novel C/D-candidates found by blast

name	Sanger	sequence	predicted targets
BICb161	CAAC01000053 160526-160457	GTGCGAT TGAATGTATTGGATAA GTTCGGCTGA TTCATAATT GATG TGTCAACTTTATAACTTGCTGAG CAC	Am416/18S; guidebox D'(13nt)
BICe171	CAAC01000066 338059-337937	GGGCGA TGATCG AAATCT TGTG CAGCGCCGA GCCGTTTGTGCT GGACGTGGCCTGAATAAGGCTG TAACCCAACGTTCCGCCTTTCGC C AGAAGA TGGATGCTTTGCGCA ATGT CTGAGCCT	Um794/26S; guidebox D'(9nt)
BICb246	CAAC01000008 264351-264423	GTGCGCGA TGAAGG ITTA ACCA TCTTCGGCTGA CGAAACGACT GATGCTAGC ATTTTCTATA CTGA GCGCGT	Am862/26S ; guidebox D'(12nt)

The Sanger database accession number and coordinates are given in column two. Gray = double stranded region, yellow = C' and C boxes, green = D' and D boxes, red = the complement nt at the target site is methylated. Bold and underlined letters indicate the antisense elements, italic letters indicate G-U pairings corresponding to the target site. Target sites are from rRNA, U-RNA or tRNA. Letters in bold in predicted targets indicate that the same sequence is targeted by the *C. elegans* orthologs. RPG = Ribosomal Protein Gene.

Table S3: Novel H/ACA box snoRNAs, group I for *C. elegans*

Group I: novel *C. elegans* H/ACA-candidates

I.1 *C. elegans* H/ACA-candidates in INTRONS of Ribosomal Protein-Genes (RPGs)

name	number of seq. clones	NCBI	sequence	predictet targets
Ce80	3	AF003151 27691-27851 rpl24.1	ttagcatgctgttAGAGCTCGTAAGGTATATTGTAATT TTACGAGTGTTGAAGTATTGCAAAAGTAAAGC ATAATCACCTTATGTATGTGTTGGTGCTATATC TTCTAGTTTTTAGAAGTTATACCATCGTTAAGC ATGCCACGTGTGAGTGCGACAAC	P1: Ψ 2237/26S P2: Ψ 1237/18S
Ce352	1	U88168 12759-12627 rpl-15	ctggccacaatgtctgggcaaggtgccctgcaccgcttgagcaacctaacc attgatggctatataaaattcattgagtaacccctgtGAGTTATATAG AACTTCCAGTTTCATATCATTGATACAatt	P1: Ψ 2294/ 26S P2: Ψ 1671/ 26S
comCe5		Z81453 23191-23317 rpl-2	ctgtccttttaactcgccctgaattatttgattctacgccctcaggaaggacc ataggaaattttgcccttaacccccgggtgatagtttgcagaatcggtcattgt gtgcacgaacactt	P1: Ψ 689/18S P2: Ψ 14/U1
ComCe8 (CeN95)		AC087079 11296-11158 rpl27A	ccgctcctatcttggcgctccattgggtaaatggctgtatgttataggaga gatagtagtgcctttggccttcggatctcctcgggtttgtctgcacctcgaca aatgtcactcctcgggttcgagacaatt	P1: Ψ 18/U6 P2: Ψ 1411/18S
ComCe11		Z70684 20611-20481 rps-23	atacagggtccagagtcacctctgagaatatgtatctctcggctgctaggattg ctcgaaaatgaattaggtactttatgcaaacagttcttgcgttatgctcatctgtt cacctcgtttctgacaaaa	P2: Ψ 2558/26S
ComCe17		Z92834 5011-5131 rps-26	ctcacttttaagctccgagactgccgaagagacgaattttatgagacacct agtaaaattatcccgcatttctaagtcaagagcgagtggtcctcctgaatacc cgtgtcacagat	P2: Ψ 130/26S

I.2 *C. elegans* H/ACA-Candidates in INTRONS of OTHER GENES THAN RPGs

name	number of seq. clones	NCBI	sequences	predictet targets
Ce104.1		AL021481 16591-16456	ACGAACTCTTGAGTGCATTTTCGTGAAAAATTTT AAACGAAAATGTCATATTGAGTCATTCTGACA TTAACTGGCCTTACAAGGCGGGTACGCGTAA ATTTTTTGCGTTCCCTCCGTCAGATGCGAGGCCT ACAATT	P1: Ψ 29/18S P2: Ψ 3427/26S
Ce286	2	Z71262 18360-18226	ccccgctctatgtctctccacttgttaatttctggaatggagatttataaga gcgaaaataaaatgtcattagcgggtgctcatctcgTTAATTTTCT CGATATGGCTGATTGGATAATGACTACAatt	P1: Ψ 26/U6 P2: Ψ 22/ 5.8S
Ce356	1	Z49886 3858-3746	aaacgcacaattagaacttgaatgtctgtgattacaatataggctgaaaa cgttctgtttgaagctgactgtttattgctgatggtttatgagtgcatagttg tgcgatagatcaagtaacgaatcgtttcaaagtATTTCGTAATCC TAACACCACGCAAAGGTGCTGATCTCGATTTTT AAACGGTTGTACACAATT	P1: Ψ 2367/26S P2: Ψ 1357/18S
ComCe13		Z71181 22197-22069	atatectcgttataagccggggactagccttctgagttcactagtaaaac gcgaggaaaattatagagacatccagacaccgattatgtgatattcgg cactcgtatgtcccagatt	P1: Ψ 580/18S P2: Ψ 1266/18S
ComCe15		Z71181 20272-20138	ttagcatgtatataatgcccggcaattgttttaattcggccttttagcttgcacgc gatataattatccattgaagaatttttagctgggttctctcattttaaactcatgat ctatcttttaaggaacaatc	P1: Ψ 1058/26S

The number of clones describes their frequency in the sequenced cDNAs. The NCBI GenBank accession number and coordinates are given in column two or three. Purple = box H and ACA, Gray = antisense element Capital letters represent cDNA sequences. The additional sequences completed by Wormbase or GenBank information are in lower case letters. Target sites are from rRNA or U-RNA. Letters in bold in predicted targets indicate that the same sequence is targeted by the *C. briggsae* snoRNA orthologs. RPGs = Ribosomal Protein Genes. Designations given in parentheses refer to Deng et al. 2006.

Table S4: Novel H/ACA box snoRNAs, group I for *C. briggsae*

Group I: novel *C. briggsae* H/ACA-candidates

I.1 *C. briggsae* H/ACA-candidates in INTRONS of Ribosomal Protein-Genes (RPGs)

name	Sanger	sequences	predictet targets
Cb352	CAAC01000118 37316-37183	CATGCCACAATGTCTGGGCAAGGTGCCTGCACCCG CTTGATCAACCTAATCCATTGATGGCTATATAAAT TCATTGATTAATCCCTGTCGAGTTGAATTAGAACTCT TCAGTTTCATCTCATTGATACAATT	P1: Ψ 2295/26S P2: Ψ 1672/26S
comCb5	CAAC01000027 288580-288706	ACGGTCCTCGTTTTCTCTGCCTGATTCATTATCGCTT CAAGCTTGAAATAGAGGACAATAAGAACGTTTGCCT CTTACCCCGGTGTGATAATATGTCAGAATCGGTCA TTGTGTGCAAGTACAAT	P2: Ψ 14/U1
comCb8	CAAC01000129 226919-227059	TTCTCCTATCTTGGCGCTTCCACTGGTGAATGTGGC TGTGTATGTTATAGGAGAAAGTAAGTGTCTCTGG ACTTTCGGATCTCTTCGGTGTGTGCTTGCATCTCG ACAAATGTCATCTCTGGTTCGAGACAATTC	P1: Ψ 18/U6 P2: Ψ 1405/18S
ComCb11	CAAC01000013 60060-60190	AAGCGAGGTCCAGAGTCACCTTTGAGAATAAGTGTC TTTTTGGTGCTAGGATTACTCGAAAATAAATTAGGG ACTTTATGCAAGCAGCTGTTGCATTTTGTCTCATCTGT TTCACCTCCGTTCTACAATT	P2: Ψ 2559/26S

I.2 *C. briggsae* H/ACA-Candidates in INTRONS of OTHER GENES THAN RPGs

name	NCBI	sequences	predictet targets
Cb104.1	CAAC01000274 43115-42975	GACGAACCTGAAAACCTGGGCACTCTGGCTGA AATTTTAAACCACAGTGCTCTAAAAGAGTCATT CTAATAGAGATTTCGGCCTTCTAAGGCGGATT GTGTCAATTTTTGCGTTTCCGTCCGATACGAG GCCTACATTT	P2: Ψ 469/18S
Cb286	CAAC01000112 64711-64851	CCCCGCTCTATGTTCCTCGCCACTCCGTTAAATT ACAGGAGTGGGGATTTTATAAGAGCGAAAATA GAATATCAGGTCATGAGCGGTGCTCATCTTCG TTAATTTTACGATATGGCTGATGGGTTATGA CCACAATT	P1: Ψ 26/U6 P2: Ψ 22/5.8S
Cb356	CAAC01000012 3236947-3237153	AATGCACAATTTAAGAAGTGTAAAATTTGTTT CTCATAGAAAAGCATCTAGGGACGTTTGTCTCG ACATGTTTTTCGTGTAGTAAGTATGATTTTATG AGTGTTCATAGTTGTGCTAGATAAATTGAGGAGA GAAGTGTTCACTAGTTCAAACCTCCAACGCTAC GCCTAAGCGCTGGGTTTGAATTACTTCTATCTT CGCACATA	P1: Ψ 2368/26S P2: Ψ 518/18S
ComCb13	CAAC01000044 1358667-1358796	GTGTCCTCGCTTATAAGCCGGGGACTAGCCGT ATGCTATGTTCACTAGTAAAACGTGAGGAATAAT TATAGAGACAACCAGACACCGTGCAAATTTG ATATGTTCCGTTCACTATGTGTGCCACAATA	P1: Ψ 574/18S P2: Ψ 1260/18S

The Sanger database accession number and coordinates are given in column two. Purple = box H and ACA, Gray = antisense element. Target sites are from rRNAs or U-RNAs. Letters in bold in predicted targets indicate that the same sequence is targeted by the *C. elegans* snoRNA orthologs. RPGs = Ribosomal Protein Genes.

Table S5: C/D box snoRNAs, independently confirmed by Deng et al. 2006 or Wachi et al. 2004; group II for *C. elegans*

II.1 *C. elegans* C/D-candidates independently confirmed by Deng et al.2006 and Wachi et al. 2004 in INTRONS OTHER THAN RPGs

name	number of seq. clones	NCBI	sequence	predicted targets
Ce39 (CeN121)	10	AC024830 40097-40174	CggtggaTGATTCCTATTG CCGTTTACCCTGCTGAGG AAAACCGTGCTTGATACA ACTTGGAAAGGCTGAGC CG	Gm2343/26S; guidebox D' (15nt) Um2654/26S, guidebox D (10 nt)
Ce61 (CeN118)	10	Z66519 5571-5640	gaatcggatGTGATATCCAG TTCTGCTACTGAGTTATT GTGAAGATTAACCTTCC CGTCTGAGATtc	Am1185/26S, guidebox D' (11nt) Gm2498/26S; guidebox D (10nt)
Ce62 (CeN98)	4	AL117204 217925-217834	aagtgcgtgaAGAGAACGTGC CACTGTACTTTGCCATC GGAAGGGCATTGAAATGG AGATATACCTGGCACAGG GCCATCTGAGCActt	Gm20/tRNAlle; guidebox D' (12nt) Cm55/U6; guidebox D (10nt)
Ce63 (CeN27)	2	U41108 18075-18140	CCAATGATGAGAGTTTGC GACTAGGCGGTCTTACA CAATCATGGTGAATTCTAG TCACTCTGATGG(TAC)	Cm982/18S; guidebox D' (12nt) Am1060/26S; guidebox D (11nt) Am31/tRNASer; guidebox D (9 nt)
Ce75 (CeN63)	3	U14635 32685-32622	gtcagtgcgatATTACTTACCG CCACAGGCATAGTGTTTG TGATGATGGTTTATCC GAGAC(TT)	Gm2731/26S; guidebox D' (11nt) Am1205/26S; guidebox D (10nt) Am730/18S; guidebox D (10nt)
Ce118 (CeN24)	1	Z47811 22777-22850	aagcaatgacgaatcgacactcggccc gactcaacctggggcgaa/GAG CTTTTAAACTCAGATGCT T	Gm272/26S; guidebox D' (14nt) Am601/18S; guidebox D (15nt)
Ce139 (CeN109)	6	AF022977 13406-13470	gcgcaatgaaTGTTTAACCATC TTTCGGCTGATCCATGA TGCCAATTTTCAAATACT GAGCGC(A)	Am862/26S; guidebox D' (12nt)
Ce160 (CeN30)	2	Z29094 54636-54714	ggttgctgacgaattactattccaacgc tggatgaACCAAAGTGATTA TTAACCAATCTTTTCTG AGCCAAtc	Am3023/26S; guidebox D' (11nt) Gm2027/26S; guidebox D (12nt)
Ce161 (CeN108)	1	Z49967 6647-6566	gaaaaagtgcgatgaatgaCTTGGA TAAGTTTCGGCTGAAACT TGGTGATGCCAACTTTTA AAACTGCTGAGCACTtttc	Am423/18S; guidebox D' (13nt)

Ce177 (CeN33)	3	AC087079 25978-26054	(AGCCGGGATTCATAGGCT)GGCGATGATTGAGATTGT TCCCACACCGCAATTTCTC CTGATCCACATGAAGGCT AAACTTTCCTTGACGTTCT GAGCC(GC)	Am 75/18S; guidebox D' (9nt) Cm400/18S; guidebox D (13nt)
Ce209 (CeN124)	11	Z72511 19566-19656	gagcggGATGAATGCACGTA TTGCTCTGACACCTTTAT GTTAGCGGTAAATTTCCGT GCCGCGATGATCCACTA GATCTCTGAGCTC	Cm111/U2; guidebox D (9nt) Um2172/26S; guidebox D (9nt)
Ce223 (CeN60)	2	AF040659 16752-16687	gccacgtagtTAGGTTTATTG CTACTCTTGATTA ACTCTC ATGATGACAAGAAAGTAT GATGGC(T)	Am 1514/26S; guidebox D' (11nt)
Ce239 (CeN119)	2	Z46935 8872-8946	Tgtcaatgatgtctaaaaaattactacgatt aattcgaattgctgGAGATCAATC TTATACAATTCTGAGACA	
Ce245 (CeN28)	4	Z81493 23484-23399	egtctggtagGATGAAAACAG GACAGGTTTCGCTAA AAT ATTACCGAATGCCAATA T GTCGAGACACCTTGCTG TCTGAGGACG	Am774/26S; guidebox D' (9nt) Cm2468/26S; guidebox D (10nt)
Ce285 (CeN106)	2	AC006651 16329-16403	gatgatgatgagaattttgatatggttca GACCTCTGAGATTCCG TGATGATGTTTAGAGTTC CTGATC(TT)	Um927/26S; guidebox D' (9 nt) Cm154/U2; guidebox D' (10nt) Um239/18S; guidebox D (11nt)
Ce325 (CeN120)	1	Z49130 12059-12135	AagcgaTGATTAACCAAAA TAACCAATGTTGAGTG ATTGTTGTGATCGAATTT TGTCACATCGCTGAGGC TT	Am3159/26S; guidebox D' (14 nt) Am448/18S; guidebox D (9nt)
Ce372 (CeN123)	3	AL023811 1145-1220	gatctatgatgaGACTTTCACGA CGTCTTCCGATGTAATA CATACCTGTGGAATATCTTT ACGTGAAGCTGAGATC	Cm3071/26S; guidebox D' (12 nt)

II.2 C. elegans C/D-candidates independently confirmed by Deng et al.2006 and Wachi et al. 2004 in INTERGENIC REGIONS

name	number of seq. clones	NCBI	sequence	predicted targets
Ce81 (CeN117)	26	AC024206 3722-3844	AGTTGATGAGA ACTCTAAT CCTTCTCTGAGCGAGAAG GATGGCCGAAGCGGGTTTCG CATTGAGGCATTAAGGT A GACGACAGAGTTCTTCTGG AAACTACTGCCTCGCGCTG ACGTCATGCCTTCGCGGGCT GAATTZGGGCTGATCCTC	Um2417/26S; guidebox D' (10nt) Gm1805/26S; guidebox D (9nt) Am300/26S; guidebox D (9nt)
Ce83 (CeN57)	6	Z81581 20806-20876	tccacatgaTGA TACAACCATAG CATGAGCTGGCAGCAGTGA TCGCTAAATGTCATAGTTA CACAGATGGG(T)	Am 2359/26S; guidebox D (11nt)

Ce138a (CeN50-1)	10	Z68296 4530-4458	ctgtgtatga CGA CAACGT GTTA GG ACATCTGC ACCAACCG TGAAGATTTAACGAAAGTA GTA CTGACACAG (C)	Cm2440/26S; guidebox D' (10nt) Am2448/26S; guidebox D (10nt)
Ce138b (CeN50-2)	1	U42830 28111-28183	ctgtgtatga CGA CAACAT GTTAG GGACATCTGC ACAAACCG T GAAGATTTAACGAAAGTAG TACTGACACAG	Cm2440/26S; guidebox D' (10nt) Am2448/26S; guidebox D (10nt)
Ce230 (CeN15)	8	U29096 17604-17690	igtccgtgatgacaaCATACATACA CCATTACGATCTCTGA AGA CTTCGTGCTGATCA TGTATC CATGCAAC CCAACTGAGG ACA	Cm1502/26S; guidebox D' (13 nt) Um3441/16S; guidebox D (10 nt)
Ce243 (CeN111)	3	U41992 15703-15771	aagcagtgatgattttatag tcagctt atctt CGGATT TGATGAGAAATTT CGCCCTATCAGA GCTT(T)	Am872/26S; guidebox D' (9nt) Gm963/26S; guidebox D (12nt)
Ce246 (CeN70)	1	Z81116 7181-7110	gtgcgcgatgacTCTTT ACCATC TTTCGGGGCATA ACACTCT TGATGATAACATACCCATT TGCTGAGCGC (T)	Gm860/26S; guidebox D' (13nt) Um17/tRNA ^{Ala} ; guidebox D (10nt) Um304/26S; guidebox D(9nt)
Ce252 (CeN122)	2	U64858 19398-19473	TgggaatgatgacCTTCTGT GTAG GAACTCTCAATGA GTGACTG TGACATAAAAAT GCAGTAA ATTCACTG acccca	Am2429/26S; guidebox D' (11nt) Um247/18S; guidebox D (10nt) Um668/18S; guidebox D (9nt) Um310/18S; guidebox D (9nt)
Ce271 (CeN44)	6	Z48717 2829-2759	gacaatgataGGATAACCTAG AG TCTCTGA ACCATTT CGTGT TGAACAATGCTCTTTGTCT GAGTC (AG)	Um1298/18S; guidebox D' (10nt) Gm66/U5; guidebox D (9nt) Gm1313/26S; guidebox D (10nt)
Ce304 (CeN114)	10	Z81143 22420-22359	gtgcaaggatgaAAA GA ACT CT CTCACTGATAGATGATGTC TTCTTACATTATCAGAGCA C(T)	Am395/26S; guidebox D' (10nt) Um1981/26S; guidebox D (10nt)
Ce354 (CeN14)	1	AC006654 7239-7310	ctgcggtga CGATCAACTCTTAC CTACTATGA CAAAAACAA T GGTTAGACGTTACTCGTAC TGCTGAGCAGT	Gm1985/26S; guidebox D' (11nt) Um2841/26S; guidebox D (10nt)

The number of clones describes their frequency in the sequenced cDNAs. The NCBI GenBank accession number and coordinates are given in column two or three. Gray = double stranded region, yellow = C' and C boxes, green = D' and D boxes, red = the complementary nt at the target site is methylated. Letters in parenthesis indicate that the cDNA is longer than the snoRNA sequence. Bold and underlined letters indicate the antisense elements, italic letters indicate G-U pairings corresponding to the target site. Capital letters represent cDNA sequences. The additional sequences completed by Wormbase or GenBank information are in lower case letters. Target sites are from rRNA, U-RNA or tRNA. Targets verified by the modification study of 26S rRNA (Higa et al. 2002) are shown in red letters. Letters in bold in predicted targets indicate that the same sequence is targeted by the *C. briggsae* snoRNA orthologs. RPGs = Ribosomal Protein Genes. Designations given in parentheses refer to Deng et al. 2006.

Table S6: C/D box snoRNAs, whose orthologs in *C.elegans* have been independently confirmed by Deng et al. 2006 or Wachi et al. 2004; group II for *C. briggsae*

II.1 *C. briggsae* C/D-candidates whose orthologs in *C.elegans* have been independently confirmed by Deng et al.2006 and Wachi et al. 2004 in INTRONS OTHER THAN RPGs

name	Sanger	sequence	predicted targets
Cb39	CAAC01000067 730855-730933	GGCTGTGATGATTTCTACTTGCC GTTTACCGTCTGAGGAAAACCG TGCTTGACGATTTTGAAAAATTAG GCTGAGCC	Gm2344/26S; guidebox D` (15nt)
Cb61	CAAC01000012 2466799-2466864	ATCGGTGATGTGATATCCAGTTC TGCTACTGAGCGTTGTGAAGAT TAACCTTTCCTCGTCTGAGAT	Am1185/26S, guidebox D` (11nt) Gm2499/26S; guidebox D (10nt)
Cb62	CAAC01000004 400480-400568	TATGCTATGAAGATAGTGTGCCA CTGCACCTTATCCATCGGAGGAA TTTGAAAATGGAGAAATTCTAGGC ACAGGGCCCATCTGAGCATA	Am770/18S, guidebox D` (9nt) Cm55/U6; guidebox D (10nt)
Cb63	CAAC01000054 685073-685009	CTATGATGAGAGTTTGCAGACTAG GCGGTATACATAATCATGGTG ATTCTAGTCACTCTGATGG	Cm974/18S, guidebox D` (11nt) Am1060/26S guidebox D (11nt) Am31/tRNASer; guidebox D (9nt)
Cb75	CAAC01000062 91988-92051	GTCAGTGAAGATAATACTTACCG CCACAGGCATAATGTTTGTGATG ATTGGTTATTCCGAGAC	Gm2732/26S; guidebox D` (11nt) Am1205/26S; guidebox D (10nt) Am724/18S, guidebox D (10nt)
Cb118	CAAC01000005 984668-984741	AGACAAATGAAGA AATTGCACCT CGGCCCGACTCCAAACCCTGGGGG CGAAATGAGCTTTTAACTCAGAT GTCT	Gm272/26S; guidebox D` (14nt) Am595/18S; guidebox D (9nt)
Cb139	CAAC01000008 264346-264426	CTTGCCTGCGCGATGAAGGTTTA ACCATCTTCCGGCTGACGAAACG ACTGATGCTAGCATTCTATACT GAGCGCGTAGG	Am862/26S, guidebox D` (12nt)
Cb160	CAAC01000045 1007383-1007309	TTGGCTGTGAAGATCACTATTCCC AACGCTTGGATGAAAATTACTG ATTATAATCCAATCTTTCTGA GCCAA	Am3024/26S; guidebox D` (11nt) Gm2028/26S; guidebox D (12nt)
Cb161	CAAC01000005 255907-255825	AAATGTGCAATGACTGACTTGGGA TAAGTTCCGGCTGAACGTCACA CTTGATGCCAACTTTAAGANTT GCTGAGCACATTI	Am416/18S; cguidebox D` (13nt) Um119/U4; guidebox D (10nt)
Cb177	CAAC01000129 214794-214719	GGCGATGATTGAGAGATTCCCAC ACGCAATTTCTACTGATCCGCAT GAAGGTTAAACTTCTTGGACG TCTGAGCC	Am75/18S; guidebox D` (9nt) Cm394/18S; guidebox D (13nt)
Cb209	CAAC01000141 769783-769871	AGAGCGGTGATGAAATGCACGTAT TGCTCTGACACCTCTTATGTTAGC	Um259/26S; guidebox D (10nt,) Um2397/26S; guidebox D (9nt)

		GGTAAATTTCCGTGCCG CGATGA GTCCAAT GGATCTCTGA GCTCT	
Cb223	CAAC01000107 39897-39959	GCCATATGATTI AGGTTATTTG CTACTCTTGATGAATCA TGATGA CAGAAATGTATGATGGC	Am1515/26S; guidebox D` (11nt)
Cb239	CAAC01000012 2984890-2984823	TGTCAA TGATGT CCTAATCTACGA TTTAAITCGAAITGATGAGAT GAATCACTGAAAACTGA GACA	Am491/26S; guidebox D` (10nt) Am758/26S; guidebox D` (9nt)
Cb245	CAAC01000115 854445-854531	CGTCTGG TGAGGATAGAAAAAGG ACAGGTTTCGCTAA AATACTAGC CGAACGCCAACAT TGTAGAGACAC CTTGGCTGTCTGA GGACC	Gm3364/26S; guidebox D` (9nt) Cm2469/16S; guidebox D (10nt)
Cb285	CAAC01000133 8586-8663	GACGGTGA TGAAGAATTTTATTG ATATGGT GTCAGACCTCTGA GA GTTCCG TGACTGAGGATTAGAGT TC CTGA GTC	Cm9274/26S, guidebox D` (9nt) Cm154/U2; guidebox D` (10nt) Um3384/26S; guidebox D (10nt) Um2525/26S; guidebox D (10nt) Um386/26S; guidebox D (9nt) Um905/26S; guidebox D (9nt)
Cb325	CAAC01000012 2717553-2717628	AGGCCG TGATTACCAAAATATA ACCAAATGTTGA GTGA TTGTTT GTGAGCA TTT GTCACIATCGCTG AGGTCTI	Am3160/26S; guidebox D` (14nt) Am442/18S; guidebox D (9nt)
Cb372	CAAC01000141 1446841-1446917	GATCGATGATGAGACTTTCACGA CGTCTTCCGA TGAAATATCAAA GCTGTGGATATCTTTACGTGAAG C TGA GATC	Cm3072/26S, guidebox D` (12 nt)

II.2 C. briggsae C/D-candidates whose orthologs in C. elegans have been independently confirmed by Deng et al.2006 and Wachi et al. 2004 in INTERGENIC REGIONS

name	Sanger	sequence	predicted targets
Cb81	CAAC01000016 1102272-1102429	AGAGGAGTT TGATGA GAACTCTAAT CCITCTCTGA GCGAGAAGGATGG CCAAAGCGGGTTTCGCATTGAAGGC TTAAGGT AGACGA AAGAGTTCTTCT GACGACTACTGCCTTGCCTGAAG CCATGCCTTCGCGGGCTGA AATTITG GGTCTGA TCCTCT	Um2418/26S; guidebox D` (10nt) Gm1806/26S, guidebox D (9nt) Am300/26S; guidebox D (9nt)
Cb83	CAAC01000016 2019786-2019856	TCCATG TGATGA TAAAACTATAGC GTGAGCTGG CAGCAG TGATCG CTA AATGTCATAG ITACA CTGA TGGG	Cm1562/18S; guidebox D` (9nt) Am2360/26S, guidebox D (11nt)
Cb138a	CAAC01000068 5095118-5095045	CTGTGTA TGACGA TAATATGTTAG GGACATCTGC ATTCA TTTGTGATGA TTTAA CGATAGIAGTA CTGA CACA G	Cm2441/26S; guidebox D` (10nt) Am2449/26S; guidebox D` (9nt)
Cb230	CAAC01000069 837614-837700	TGTCCTG TGATGA CAACATACATAC ACCATTACATCTCTGA AGACTTC GTG TGATCA TGTATCC ATGCAAC ACCAACTGA GGGCA	Cm1503; guidebox D` (13nt) Um3442/16S; guidebox D (10nt)
Cb243	CAAC01000028 746138-746206	AAGCCAT TGATGA TTTTATAG ITCA GCTAA TCTACGGATT TGATGA TAAA TTTCGCCCTATCAGA GCTT	Am872/26S; guidebox D` (9nt) Gm963/26S; guidebox D (12nt)
Cb246	CAAC01000140 279342-279411	GCGCGG TGAATTCATTACC ATCTT TGGGGCATA TCAATCC TGATGAT	Gm860/26S; guidebox D` (13nt) Um1076/18S; guidebox D (9nt)

		AACATAACC TATGCTGA GCGC	
Cb252	CAAC01000054 806865-806941	TGGGAATGATGACTTTCTGTTGTAG GAA CTCAATGA GCGACTGTGATA TAAAAATGCAGTAATCTCA CTGAC CCCA	Am2430/26S; guidebox D' (11nt)
Cb271	CAAC01000006 1386652-1386582	GACCATGATAGGATAACCTAG AGT CTCTGA ACCATTTCTGTT TGCACA AACAA TGCTC TTGTCTGA GTC	Um1292/18S; guidebox D' (10nt) Am712/26S, guidebox D (10nt)
Cb304	Megablast(traces): 58349734 lbb07g02.g1 595-535	GTGCAAGGATGAAAAGAACTC CT CACTGA TAGATGATGTCTT CCCTAC TTATCAGA GCAC	Am395 /26S; guidebox D' (10nt) Um1982/26S; guidebox D (10nt)
Cb354	CAAC01000009 150398-150326	ACTGCTGTGACGATAA TCCTTAC C TACTATGA CAAAAACAATGGTTAG ACGTTACTCGT ACTGTCTGA GCAG T	Gm1986/26S; guidebox D' (11nt) Um2842/26S; guidebox D (10nt)

The Sanger database accession number and coordinates are given in column two. Gray = double stranded region, yellow = C' and C boxes, green = D' and D boxes, red = the complement nt at the target site is methylated. Bold and underlined letters indicate the antisense elements, italic letters indicate G-U pairings corresponding to the target site. Target sites are from rRNA, U-RNA or tRNA. Letters in bold in predicted targets indicate that the same sequence is targeted by the *C. elegans* orthologs. RPG = Ribosomal Protein Gene.

Table S7: H/ACA box snoRNAs, independently confirmed by Deng et al. 2006 or Wachi et al. 2004; group II for *C. elegans*

II.1 *C. elegans* H/ACA-candidates independently confirmed by Deng et al.2006 and Wachi et al. 2004 in INTRONS OF RPGs

name	number of seq. clones	NCBI	sequence	predictet targets
Ce170 (CeN126)	5	U00036 11553-11684 rpl-6-	acagcatcgaaaatggacgGACTTCCCGATGGATCGTT TCGTATAATTTGGTGCAAA ATAGTA GAGAGA CGCAGTGTACTCTTCTTACGTTACCTGTATC	P2: Ψ 1156/18S

			TGGAGAGTGTCAAGCGTTTCCCACAATT	
Ce175 (CeN93)	2	Z68315 14113-14246 rpl-26	ctgtttccattaagtaGTCCCGTACGTTGAAATTTFCACG TACGGTTTGGACAATATGGAGAAATGAATGTT ACTCTTTTTGCAATGACGCTGAAACATATTTTC GCTTTGTTAGCCATAAGTTAAAACAATT	P1: Ψ 2417/26S P2: Ψ 2483/26S
Ce182 (CeN99)	1	U00067 26061-26191 rps-12	gttccactattttcaacgtcgccgggtctagaatcgatgacccaataagc tggtagataagttgttactctgccacacgtgactggtatcatGCTGTAT GTGTTCCAAAGAttttacaacaatt	
Ce192 (CeR-4; CeN100)	3	U00036 11144-11276 rpl-6	aaacgaggtccagagtCACCTTTTCAGCAAAATGCAGT TAGGGTGTAGGATTTCTCGAAATGAAATTG GTCGTATTATGCAAGTAGGGCTTGTCTTTGCGC TCCCCGACTTCACCTCATTCCCAAACAAtt	P2: Ψ 2558/26S
Ce210 (CeN96)	9	AC006729 13571-13352	tcgacatgtgactAGCGATCCTCTTCGGGGTTGATTGC TTTTCTTAGTGGAGCATCGGGGGCTTCTGTAA AGTTGACTCCGATCCACCTTGTCTGTATACCAAC AGTCTGTGTGGCCCTTACCCTATTTGAGATG CCCGGGCTGGATTGCATATTCCTTATCCTTCCG TAGATCCTATGGGTCCGTGACGGTTAGGACAA ACCATGCAAATTACAAT	
Ce236 (CeR-6; CeN90)		U80953 5475-5603 rps-29	gaatcgatgtccaTACGAAAAGGCTCTTTACCTTT TGACGTTTAGTtaaatttgcgaaataaattgatgtctgaagacatgt gcttcatattttagtctcatgttcaagatcagcaacaac	P2: Ψ 2977/26S
Ce248 (CeN84)	1	U88168 12429-12300 rpl-15	gttcctcagtgctgggcaaaAGCAGACTGTTTTAATAGT ACTGACTTAATCCACTGATGGCTATAGAAA CATTGTGTAATCCCCGAACACCTTGTGGTGTAT TGGATTCATGACATTGTGACAATT	P1: Ψ 2294 / 26S
Ce280 (CeR-8, CeN82)	2	U41534 6548-6414 rps13	tacgctctcaaaagcactggtttagcagactgtccatgccagccgtc aaaatgagcaaatgaaatatctgttttgggtgaggtgtaactgtattagatt agatctcaataacacgatgacatt	P1: Ψ 2098/26S P2: Ψ 3035/26S
Ce283 (CeN79)	1	U00036 11930-12065 rpl-6	gcttttgcattgaaaaggacgggctatctttatgattgttctgataatttga tgcgagataatagagaGGCGCACTGTTACTCTTCATCAC TTTTTCTGTGAACGGAGAGTGTCAAGCGCTTCC ACAATT	P1: Ψ 1523/ 18S P2: Ψ 1156/ 18S
Ce345 (CeN92)	1	U00067 25691 -25825 rps-12	atcttcacactaccaattatatcggaagaTTTTGAAGTCATAGT TTTCCTATCGTAGTGTGCAATAAAAACCGTTCT ACTGCCACACGGGTACTGGCCTTGAAGCTGTA TCGGTTCCAAAGTTGTTGAAACAATT	
comCe6 (CeR-3, CeN87)		AF003139 3611-3745 rpl-7	aatgctctcaaaagcactggttttaggatccactattatccaagccagccgtc aaaactgagctataagaattatctgttttgggtgaggtgtattcaaticagaat gcgtctcaataacacgatgacaatt	P2: Ψ 3035/26S
comCe7 (CeN78)		AF003151 28272-28431 rpl-24.1	ttagcatgctgttagagcttgaaggtatatgtatttacgagtggtgaagtatt gcaaaagcaaaagacgggcacaattgccatgtgttgattattgcttcaagtt atttgaagctgtaatacaataagcatgctcgtgtgaagtcggacaatt	P1: Ψ 2237/26S P2: Ψ 2484/26S
comCe9 (CeN88)		AC087079 10925-10785 rpl-27A	atttctctgcttggcgttccactggtgaatgtggtgtgtatttacgagaga caagtagcgcctaacggcttggatctcttgggtgttcttgaatttca caaatgtcctctctgggttcgagacaatt	P1: Ψ 18/U6 P2: Ψ 1411/18S
comCe12 (CeN110)		U80953 5818-5944 rps-29	tgagcagatgtccattacgcgaatgcctgtgcttttcgacgttttagtttagctg caagatagaattgatgtctcgaagacaggtacatcagcttttaggttctgtt aagatcagcaacaac	P2: Ψ 2977/26S

II.2 C. elegans H/ACA-candidates independently confirmed by Deng et al.2006 and Wachi et al. 2004 in INTRONS OTHER THAN RPGs

name	number of seq. clones	NCBI	sequences	predicted targets
Ce23 (CeN55)	26	Z68160 8479 -8607	cccgcgctagaaacTCAGCGGTGTTTTGTCTTTATGA TCATGAGCTGGTAGCAGGTGCAATATTGATTC GGAGTCTTACCGGCGTCCACCTTCTGAAGGT GTGCGTAAAAGTTCATCCGAACAATT	P1: Ψ 6/U4 P2: Ψ 2519/26S
Ce25 (CeN48)	8	U29380 25865 -25740	aatgcacacagaaaGTCGAGATTGCCGGCTCAAAGG CTTTATCGTTGATTACGTGTGCTATAACAACGC CATAGGTATCATTCTTCGTCTTCTAGGCGCGG AACATCTAAATATGGCTACAATT	P1: Ψ 2401/26S P1: Ψ 127/18S
Ce36 (CeN46)	1	Z68297 6183-6302	acgaCTGCAACCTGCTTTCGGAACCTTACCCTCT GCGGTACTTGTAGTGCTATATGACGCTGGGCC ATCCGTGTGCGTGAATTTAATTGAACTAGCAC TCCGTTGGTCACCGGATAATT	P1: Ψ □□□□ P2: Ψ □□□□ P2: Ψ □□□□
Ce48 (CeN58)	14	U28940 16314-16453	actgcgtctctcaaccCGGACAACCTCGCAACTTGTTC AATGGTCAGTTCGACTGTTAGAGACGCTAAAT AAGAAAAATGGCGGATTCGCTAACGTCGCGTC CCATGACCGGAGTTTGAAGTAGGCCGCTGAA CAATT	
Ce57 (CeN39)	29	Z83217 38440-38308	ttatggcgaTAGGAACCAGGTCATGTTGTACGTG ATTTGGGCCGACATCCCGCCGAAATAGTCCT GCGAAGATCTAAGGTCGCTTCTGGATGGATT GCCACCGGTGCACACCATCTTCGTGCACAATT	P1: Ψ 2992/26S
Ce58 (CeN86)	3	U40800 21389-21266	gcctgcaactattaAGAGATTTGCCTCCCGTGGGGCA CGCCTTTTTCGTGCGAAATAAAACATGTCCT TTATTCCCGCTCCTGGATTGTGTTTCTTGCGCG ATGATATGGCTATGACAATT	P1: Ψ 499/18S
Ce141 (CeN38)	7	Z35663 12289-12152	taecgctcatttcaattgcaAACGTGATTCTAATGTTG GCGATTCAGCGTATTTCTGACGCAAAATTGATA ACTTCTCCATTGACGCTCTAGTCAGACTAAACTG GCTCGGATACAATTAGGGAGTTTACTT	P1: Ψ 1198/26S P2: Ψ 230/18S
Ce149 (CeN125)	4	AL032637 46348-46211	ccaccacgcaCAAATTCCAATTGTGTGTAACATT CAATGCAATTGAGCCGACGCCGTGGGAAATCA CTTTCGTGGAACCAATTGATCCCACGCTCGTTA CTGTTAATGATTGTGTTTGCACGTGGTTACA ATT	P2: Ψ 940/26S
Ce162 (CeN43)	3	AF000263 5550-5521	gtgcccgtcttggcccgatcaactttaatagttatgacggttccgactcg GGAAATAAGATTCTGCATAACGACGGAAATT TCAGAGTTTGTCTGAATGTCTCCAGTTCGATGT GCAATACAATT	P1: Ψ 1996/26S P2: Ψ 1667/18S
Ce166 (CeN126)	1	Z74028 8885-8755	aaagcagtcgtcaGTGGCGCAAGCGATTTCCCATGC GCTTGTGCCTAATCTTTGACTGCGAGATAAAAA TGTCAGAGTCAAGCGGTCCGCTATCTGTGTAGC ATTCTGTTCAAGATTGACTGATAATT	P1: Ψ 3220/26S P2: Ψ 2828/26S
Ce222 (CeN101)	1	Z71181 21221-21092	gtaacctcttataagccgggactagcatttgtaagttcactagtaaat gagaggtaaagcatagagacaaccagacacCGAGAATGTTTTG ATGTTTTCGGTCATTTGTGTGTCCCAAAAT	P1: Ψ 580/18S P2: Ψ 1266/18S
Ce244 (CeN83)		Z79754 35280-35505	ttccacactccttaagctAGTTTGACTGTGATTGTGCATT TTAGATCGCTTCATGAGTTCGCTGCGTTTTGCT GTGAATTCATTGTTGCCCTAATTTGTATAGTCA TGGGTGTCAAATTGGCGAGTTACGTGTGGTAA ATGGAATGACGATCAAATTTTGTCTGTGAACTT TGCCGTAGATGTGATGCTGTTTGTATAGATT GATAATGATTGTCGAACAATT	P1: Ψ 2369/26S
Ce273 (CeN85)	3	Z49886 1728-1511	aagcacaacttaagaactgcGAAATCTACACATTCTTGG CTCTTCTTAGTGCCTTTTGCAGTTCAGATTCT	P1: Ψ 2367/26S P2: Ψ 1422/26S

			GCCAAGTTTTGTGTTTCATGGTTACGCGAGTGTC ATATTTGTGCTATATAAAAAATCGTCTCACAGT AAATTATAATAGTTAGAGTATCTAAAGTCGCG CTAAGGCCCGATATTCTATTTTTCTGGTGTG AACGATGACAATT	P2: Ψ 1392/18S
Ce309 (CeR-9; CeN41)	4	Z92817 26676-26814	gcatgcacctgcactCTACGCCTTTCCTTCAATGGGT TGGTATGATTTAATAAGGATGCAAGAGAAatagta gggaaGTTCGAAGACTTGCAGATTGCTTCCACG GCTCCGCGAGTTCATAAAGTCACTCACTCACT	P2: Ψ 513/18S
Ce323 (CeN81)	1	Z72507 33208-33334	tgctgaagagtAGTCATTTGTATACGTGATACACTTA TACAGAGTTACACTTTTCGTATATAAGTGCTTC TTCTCGTTGGAGTTGTTTATTTAATGAGCAATT ACCTCTAAACTGAAAGCAACAATT	P1: Ψ 2361/26S P2: Ψ 1443/18S P2: Ψ 55/5S
Ce375 (CeN94)	1	U53336 25600-25725	atatctctgctctcacggttcatctgtgagaagctcaagaactgcaatag aagtctagctcgagatgcgtGTGCCGTTTTGCTTTAATGC AATATGGTTCCTTTCTCCTCGGGACAGTT	P2: Ψ 69 / U6
ComCe14 (CeR-7)		Z71181 20712-20577	atggcatgtatataatgcccgttgatgatttagtcagccgttagcttgcacgc aaaattatttctattgaagatttattcgtgctgactcggtcatattcagctctatga ttttctgaaattggtacatt	P1: Ψ 1058/26S P2: Ψ 3217/26S P2: Ψ 1718/18S
ComCe22 (CeN104)		U53336 7829-7959	ctgcaatgtctcagtcaccttggttctccgagccgaaagaagtcactagc tgaaaaagagtttatactctgatcacacagtaacattgcaataaaagcttagctc gagatcgtgtgccgttctcttttaagcagatcgtgtcctttctcctcgggac aatt	P2: Ψ 69/U6

II.3 C. elegans H/ACA-candidates independently confirmed by Deng et al.2006 and Wachi et al. 2004 in in INTERGENIC REGIONS

name	number of seq. clones	NCBI	sequence	predictet targets
Ce27 (CeN49)	18	AL132949 214880- 214746	caccgcctctCTACCAAACACTTGCAAGTTCTGTTTA TTGCAAGTGCATGGAAGAGGCGAATAGAAAAAC GGAATGATGTCCACTCCTTCGATTATCGTTCAT TGGATTGCGGGCACTTTACCTCGTTCGACAATT	
Ce87 (CeN51)	2	Z47811 6577-6711	gcgtgagtaCTGGCTGTTTGTGTCTCCGCCATTGCC AATCAGCTGTCATTAACCACGCAATACCGTAC AGAGGTGCTAAATTACCGTGAAAACCACTTTA AAAATTGGTCACTCGGAGGAGGCACCTCAACA TTT	
Ce105 (CeN66)	6	Z49969 14476-14605	aacgcacgcttaTTTCGCGCCGCAAGTTTTGCAATGA CGATGTGGCTAAAGTGTAGTGCAATATGAGCT CGCTCACGGCGTTGCGGACCATAGTCTGAACA CGGTTCCGCTTTATGTGAGTGAAACAATT	P1: Ψ 1435/18S P2: Ψ 1361/26S
Ce176 (CeN36-1)	5	Z11126 13110-13240	atategctctcagctccatGCCGATGTAAAAAAGTCAGT GTGGCGTTTTTCATGAGCGGAAATTA TCACTGTT CCAAAAACAATTGCTAGTCTCCTGTGAGCTA ATGATCACCTGATGGTTCAGACACTT	P1: Ψ 3056/26S
BICe176 (CeN36-2)		Z79602 7829-7959	atategctctcagctccatgcagacgtgaaaaagtggtgtggtgttctatg agcggaaattaacattgttccaaaaacaattgctagtctctgtgagctaag atcacctgatggttcaaacact	P1: Ψ 3056/26S

The number of clones describes their representation in the cDNA library. The NCBI GenBank accession numbers and coordinates are given in column three. Purple = box H and ACA, Gray = antisense element. Capital letters represent cDNA sequences. The additional sequences completed by Wormbase or GenBank information are in lower case letters. Target sites are from rRNAs. Letters in bold in predicted targets indicate that the same sequence is targeted by the *C. briggsae* snoRNA orthologs. Designations in parenthesis denote the nomenclature of Wachi et al. (2004). RPGs = Ribosomal Protein Genes. Designations given in parentheses refer to Deng et al. 2006 (“CeN”) or Wachi et al. 2004 (“CeR”).

Table S8: H/ACA box snoRNAs, independently confirmed by Deng et al. 2006 or Wachi et al. 2004; group II for *C. briggsae*

II.1 *C. briggsae* H/ACA-candidates independently confirmed by Deng et al.2006 and Wachi et al. 2004 in INTRONS OF RPGs

name	SANGER	sequence	predictet targets
Cb170	CAAC01000078 622936-623070	AAATTTGCATCGAAAAGGGACGGGGTTTCCTACTG GATTGTTCCGTATAATTTGGTGCGAAAGCA TAGAG AGCCGCAGTGTACTCTTCATCACAGATTTTGTGAA CGGAGAGTGTCAAGCGGTTCCCACATTC	P1: Ψ 1517/18S P2: Ψ 1150/18S
Cb175	CAAC01000005 191849-191717	CTTCCCATTCAGTAGTCCCGGACGAATTAGAATTTA GCGTACGGTTTGACATAATGGGGAAATGGA CTTT ACTCTTTTGCAGCGAAGTTGATCCTTATGATCTCTT TGCTAGCCATAAGTTTAAACAATG	P1: Ψ 2418/26S P2: Ψ 2484/26S
Cb182	CAAC01000041 151470-151599	GTTCCACTTGTATCTAGAAATCATAAGTTGTAGTT ACTTTGTGATACAAATAGGTGGTATAATGATTGTTTC CTCTGCCACACGTGTACTGGCTTATGCTGTATGAG TTCCAAAGATCTACGAACAATT	
Cb192	CAAC01000078 622532-622666	ATACGAGGTCCAGAGTCACTTTTTGGATATAATTA CTAATTCGGTGCTTGGATAACTCGAAAATAAAATTG GTCGTATTATGCAAGTAGGGCTTGCTTCTGCGCTCC CCTCCTCACCTCATTCCCATACATTC	P2: Ψ 2559/26S
Cb210	CAAC01000009 565206-564987	TCTACACGTGATTAGCGGTCCTTTCGGGGTTGACT GCTTCTCATTGTGGAGCATCGAGGGCTTCTATTA GTTGACCTTGGTCCACCGTGTCTGATACCAACAGTC TGTGTGGCCCTTAATGCTACTTGAGATGCCCGGGC TGAATTGCATATTCCTTATCCTTCCGTAGATCCGAC GGATCAATGACGGTTAGGACAAAACCATGCAAATTA CAATA	
Cb248	CAAC01000118 36984-36854	TATGCCACAGTGTCTGGGCAAGTAGGCTGTTTTTA ATAGTACTAACTTAATCCACTGATGGCTATAGGAA GCATTGTGTAATCCCCGAACACCTCTGTGGTGTATT GGATTCATGACATTGCGACAATT	P1: Ψ 2295/26S

Cb280	CAAC01000101 188656-188522	TATGCTCTTTAAAAGCACTGGTTATAGGACTCTGAC TTGTCCATGCCAGCCGTCAAATGAGCTATATAGAA TATCTTGTITTTGGGTGAGGTGTAATTGTATTTAGAT TAGATCTCAATAACACGATGACAATT	P2: Ψ 3036/26S
Cb283	CAAC01000078 623323-623455	TAGTGCATCAGAAAGGGACGGGGTTCCAGTTGGA TTGATCCGTATAATTTTGATGCGAAAGCATAGAGAG GTGCAGTGTACTCTTCATCACGGATTTTGTGAACG GAGAGTGTCAAGCGCTTCCCACAATT	P1: Ψ 1517/18S P2: Ψ 1150/18S
Cb345	CAAC01000041 151102-151228	TCAGCACATAAATACGGAGAATTTCCGAAGTCGATA TTTTCTAGTCGTAGTGTGCGATATAAACCGTTCTAC TGCCACACGGGTACTGGCCTTGAAGCTGTATCGGTT CCAAAGTTGTTCCGAACAATT	
comCb6	CAAC01000016 1050031- 1050165	GTTGCTCTTCAAAGCACTGGTTTTAGGATCCATTA TTATCCAAGCCAGCCGTTAAAACCTGAGCTATAAAA AAAATCTTGTITTTGGGTGAGGTGATTCAAGTCAG AATGGATCTCAATAACACGATGACAATT	P2: Ψ 3036/ 26S
comCb7	CAAC01000129 1369405- 1369566	TAGTGCATGCTATTAGAACTCGTAAGAACTTCGTA ATCTTACGAGTGTGCAAGATATGCAAAATAAAAAG CATGGGCACAAGTATCATGTGTTGGTATCATTGTTT CAAGTTATTTGTTGCTATGGTATCGATAAGCATGCT ACGTGTGAAGTGCACAATT	P1: Ψ 2238/26S P2: Ψ 1578/26S
comCb9	CAAC01000129 227294-227435	TTATCTCTCGTCTGGCGCTTCCACTGGTGAATGTG GTTGTGTATGTTACGAGAGGAAGTAAGTGTCTTTT AGACTTTCGGATCTCTTCGGTGTTCCTTGAATTT CGGCAAATGTCATCCTCTGGGTTTCGAGACAATT	P1: Ψ 18/U6 P2: Ψ Ψ 1405/18S
comCb12	CAAC0100006 849609-849735	CACGCAGGTGTCCATTACGCGAAGACCAGTGTCTTA CGACGTTTAGTTTAGCTTGCAAGATAAACCTGACAT CTCGAAGACAGGAGTATCGTTTCGTAGAGCTACTGT TCAAGATTGGCAGACAATT	P2: Ψ 2978/26S

II.2 C. briggsae H/ACA-candidates independently confirmed by Deng et al.2006 and Wachi et al. 2004 in INTRONS OTHER THAN RPGs

name	NCBI	sequences	predictet targets
Cb23	CAAC01000124 375013-375142	GCCGCGCCTTTGAAACTCAGCGGTGTTTGTAT TAATGATCATTAGCTGGTAGCAGGTGCATAAGC GTTTCGGAGTCTTACCGGCGTTCACTTCCAAA GGGTGTGCGTTAAAAGTTCATCCGAACAGTT	P2: Ψ 2520/26S
Cb25	CAAC01000012 72878-72753	TCCGCACGCTGAAAGTCGAGTGAGCCTGCTCCA AAGGCTCTTTCGTTGATTATGTGTGCCAGAACA ACGCCATAGGTATCATTCTCGTCTTCTTAGGC GCGGAACATCTAAATATGGCTACAGTT	P1: Ψ 339/26S P1: Ψ 1145/18S
Cb36	CAAC01000028 1870686-1870805	ACGACTGCAACCTGCTTTCGATACATTATCGTC TGCGGTACTTGTAGTGTAAATGAATGTGGGCC CTCCGTGTGCGTGTGAACATAATGAACTAGCAC TCCGTTGGTCACCGACAATC	P1: Ψ 1076/□□ P2: Ψ 338/18S P2: Ψ 683/26S
Cb48	CAAC01000012 1315842-1315982	CCCCTGCTCTCCAACCCGGACAACCTCGCAACA TGTTGCAATGGTCTGTTCCGACTGTTAGAGACGC TAGATAAGAAAATTGGTGGATTTCGCTAACACCG CCGTCTATGACCGGAGTTTGTATAGTAGGCCCG TGAACAATT	
Cb57	CAAC01000028	ATAGGCGGATAGGAACCAGGTCATGTTTGTATG	P1: Ψ 2993/26S

	1543885-1544016	TGATTTGGGCGGACATCCCCGCCGAAAGAAATT CGTGAAGATCTAAGGTCGCTTCTGGATGGATT GCCACCGGGTGCACACCATCTTCATGTACAATT	
Cb58	CAAC01000118 97064-97188	TTGGCAGCGTTGTTTGAGAGTTTACTCCCCTGA GGAAGCATCTATTTATCGCTGCGAGATAAATA TGTCCCTTATCCCGCTCCTGAATTTTGTTCCT GCGCGATGATGCGGCCATGACAATT	P1: Ψ □□□□ P1: Ψ 98/5.8S P2: Ψ 112/18S
Cb141	CAAC01000088 233028-233168	TACGCGTCTTTTCATCCAATTGTCAATGTGTAAT CCAATGTTGATGATTCAGCGAATTCATTCAGAC GCAATACTGCAACTTCTCCATTGACATCTAGT CAGACTAAACTGGCTTGGATACAATTAGGAAGT TTACAATT	P1: Ψ 1198/26S P2: Ψ 225/18S
Cb149	CAAC01000027 731351-731491	CCACCCAAGGCAACAAATTCCAATCGTGTGATC TTCTCGCAACACGATTGAGCCGACGCCTTGGGA AAGCAATTGCTTTGACCATTTGATCCACTCTCG CTACTCAATTGGTGATTGTGGTTTGACATGGT CCACAATT	P2: Ψ 940/26S
Cb162	CAAC01000061 336194-336066	CAGCCCCTTTTGGCCCGGATCAACTGAATA GTTATGACGGTTTCCGACCAGGGAAAATAGATT CTTGACGTAGAGGTGATTCAGACTACGTTCC GAATGCTCTTGTCTACGTACAATACAATT	P1: Ψ 1197/26S P2: Ψ 3294/26S
Cb166	CAAC01000014 1758124-1757993	AAAGCAGTCGTTCAAGTACGCAAGCGATTTTC AATGCGTTTGTGCCTAATCTTTGACTGCAAGAG AATCATTGTCATAGTCAAGCGGTCCGCTATCTG TGTAGCATTCTGTCAAGATTTGACTTACAATT	P1: Ψ 3221/26S P2: Ψ 2829/26S
Cb222	CAAC01000044 1357791-1357661	TTTTACCTCACTTATAAGCCGGGGACTAGCTT TATGTTGTGTTCACTAGTAAAATGTGAGGTAGA GATAGAGACAGCCAGACACCGAGAATGTTTT GATGTTTTCGGTCACTTTGTGTGCCACAATT	P1: Ψ 574/18S P2: Ψ 1261/18S
Cb273	CAAC01000012 3239154-3239367	AAATGCACAAATTAAGAAGTGCACAGTCGGCT TTCTCATTTTATCTCTTGGCTGTGTTTTGCAGT CGCGTTTAAAATGAGCTCAGCTATTGATCATGC GAGTGTATATTTATGCGAGACTGTTCGTCT ATGCATTTCTGTGCTAGTGAGGAATCCGAAAGC CAGCTACGGCTCTGAATATCTCATAATGTTCA TAAACGAAAACAATT	P1: Ψ 2368/26S P2: Ψ 1191/18S
Cb309	CAAC01000140 21346-21480	ACAGCACCTTCACTTCTATCATTCTGTGTGA ATGCCTAGATTTATTAAGGATGCAAGAGAGAA GACGCGGAAGTTCGAAAGACTTGCAGCAAGTTT CTCACGACTCCGCGAGTTCAAACTATCACCAC AATT	P1: Ψ 726/18S P2: Ψ 2978/26S
Cb323	CAAC01000141 42923-43049	AACCGAAGAGTAGTCATTTGTATATGTTCTTA TATGTACAGAGTTACACTCTTCGAATATCAGTG CTTCTTCTCGTTGGAGTTGTTTGATTTATGAGCA ATTACCTCTATTCTGAAAGCAACAATT	P1: Ψ 2362/26S P2: Ψ 2422/26S
Cb375	CAAC01000364 4400-4545	TGTGCAGTTTCTCATGGTTTTCGACTGCTGAC CGTAAATTTCCGGTCAGAGGTCGTTAGAGAAC TGCTATATAAGCCTAGCTCGAGATGCGGTGCT GGTTTGCTTCCAATGCGAACTGGTTCCTTTTCTC CTCGGGACAATT	P1: Ψ2245/□□□ P2: Ψ 69/U□
ComCb14	CAAC01000044 1357274-1357141	TAGGCATGTATTTAATGCGGGTGAATGACGTTA ATTTGGCCGTTAGCTTGCATGCGAAATCATTC TCCATCGAAGAATACATTCGCTGAGCTCTGTT AAAGAATTCATGATTTTCTGAAATGGAAACAT TT	P1: Ψ 1058/26S P2: Ψ 1979/26S P2: Ψ 1705/26S

II.3 *C. briggsae* H/ACA-candidates whose orthologs in *C.elegans* have been independently confirmed by Deng et al.2006 and Wachi et al. 2004 in in INTERGENIC REGIONS

name	NCBI	sequence	predictet targets
Cb27	CAAC01000085 33096-33230	CTCCGCCTCTTACCAAACACTCGTAAGTACTATTTAT TGCGAGTGCATGGAAGAGGCGAATAGAGAACGGAAC GTTGTCCACCCCTTCAATCATCATCAAATTGGATTGCG GGCACTTTACCACGGTCGACAATT	
Cb87	CAAC01000064 21658-21521	gcgtgagtACTGGCTGTTTGTGTCTCCATCCATTGCCAATC AGCTGTCATTAACCACGCAAGACTGTAACGGAGTGCT AAATTACCGTGTGAATACCATAACAAAGATTGGTCAC TCGGAGGAGGCGCTTCCACAATT	
Cb105	CAAC01000005 281980-282108	GTAGCACTCATATTTTCGCGCCGCCGTTTGTGCAATGA CGACGTGGCTAGAGTGAAGTGCAATAATGACTCGCCC TGGCGTTGCAGACCACAGATTGAAAATGGTTCGCGTT TATAGGGGTGTTACAATT	P1: Ψ 2154/26S P2: Ψ 1361/26S
Cb176	CAAC01000030 316415-316547	CCATCGCTCTCCAGCTCCATGCAGACGTAAGAAAGTC AGTGTGGCGTTTTTCATGAGCGGAAATTGTACTACTGTT CCATAAAACAATTGTTACACTCTTTATGAGAGAACGA TCACCTAATGGTTCAAACAATT	P1: Ψ 3057/26S

The Sanger database accession number and coordinates are given in column two. Purple = box H and ACA, Gray = antisense element. Target sites are from rRNAs or U-RNAs. Letters in bold in predicted targets indicate that the same sequence is targeted by the *C. elegans* snoRNA orthologs. RPGs = Ribosomal Protein Genes.

Table S9: Additionally found C/D-box snoRNAs by Wachi et al. 2004 and Deng et al. 2006, group III for *C.elegans*

III.1 In INTRONS OTHER THAN RPGs

name	NCBI	sequence
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CeR5 (CeN56)	AB125754 AY948634	tccccg tgatt caaacatt ctga aacctcccaccgaaagcttcgagattggcgtggggccgatcaggaaaag ctg acaacgg tgga accatgatacagattatgagagat gagggga
CeR19 (CeN69)	AB125759 AY948700	gacaggat gatga gtcactc ctga gtgacaataagccgagtgtagcggttttatgtaatc gatgat cattccctcaaaa gcgataatt tgaa ct gactgtc
CeN54	AY948689	gttt gatgact gcatacggatcactgggct ctga atctctatgaaccgataatatccgt ctgata
CeN62	AY948695	gtc gat ga agg ta atgataagtt ctgg ct act caaatt gatga acc tt aatat ctgag cact
CeN89	AY948711	gc gat gag gattgataaacacatacacacact ctga agttatgtgaagagataattgaagaaccgata ctgag ggc
CeN103	AY948605	tacccat gat gatcaatttagctaatt ctga gctactc ctc gagattt gtct gaa gt ctg agtcgattgaacgaacttt gtcgaag ctgat ct gagggag
CeN113	AY948654	tggctaat gat gttctc tc gaaatacacaa ct tactacaa ctgat cttatttgaattgaggg tact gtagctact ctg tagct accgtaatcctcacag gtga acttaattaaag actga agctt

III.2 In INTERGENIC REGIONS

name	NCBI	sequence
CeN13	AY948665	agtcaat gat gtttttcaagacggg acc gactgg tgat gcataaatgaaat ctgag act
CeN22	AY948615	attgcagacc ggtgat gaaactgttctaggaag tc ccgt ctt gaaacaat gatta gaa ttgg ac gtga gg ta
CeN53	AY948688	tggcaat gatc gaattatcattgagccaatc cttt ctgaatt ctgag gatgtaaatgatag gtctgag cca
CeN65	AY948697	aagcgat gac gattgatat ctg ctta atg at ctga attaccatg ttg agat ctgtctgag ct

The NCBI GenBank accession number is given in column two. Gray = double stranded region, yellow = C' and C boxes, green = D' and D boxes. RPGs = Ribosomal Protein Genes.

Table S10: Additionally found C/D-box snoRNAs by Deng et al. 2006 for *C.briggsae* (found by our group)

III.1 In INTRONS OTHER THAN RPGs

name	SANGER	sequence
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CbR5	CAAC01000078 1552097-1552220	CCGTA TGATTA CAAAC TTCGCTGATACCTGCCACCCGAAAGCTCAGAG ACTAGGAGTGGGGTCCC GGTTGAGGACGGCGCTGACAACGGTGGGAAC CATGATACAGATTATGAGAG ATGATGG
CbR19	CAAC01000044 1766662-1766767	GACAGGA TGATGAGT CACTCGCTGAGTGACAATAAG CCGA GTGTTAGC GGTTTTCAACAACCG TGATGA TCATTCCCTCAAAGCGATACATGTGGT CTGACTGTC
CbN54	CAAC01000059 790768-790840	GGGTTTG TGATGA CTGCATACGGATCACTGGGCT CTGA ATAT TCATGAA ACGATAATATCCGTT CTGA TACCC
CbN62	CAAC01000053 160526-160456	GTG CGATGA AATGTATTGGATAAGTTTCGG CTGA TTCATAAT TGATGT CA ACTTTATAACTTG CTGA GCAC
CbN89	CAAC01000042 298981-299054	CGCGA TGAGGA AATTCATCACACACACT CCGA ATTTTCG TGTAGAGA ATTATTAAGAACGGATAT CTGA GCG
CbN103	CAAC01000016 614549-614435	TCCCCA TGATGT CAAAACTTAGCTAATTGTGAGTCGTCTAATATTCTAA AAAGCATTGCCTTGTTTGGAATTTAGCTGATACTGA ACTAATATTCTGTC GAAGCTGAT CTGA GGGA

III.2 In INTERGENIC REGIONS

name	SANGER	sequence
CbN13	CAAC01000056 269674-269738	AGTCTA TGATGT TTTTCAAGACGGGA CCGA CTTGTGAA TGATGC ATAA CAGAATTG CTGA GACT
CbN53	CAAC01000016 1481948-1482021	TGGCAAT TGATTGA AATTATCATTGAGCCAATCCTTTT CTGA ACTCCA TGA GGATGGAAATGATAGGTCTGA GCCA
CbN65	CAAC01000016 1385750-1385813	AGCGA TGACGA ATGATATCTGCTCTAATGAGT CTGA ATCC CCATGT TGA GATCTTAT CTGA GCT

The Sanger database accession number and coordinates are given in column two. Gray = double stranded region, yellow = C' and C boxes, green = D' and D boxes. RPG = Ribosomal Protein Gene.

Table S11: Additionally found H/ACA-box snoRNAs by Deng et al. 2006; group III for *C.elegans*

III.1 In INTRONS OTHER THAN RPGs

name	NCBI	sequence
CeN45	AY948682	gtgggcacagagttgcagttgattgaaactaatcatgtcgcctaagttgcccgaagta ctcttggatttctacaaaacagf gttcctcttaggatgctgatccgtagagatctgaca aat
CeN59	AY948692	cacggccagttgagttgattcgtctcttcgcaatagagctttgagtcaaactactgtccggaatta tagagatgaagctcattt ggagcaataacaattgtgaagctccgaaaatgatccttcccaca aatt
CeN91	AY948713	caaccactattcaagttaatctatgaaaattattgataagatgattatagaactgtggaatataa acgcgaagcgaattataaaa gcagagtggtacttccaaaatgttttttaataaattttgtcttagacactcagaca ac

CeN97	AY948592	ttccactgcgaagtcagcagactagtcgaatcgattagtaggcgttacagtggtggaatatcaagattatgtacacgctcttgc ttgaaacagttttgttttctttgttcggaacgttttcatgggactgagagttggaattagcactggctgttacagggttgc ctgcagtcgaattctaagttaccttagttatgtcccacacat
CeN102	AY948646	tatccatgtttactactctttcatctcttttctactgaaatgctgagatatttgcgatgcatggttaagaaatcaagggtgaccag gtttctttcaattttcccataattgaagagttacaatgccatctgacaagg
CeN105	AY948648	gattgctggaactctgatcgcgtgtttatttaccgcggtgattgtaaaggccgacatatacaaaattgacattaatgctgg aagtttctgaaatagttccattttctccaattttcaaatgtcaaacaaac
CeN127	AY948595	ccgaagtgcgatatccagacagaactttaagagtactgctggactgagttactaactcgaatataaagatgtagcgataa ccggaatatactcaaaaaaaaaagggtgtcctccggacaaaaatcaactaaca

III.2 In INTERGENIC REGIONS

name	NCBI	sequence
CeN67	AY948698	gccccattatcttccatcaaatgatttaggacgtcattgatggcttagaatggggaatgaatcggtagaatgtattgtg agttgttcaactgacacgtggcaactcgtattcgtacttccatatt
CeN68	AY948699	gtgccgattaaacactctgagttgctcacatgctcagaagaacaagggtcggaaatagtgatcatttgatgctgaact ccaagagtcaaaactgagttggtgatcgtacatt

The NCBI GenBank accession number is given in column two. Purple = box H and ACA: RPGs
= Ribosomal Protein Genes.

Table S12: Additionally found H/ACA snoRNAs by Deng et al. 2006; group III
for *C.briggsae* (found by our group)

III.1 In INTRONS OTHER THAN RPGs

name	SANGER	sequence
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CbN45	CAAC01000079 104179-104305	GGGGGGCACAGAGTTGCAAGTGATTGAAACTAAATCATCTGCGCTAAG TTGTCCCGAAATGGTGTTCGGATTTAAGA AAATGAT GCCTTGCTTCAT GAAGTGTCTTGATATCTATTGCA ACA ATT
CbN59	CAAC01000016 2251938-2251797	CCACGGGCAGTTTGAGTTGATTCGCTCTTTATTGATGGAGCTTGGGTCA AATTACTGTCCGA AAATGA TAGAGAAGAAGATCTAATCAATTGAAATT GTCTTCCTTATGAAGATGATTTATCAATAGTCTCTTCCC ACA CTT
CbN91	CAAC01000001 123111-122972	CATTTTTCGTCGATTTCTAAGTGGAAAATAAAGAAGCGAAGCGAAAAA AAAGCA GAGTGTTACTTCCAGAATTTCCCCCTTTTCAATGGAATTCTT GGTCTTAGACACTCGG ACA TTT
CbN97	CAAC01000141 42139-42351	CACTGCGAAGTCAGCAGGCTAATCATCCGGTTAGCAGGCGTTACAGTG GTGAAATAGCAAGAAATTTGCATCCCGTTATTGCTTGAGACAGTTTTT GTTTCTGCTCTTTTCGGCGCGTTTTTCATGGGACTGAGAGTTGGAGATTA AGCACTGTTCTGTTTACAGGATCTTCTGATGTCAATCCTTAGTCACCTTA GTTTATGTCCCA ACA GTC
CbN102	CAAC01000033 393866-394008	Not orthologous locus! AAACCATGTTTACTACTACTTGTACCTCTCCCCTTGAGATTTTCGAGTAT TTTTGCGATGCATGGA AAATGA AATTTCAAAAAATCTGACCAGGTTTCT TTCTAACCCCTTATAGCTAGAAAAGTTACAATGTTAGTTG ACA ATT
CbN105	CAAC01000088 165697-165545	GATTGTCGTGAATCTTGGTCGATGGGCTTATTTTACCCCATTTGATTGTA AAGGCCGACAT ATACCA GTTTCGACGGTACTTACAGGAACAGCCTGA ACATTTTGATTTTTGAAGGTTTTTCTGTAAAGCTTGAATTGCTGTCAA C ATTA
CbN127	CAAC01000045 1575251-1575389	CCGAAGTGCATATCCAGTCATTGAATTCATTTAATGTTGGCGTGTT GTTTTTTTATTACTTCGAAG AGAGAA TAGCTGTACGATAACCAAAACAG CTCCCTATCGGGTTGCTTGGGACAAAAATCAGCTG ACA ACC

III.2 In INTERGENIC REGIONS

name	SANGER	sequence
CbN67	CAAC01000088 1694553-1694683	CAATCCCATTATCTTTCCATCAGCCGATTTTGAAGTCACTGATGGCTTAG AATGGG AGATA TTGTCAGGTCGAATCTGATAAATGATTCATAAGCCCTA GTTTGTGCATCATTTCTATTCTACCG ACA AAC

The Sanger database accession number is given in column two. Purple = box H and ACA: RPGs = Ribosomal Protein Genes.

Table S13: Full-length novel spliceosomal paralogs, group I for *C. elegans*

Group I: novel spliceosomal isoforms for *C.elegans*

L1 Novel *C. elegans* isoforms of U4 and U5 in INTRONS

name	number of seq.	NCBI	sequence

	clones			
Ce13 (CeN3-1)	20	U5	AF003148 24895-25016	aactctggttCCTCTGCATTTAACCGTGAAAATCTTTCGC CTTTTACTAAAGATTTCCGTGCAAAGGAGCATAACAT TGAGTATTACTTAGAATTTTTGGAGCCTTCTCGAAA GAGCAAGGCA
Ce119c (CeN3-4)	1	U5	Z70270 5918-5797	aactctggttctctctgcatttaaccgtgaaaatctTCGCCTTTTACTAAA GATTTCGTGCAAAGGAGCATAACATTGAGTATTATA TATAATTTTTGGAGTCCCCTTGAGAAAGCGGGACa
Ce307b (CeN2-2)	7	U4	AF022972 10802-10661	cttgcgctgggGCGATAACGTGACCAATGAGGCTTTGCC GAGGTGCGTTTATTGCTGGTTGAAAACCTTTTCCCAA TTGCCCGCGATGACCTCTGAAACATGGGTGCCATAC GCAATTTTTGAACGCCTCTAGGAGGCAgaa

I.II Novel *C. elegans* isoforms of U1 in INTERGENIC REGIONS

name	number of seq. clones		NCBI	sequence
Ce11g (CeN1-7)	9	U1	U14635 20452-20616	aaacttacgtgctggggctatcttgcgatcaagaaggcagaatccccatggtgag gcctaccCATTGCACTTTTGGGCGGGCTGACCTGTGTG GCAGTCTCGAGTTGAGATTTCGCCAACAGCTTAATTT TTGCGTATCGGGGCTGCGTACGCGCGGCCCTGAa
Ce11h (CeN1-4)	7	U1	U64837 27738-27902	aaacttacgtgctgggggttacTCGCGATCATGAAGGCGGGAT CCCCATGGTGAGGCCATCCATTGCACTTTTGGATG GGCTGACCTGTGTGGCAGTCTCGAGTTGAGATTTCG CAACAGCTTAATTTTTGCGTATCGGGGCTGCGTGGC CGCGGCCCTGAa

I.III Novel *C. elegans* isoforms of U6 found by blast search

name		NCBI	sequence
BIce378	U6	U53333 1100-1201	tttctccgagaacatataactaaaattggaacaatatagagaagattagcatggcccctgcgcaaggat gacacgcaaattcgtgaagcgttccaaatttt

Splicing of mRNA is mediated by small nuclear RNAs (snRNAs) and associated proteins. Altogether, we extracted 20 expressed snRNAs and localized them on the nematode genome. Previously, Thomas et al. (1990) described 21 *C. elegans* spliceosomal RNA genes after screening a genomic library with known snRNA DNA probes. We verified 15 of these in our cDNA clones and identified 6 novel candidates (see above). The number of clones describes their frequency in the sequenced cDNAs. The NCBI GenBank accession numbers and coordinates are given in column four (U6). Capital letters represent cDNA sequences that were completed by Wormbase or GenBank information (lower case letters). Capital letters represent cDNA sequences. The additional sequences completed by Wormbase or GenBank information are in

lower case letters. However, the 6 novel candidates of spliceosomal RNAs were also sequenced by Deng et al. 2006, but categorized as known and not recognized as novel isoforms.

Literature

Thomas, J., Lea, K., Zucker-Aprison, E., and Blumenthal, T. 1990. The spliceosomal snRNAs of *Caenorhabditis elegans*. *Nucleic Acids Res.* **18**: 2633-2642.

Table S14: Transposable elements (TE), group I for *C.elegans*

name	number of seq. clones	NCBI	sequence
Ce157	2	U50068 37825-37971 SINE CELE45	Gtaagtgaactgaaattgagaattttaatttaaaccggggcagatagctcagtcggtagtggtggcc gctagcagctggaggtcacgagttcaagtcggcctcacccctaggctcaccagcctctattggg aagtggAGCAATCCACGACTGGATTATCGGCCACAGTCCCCGGC TAGGACGTGGCTTAAATTACAGCCCAGAGGGATCACCACCAG GCAGTGTACCTGAATCCCAGATCCGCAGTGCATAGCACTTA AGAACGGATCGTCCTTTAATCCTTTaatcctttaaacttttagg*
Ce268	1	AF067215 25851-25898 SINE CELE 45	Acacaaacctagacacacgcgcaattcattgcattcagtttagagacagctctcccgaatcgattta tatatattccattagtaactatactccgggggtgatggCTCAGTGCCTATGCGCGC TGCTTGCAATCACAAGGTCACAAGTTCGACccccaccctaggtcctc cagcctaaatgggaattcagtggttccttataataataatcaaagggttaaccaggc*
Ce293	2	AF025465 3346-3405 PALTTAA1_C E PIGGYBAC	gcacagttatttttgcacaatccgattgtctgaaaacaccgattcaagatgaaactctggaaaact ctcaaaaaatataatggtgctcaaaaatgcctaaaatttaaatatcaaatcttagtcatttttga gccgctataactgttttctagaagtttCAAGAAGTTTCATTAGGAAATTGGGT GTATTTCAGACATTTAAGTCTGATAAAGCAATGAaaaattcggcaat accaccttaatatattaataggcagtcctcgtttgaacagctcttcgattttatcaaaaactataacca aaccacaacaatatttaggtttacaatttaaccaccgaaacacattatcattcgcca

The number of clones describes their frequency in the sequenced cDNAs. The NCBI GenBank accession number and coordinates are given in column three. Sequences in blue letters delineate the corresponding transposed elements.

Transposed elements: The *C. elegans* cDNA library contains three RNAs (Ce157, Ce268, Ce293) that exhibit similarity to *C. elegans* transposable elements. cDNA clones Ce157 and Ce268 represent 48 and 147 nt fragments of the CELE45 consensus sequence (265 nt full-length). Northern blot hybridization revealed the 265 nt full-length form only. There are several hundred copies of CELE 45 in the *C. elegans* genome. Their lengths vary from 24-265 nt. The high sequence similarity (97%) indicates a recent activity of these elements that are related to RTE1 non-LTR retrotransposon SINE-like retroelements (<http://www.girinst.org>). Ce293 represents a 59 nt fragment of a putative nonautonomous DNA-transposon termed PALTTAA1_CE that is probably piggyBac-related [DNA transposon]. The 100 *C. elegans* PALTTAA1_CE copies are at least 90% identical to the consensus sequence (<http://www.girinst.org>). It is intriguing why part of a DNA-transposon is represented in the cDNA-library of small RNAs. The presence of retroposed elements in the cDNA library supports the idea that those elements are still active.

Field Code Changed

Field Code Changed

Table S15: miRNA, group I for *C.elegans*

name	number of seq. clones	NCBI	sequence
Ce228	3	Z93375 13351-13068	aacctagtggcaggcgaaaccgcaaggtgctggccgcacgtctaccctcccctttataacgaccgtc ggttttgaacgtactcggcgggtgctcgtacgt <u>ATTTTCGGTCTAGATTGATCTCGCT</u> <u>ATAAAATAGTTGACGAACTTTAGATTGAATCAAACCATGACG</u> AGGACCGGGAGCTCCCGTTCCGGCTCGTGATGATGCCACGGTC CTAGAGCTCCCTCGATCAGAGGTTTCCCACTGACTGGCTATCC GGTGGATAGATTATCCAGTCCTGGTGGGTTCTGTCACGTTAC AGGCCTCACTCCCCCTAGGTTAGACAAATTCAAAATTATCTG AGCACCGCGATGTGAGCTCCGCTTGTTAGGAGTTGTCAAAA Ttttttgccgtgtattattgaggaagtaagcatgaacattaccaagaaaaattccgggagtcaaat cgtttaattatttgaaaaaaacttc

The number of clones describes their frequency in the sequenced cDNAs. The NCBI GenBank accession number and coordinates are given in column three.

microRNAs in *C. elegans*: Due to the size selection of the RNA (70-600 nt) from which the cDNA library was constructed, we did not expect to find any mature miRNAs. We identified a cDNA clone (Ce228) that encodes an RNA ~280 nt in length, which would make it possibly the longest precursor form. In addition, RNA blots detected a 60 nt RNA species, possibly a fold-back hairpin precursor. A specific sequence region of Ce228 (underlined) exhibits all characteristics of a miRNA (Ambros et al., 2003). We could not detect phylogenetic conservation, for example in *C. briggsae* or any invertebrate or vertebrate genome.

Literature

Ambros, V., Bartel, B., Bartel, D.P., Burge, C.B., Carrington, J.C., Chen, X., Dreyfuss, G., Eddy, S.R., Griffiths-Jones, S., Marshall, M., Matzke, M., Ruvkun, G., and Tuschl, T. 2003. A uniform system for microRNA annotation. *RNA* **9**: 277-279.

Table S16: Other ncRNAs, group I in *C. elegans*

name	number of seq. clones	NCBI	sequence
Ce106	1	AF164959 23496-23531	tggattgagcaaccaatgaaccttcacaactgccgtccatcctaataaatatgtttccaaaagattcaa accttgatatcctctcagagccgtcaAAATGGTCATAAAATGTTTCATCGCGACAC CCGCGTAAAtcaaatgtaacttttgatattagtcattgctcacaataggaatcaccactacaacat cagctattcacatcctttagtcatttagttagccccc
Ce150	1	Z83128 3895-3952	caaccaccgccattcctcgaaaaatgctggccgctgtcagaaaagtgttatatatacccccgacgcaa cacaattccgaccaccggctccggattgtGGGTACCAAAATTGTCATTTGAAT CCCCCATAGACATCCCTTGACCGGGGGTTTTgcaatttcatttattttct gaaaagtgatattccagcttttagtgttccaagtattcgaaacatgtgttctatagaaaatcgattatga ggg
Ce296	1	U37548 42383-42367	ttattccccctctcaccctttcaagttttgattctattgtgaccagtttaacatgttcgccattgagtactgca acaattttggatgtagttgactGACCTTTGGAACAAAGTattctatgacctaaaagcctgc caaggcaaaatacctaagaatttgaagatttcattggatcacaaagtttgagaagcgcattttatgt gtta
Ce342	2	AF024498 18777-18793	*gtacagtcgactttccgctattttcaaaagtttgaaggcgcctgaaaggcaggcattctttgtatct atATGGACCTAGGACAACtattccagctctctcgattcactagtttatatacttccag*
Ce376	1	U58732 1891-1867	*aataattctttcccaactctatcatcaaatgattgtaattaataatattgtactagatagga aCATTTGACTCTCTTCATTTGAAAACacattgctttacactttacactgttctatt gtgatttttccgatgtacaattgaaaaaaacgactacttgatggtagctgctccgataaagac
Ce377	1	AL024499 12164-12206	ctctgatcctagtgtctctcgtacattccgttactttcgaccatattactctcctctgcacatacttt gacgggttgcctcatttctctATCTCTCTCCATCTCTCTTCTTCCAAGAAG AAGATCACAATGAaaaagtagaaaaatgataaagtatggaaaaagtaagaatattttcattg agtattatgtgaatcctgtaaatgtatttgaaaattgctccccc

The number of clones describes their frequency in the sequenced cDNAs. The NCBI GenBank accession number and coordinates are given in column three. For these cDNAs we could not find characteristics to categorize them. All sequences are extended by 100 nt in both directions (lower case) or to the end of the intron (asterisk). The numbers in parenthesis (129) and (220) in column four designate two of three different paralogs (bold) found in the sequenced cDNAs.

Table S17: Other ncRNAs, group I in *C. briggsae*

name	Sanger	sequence
Cb106	CAAC01000060 1060262-1060227	gttatccaagtgttgattgtcctgtgaggttttttgagtataattcctagattgtttgaaatcatctgtattttcca tctcagagccgtcaAAATGGTCATAAAATGTTTCATCGCGACACCCGCGAAActc aaatgtaacttatcgatattgtttgtcgcctatttttaagcagtcactcccactcactgagcagcttaatccattc gtcaacatcagagagg
Cb296	CAAC01000078 1654694-1654678	cccgttttctcaagttttattctatttgaccggttcacatgttcgttcattcaaaaagttgcaacaatttcgtattccc atgctgtagtgtgattGACCTTTGGGTCTAAAAtttctatggtcccacaaaaattgtgggtgaaaa gagattaaaaacctcaaattttactggatcgaataaagcaggaaaagtaccacaaaaaatt
Cb376	CAAC01000068 1780028-1780003	aaactgtcccatcttcgtatctaaatcacaccaataacctttttgatgtaccccacacactttgtgtgtttgt aattaatttatgatctagtttcagaaCATTTGACTGTACCCTTTTTCTAAAtcgaaaac aactaaaaacatacactgttctattttaccctttttgatgtacacactactgtttgaaaaaatgaagaaa ataaaacaaaaataattgaa

The Sanger database accession number and coordinates are given in column two. All sequences are extended by 100 nt in both directions (lower cases). Letters in upper case correspond to the orthologous cDNAs in *C. elegans* (library sequences).

Table S18: Other ncRNAs, additionally confirmed by Deng et al. 2006; group II in *C. elegans*

name	number of seq. clones	NCBI	sequence
Ce1a (CeN26-4)	13	Z79754 31359-31536 (intergenic region)	gccggcactcacgtccaactggaagcagcgggaaccgtagtgtgctggccgcccgcctctcacc tcgaagaccagcgtctcttcacgcagaccatACTATACAGAATCATTCTGCAGT ATGTATCTCGTAATTCCCATCAAAATGGTAGAGATGCCAACTG CGATGAAAGGGAGACGGGCAGGTCGCGAGCGTGAAGCAGTCC TCTAATGACTTGATGACCGCACGGAGCCAATGAATTTGGAGC CGTAGTGGCCTGCTCTTCTGAGCAGTtataaatgtgcacaaatagaataatata ctaaatcacaaaacaaaactggataataaacatgaattgaagatttctataatgttccgaact
Ce1b (CeN26-5)	33	AL117206 8781-8608 (intergenic region)	ccactcacgtccaactggaacgagcgggaaccgtagtgtgctggccgcccgcctctcctcgcac ggccagcgtctatcatcgcagaccatactTACAGAATCATTCTGCAGTATGT ATCTCGTAATTCCCATCATATTGGTAGAGATGCCAACTGCGAT GAAAGGGAGACGGGCAGGCCGCGAGCGTGAACAGTCCTTTG AGGACTTGATGACCGCATGGAGCCAATGAATTTGGAGCCGTA GTGGCCTGCTCTTCTGAGCAGTtataaatctgagattttctataataacatgattgtttg aaggagatttgaatggtgatgaatttaacgagaactgaatattctcaaaaacagca
Ce1c (CeN26-1)	33	Z79600 12224-12052	ccccgtacacaaacatctctcagcgggaaccgtagtgtgctggccgcccgcctcagtcacctcg aagaccagcggttcttcacgcagaccatactTACAGAATCATTCTGCAGTATG

		(Intron)	TATCTCGTAATTCCCATCAAATTGGTAGAGATGCCAACTGCGA TGAAAGGGAGACGGGCAGGCCGAGCGTGAAGCAGTCCTT AGGGCTTGATGACCGCACGGAGCCAATGAATTTGGAGCCGTA GTGGCCTGCTCTTCTGAGCAGTgtaaactgtgctaaaaatgctaaatctcatag caaaacctgtaatacaaacatgaatagctttatctagaatacacaattgttcggaactacg
Ce5a (CeN26-2)	43	Z75549 31244-31421 (Intron)	tgtctgtgacctacttagatgctgaatgactgaaccgaggtgtcggctgtcgtgtacacactagcc ccgccagcactctcgtacacgagaccaTACTATACAGAATCATTCTGCAGT ATGTATCTCGTAATTCCCATCAAATTGGTAGAGATGCCATCCG CGATGAGTGGGAGACGGGCGAGCCGAGCGTGAACAGTTC TTCGGAACCTTGATGACCGCACGGAGCCGATGAATTTGGAGCC GTAGTGGCTTCTTCTGAGCGGAtaatacgaacaaggttcaatctgatgtttt ttaaactgttttaatacatttgcgggtagtgattttataatgaattacattaaaaattgagcag
Ce5b (CeN26-3)	9	Z74034 2259-2089	acttacacactaggcagtgaccggcgaactcgtagggtgtcggctgtgtacacactaaccttca gcacaccgcttctcattgagaccataataCAGAATCATTCTGCAGTATGTATTT CGTAATTTCCCATCAAATTGGTAGAGATTCCATCCGCAATGAGT GGGAGACGGGCGAGCCGAGCGTGAACAGTTCCTCGGAAC TTGATGACCGCACGGAGCCGATGAATTTGGAGCCGATGTGGC TTGCTCTTCTGAGCGGAtaataattttgagtgagcataaattgaacatgtgaatgaca cttccaaagttaattcgtttcaagtattctt*
Ce9a (CeN21-1)	30	U46674 10045-9934 (intergenic region)	ggcacacaaaaacttagtgaccggcgaacctgaagagtgtcggccgagcgtttgtgacctagca cacttacccttctcagctcctcagatgGTCAATCTCTGATCTGCAACTGAAT ATGATGAGTTCGGGCGATGATCTTCTGTGATTACATCGCACGG CGAGGTGGGAACGCAATACCCGCTGCCAGCCCGATTCTGAAC caagttgcctagaataatttggaaacataagactcttttagagttattatagaattacattgtgtgta ttgatgtgtttgtcattaaag
Ce9b (CeN21-2)	8	AF038623 4988-4878 (intergenic region)	acgtacacaaaggaggtgtgagcgcggaactcgtcattgtgtcggctgtcgggtttacactggtcatcta ctgagggtgaaaacttttagtctcagatgGTCAATCTCTGATCTGCAACTGAAT ATGATGAGTTCGGGCGATGATCTTTTGTGATTAATCGCACGG CGAGATGGGAACGCAATACCCGTCTGGCAGCCCGATTCTGAAC cagttttgaaagcagcgtaaagtgatttgagtgaaaggggaataagaagagatatttttagagtcacagatt cgcttgtgtgagctcctctttcata
Ce26 (CeN34)	6	U28943 13315-13488 (Intron)	acaacaatagtacagcgaacacctcaaagtgtcgcgcatcaaagcgggtgtatataaaacaaga ggagaagaggggaaaggccgcatgacggcaaGGCGAGTACTCGCAGCCACGAA ACGTTCCCTGTTGAGCGCGCTAACTGTGAGCGAAAGTCCCTGG ACCACTGGCAGAAAGTGTACCCTCTAGGTTGGGTACTCTTTG GAGTTTTAGTCATAGCACAGAGACGCTCCTTAGAACAGCATAG GGCTACTCTGATCGTCATGCTTTTgcaacattttaaagtcagagaaacggg gctctgtgaaccataaataatgtatttctctatcaaagacccttgacactatgctcagcagatgt
Ce129/220 Ce129= (CeN74-2) Ce220= (CeN74-1)	1 1	<i>Ce-220:</i> Z79603 14756-14820 <i>Ce-129:</i> Z79603 15472-15497	actttaaactgtccgaacgctatttgagtgcaaatggctctatgtccaataaattgtgaaaattgcaaa atacttcataacagaaccagaggtgtcgaattgcaagaaatgtctgcccctgactctcctcggt atataaacagcctacaatcactaccggtctcggcggcGTCAGTGGGTTATCG TATTTCTCTCCCTTCGGGGAATTTCCCATCGGCATCAACTT GACCGTTGC(220)gtttgaaattttg aaaagacatacagtgactactgaltatataatttt tcagcatttgattgtataatttttattctctgaaacgttccaataactactagtgttcagagagttatgga aattcatcaattttgaaaattgcaaacacagtttaacagagctatctgccattgcaagaaatgtctgt cgectcactctccttggatataaacagcctacaatcaccgaagtatgtatcggtccggcgtcagt gggtatacaagttgectcctcgggaattccatcgcatcaactgacagttacattttgaaa atttgattgagacaaaaaagtgggctgacacattttgaaacaatigtgaaatgaataggagctctc cgtattataatttacaattctgaagcgtggaagtactactgactgcaagttgcaaacgcttatctaatt atagattttgaaaattgcaaacacagtttaacagaactatctgcaattgcaagaaatgtctgccc tcactccttggatataaacagcctacaatcaccgaagtatgtatcggtccggcgtcagtggt tatcaagttgectcctcgggaatttCTCATCGGCACCAACTTGACCGTT GC(129)ttttgaaattttctg aaaacacaatagtaattacaataaatcgactctactccagcag ttggtttatggtttaaaaacctgaaacggaacaa
Ce142 (CeN71)	3	Z81495 8330-8270	agagaaaccaccactctcagaaacgtccaccgcttgcattgectctagtatatatactctcctc cccaacagtttctgaattcctggtccGGATCGTATGGGTTATCAATTCTCAAC CACCCATACGAACTAACTTGACTACCGGAATTTgcaattttgataaa

			aattactgTTTTgtagtatgcaaattaaataaaaaattattatttggattttttaaaaaataaattcgtgtgc aataat
Ce148 (CeN37)	1	U40800 17973-17860	tgccgctctgctgttgcacgcttggcttagtggtaagagacgtggtcttcagtaataactacaaagattcg caaccctcactgcatctatgtgtactCGCTCGTCGTAAATCGACAAGTGTAGA AGGGAAATGATGCGAAATTGGCCGTGAACTCCGCAGGCGGAC GAGGACTTTATGGTTCCTGTCCTAGTCAATTGGAGTTCCTCATT Ttgttttctttctgtgtcaaaattttatacacagctacatagaataaacattttattatagcattacaatac acattaaattgggaaactcaaa
Ce178 (CeN72)	1	AF036694 6251-6269	ccataaattcctaatactttatcatcgggtccggtgtgatgggttattatcctggtgcttgcgtcgtgctgac acattcaccgtcctctacacatcatCACAAATTTGACCGATGTTtgaattttcacaagtg gtataagttttataccgtatttctctattacaggggtggccaaaagatggtaacacglttgcagctctata actttact
Ce347 (CeN29)	1	U28739 17543-17565	ctgcttcaactaaatgtagtcggcaagtgtatagttttctaccgtgatgaagaaattagatccaactccca ggccagttgatacgtcttctgttcatGCAGATAAAGGCGAACGAACGGGttttgat aattttgaaaccaattagcaacgattgtaacttattattatagaggctggaagaaaaaatcattat ggcagtttcag

The number of clones describes their frequency in the sequenced cDNAs. The NCBI GenBank accession number and coordinates are given in column three. For these cDNAs we could not find characteristics to categorize them. All sequences are extended by 100 nt in both directions (lower case) or to the end of the intron (asterisk). The numbers in parenthesis (129) and (220) in column four designate two of three different paralogs (bold) found in the sequenced cDNAs. Designations given in parentheses refer to Deng et al. 2006.

Table S19: Other ncRNAs, additionally confirmed by Deng et al. 2006; group II in *C. briggsae*

name	Sanger	sequence
Cb1a		<i>Ortholog locus of Cb121a doesn't contain the corresponding lib-seq.</i>
Cb1b	CAAC01000141 259435-259606	tagcacacacaaagtatagcggcgccggaacccgggagatgctggctgctgcgcgtggttaggtccggcgc ccgcgttcttcatcgagaccatactaTACAGAATCATTTCTGCAGTATGTATCTCG TAATTTCCCATCAAATTTGGTAGAGATGCCATCCGCGATGAGTGGGAG ACGGGCAAACCGGAGCGTGAAACAGTTCTTCGGAACCTTGATGACC GCACGGAGCCGATTCATTTTGGAGCCGTAGTGGCTTGCTCTTCTGAG CGGatataaatgaaacaacgaatactattgtcaattcaaaaagatcgaccggggaacacacacaaaca gtaacaagaggcgccgagcgcacccct
Cb1c	CAAC01000011 109363-109535	aggcacacacaaagtatagtgctggcgccggaacccgggaagtgtcggctgctgcgcgtggttaggtcagcgc cgcgctgcttcatgagaccatactaTACAGAATCATTTCTGCAGTATGTATCTCGT AATTTCCCATCAAATTTGGTAGAGATGCCAACTGCGATGAAAGGGAGA CGAGCATGGCGCGAGCGTGAAGCAGTCTTGAGGACTTGATGACCG CACGGAGCTGATTAATTTTGGAGCCGTAGTGCCATGCTCTTCTGAGC AGTatataaaagtttccaagcgaagagaaggttctgaaaaataactttacacacaaataccttattgtg atgacgaccggctacggatcctctgtt
Cb5a	CAAC01000141 247781-247604	gagtcggcgacacacacaaagtatagcggcgccggaacccgggaagtgtcggcgcgtgcgcgtggttaggt cggcgccgcgttgttcatcgagaccaTACTATACAGAATCATTTCTGCAGTATGTA TCTCGTAATTTCCCATCAAATTTGGTAGAGATGCCATCCGCGATGAGTG GGAGACGGGCAAACCGCGAGCGTGAAACAGTTCTTCGGAGCTTGAT GACCGCACGGAGCCGATTCGTTTTGGAGCCGTAGTGGCTTGCTCTTC TGAGCGGAtataaatgaaacaagtgaatagaaccgggaactgtgtcttgaaaaaattaggttgcaaa aatacaaggaaactattgccttcgaaaatttctgnnn
Cb5b	CAAC01000141 412943-413113	Gcacacacaaagtatagcggcgccggaacccgggaagtgtcggctgctgcgcgtggttaggtcagcgc cgcaccgttctcatcgagaccatactaCAGAATCATTTCTGCAGTATGTATCTCGTA ATTTCCCATCAAATTTGGTAGAGATGCCATCCGCGATGAAATGGGAGAC GGCTTGCCGCGAGCGTGAACAGTTCTTCGGAACCTTGATGACCGC ACGGAGCCGATTCATTTTGGAGCCGTAGTGGCTAGCTCTTCTGAGCG GAtataagtaaattagaactacacgctctcccacagaacaatccgaactgcaaatattttgatctacagaaa aagttggcgccgacacaaatgcag
Cb9a	CAAC01000090 78109-78220	gctcacacaaagtatagtgccggcgccggaacccgggaagtgtcggcgcacgttctcatcacatccgcgcgc ttgctgacttctcagcttctcagatgGGTCAAATATTGATCTGCAACTGAAATATGAT GAGTTCGGGCGATGATCTTTCGTGATTACATCGCACGGCGAAGTGG GAACGCAATACCTGCTTGCCAGCCCGATTCTGAACaaagttgctgaaaactaatt gataattttgaaaagtgaagactctgcaaatatggagttggatcgaataaaaaaaattggttatttccagctattt
Cb9b	CAAC01000055 550385-550274	tcgcacataaagatgcccggcgccggaacccgggagatgctggcccctctgtttacccectaccactactc cgcattgtctcagcttctcagatgGGTCAAATATTGATCTGCAACTGAAAAATGAA GAGATCGGGCGATGAAATTTCTGTGATTACATCGCACGGCGGGGTGG GAAACGCAATACCTGACCGTCAGCCTCGATTCTGAcacaaagtgtctgaagac ttttatatagtcagttttatgaaatgatttgaggaaatggttcaacacatctggccacctgtttagaatattcctt
Cb26	CAAC01000145 2068-2893	caaagtatagaggcgccggaacccgggaaatgtcggccgacgcaaaaggggttgctatataaactgagcgcg agagaggaagcagttgcatgacggcaaaGGCGAGTACTCGCAGATACGAAACGTTT CCCGTTGAGCGCGCTAACTGTGAGCGAAAGTCCCCTGGACCACCGGC AGAAAGTGTCAACCCTCTAGGTTGGTACTCTTTGGAGTTTTAGTCAT AGCACAGAGACGCTCCTTAGAACAGCATAGGGCCTACTCTGTTTCGT CATGTTTTTgcaattcgtgaaggacaaccgggaaggcacagctcactgctcatgaaatgcttcttctt ggagagtcaattcacactttacacacgacatgtctct
Cb129/220		<i>Seq. was found 11 x in C. briggsae; determination of the ortholog not possible</i>
Cb142		<i>Seq. was found 6 x in C. briggsae; determination of the ortholog not possible</i>
Cb148	CAAC01000118	tccactgttgcagcttggctgtaggggtaagcggcttgcgaccgatccgctcgcgccactcgcgggttcgac

	101365-101482	tccccacctgcatctatgtgtactCACTCGTCGTTTAATGGATGAGTGTAGAAGGG AAATGATGCGAAATGGACTGTTAAACTCCGCAGGCGGACCCTAGCT ATTTGTAGCTCTTGTCCTAGTCTAATGGAGTTTCTCATTtttagttttattca ataaatgaagtattttaattccatctccagcctacacctcacctagtagttcttgatgtttcgaagaatttgct gtt
Cb347	CAAC01000012 698376-698398	gctcaagaaatactagtcccgccgactgactgccgcgacaccgtgatgaagaaattagatccaactccagct agttagatacgtctttctggaacatGCAGATAAAGGCGAACGAGCGGGtcccacagaatt ctataatfttttagccttgaaggataagaagaacttagaaactgattttatttgactttaataaatagaaccta aataaa

The Sanger database accession number and coordinates are given in column two. All sequences are extended by 100 nt in both directions (lower cases). Letters in upper case correspond to the orthologous cDNAs in *C. elegans* (library sequences). The given positions refer to the sequence in upper case letters.

Table S20: Experimentally found, previously annotated histone-hairpin cDNAs for *C. elegans*

Group III: histone hairpin RNA

name	number of seq. clones	NCBI	sequence
Ce172a	1	U64843 13807-13845	*gcattcaattgctgaaAGCAAATCACCGAACCCAACGGCCCTCTTAAG GGCCACAaatgtattaaaatccttttcaattagtagtttatttaataaataaagtttctcattctcat cactattattcttatttttctcttatttaaaa
Ce172b	1	U64843 19434-19460	TttatctctcgattcatacaacaaccaaccgAACCCAACGGCCCTCTTAGGG CCACAattcaaaaatccaatttatgtataataataataattcttcttattcactgtgcagaaacc aaaagtaccaataatagacaacaacatcaacagg

The number of clones describes their frequency in the sequenced cDNAs. The NCBI GenBank accession numbers and coordinates are given in column three. Capital letters represent cDNA sequences. The additional sequences completed by Wormbase or GenBank information are in lower case letters.

***C. elegans* histone hairpin RNA sequence element:** We found two library sequences (Ce172a, b) that represent a part of the highly conserved histone hairpin RNA sequence involved in processing of histone pre-mRNA. Both library sequences are processing-remnants after endonucleolytic cleavage. Interestingly, both sequences differ at the 3' end of the loop region (U or A) that was previously described as highly conserved (U) in *C. elegans* but less well conserved in other species (Michel et al., 2000).

Literature

Michel, F., Schumperli, D., and Muller, B. 2000. Specificities of *Caenorhabditis elegans* and human hairpin binding proteins for the first nucleotide in the histone mRNA hairpin loop *RNA* **6**: 1539-1550.

Table S21: Experimentally found, previously annotated full-length spliceosomal cDNAs

name	number of seq. clones	U-RNA	Wormbase	NCBI	sequence
Ce11a (CeN1-1)	65	U1-8	F58G1.10	Z81556 (33218-33382)	aaacttacctGGCTGGGGGTTATTTTCGTGATCA TGAAGACGGAATCCCCATGGTGAGGCCT ACCCATTGCACTTTTGGGCGGGCTGACCC GTGTGGCAGTCTCGAGTTGAGATTCGCCA ACAGCTTAATTTTTGCGTATCGGGGCTGC GTGCGCGGGCCCTGAA
Ce11b (CeN1-6)	2	U1-9	T08G5.11	Z81589 (11803-11967)	aaacttacctggctgggggttatttcgcatcaaGAAGGCGG AATCCCCATGGTGAGGCCTACCCATTGCA CTTTTGGGCGGGCTGACCTGTGTGGCAGT CTCGAGTTGAGATTCGCCAACAGCTTTAT TTTTGCGTATCGGGGCTGCGTGCGCGCGG CCCTGaa
Ce11c	1	U1-1		X51371 (181-346)	aaacttacctggctgggggttatttcgcatcacaaaGGCGGA ATCCCCATGGTTAGGCCTACCCATTGCAC TTTTGGTGCGGGCTGACCTGTGTGGCAGT CTCGAGTTGAGATTCGCCAACAGCTTAAT TTTTGCGTATCGGGGCTGCGTGCGCGCGG CCCTGaa
Ce11d (CeN1-5)	19	U1-4	F08H9.10	Z77657 (7068-7232)	aaacttacctggctGGGGGTTATTTTCGCGATCAA GAAGGCGGAATCCCCATGGTGAGGCCTA CCCATTGCACTTTTGGGCGGGCTGACCTA TGTGGCAGTCTCGAGTTGAGATTCGCCAA CAGCTTAATTTTTGCGTATCGGGGCTGCG TGCGCGGGCCCTGAA
Ce11e	15	U1-7	F40G12.14	Z77661 (22220-22384)	aaacttacctggctGGGGGTTATTTTCGCGATCAA GAAGGCGGAATCCCCATGGTGAGGCCTA CCCATTGCACTTTTGGGCGGGCTGACCTG TGTGGCAGTCTCGAGTTGAGATTCGCCAA CAGCTTAATTTTTGCGTATCGGGGCTGCG TGCGCGGGCCCTG TA
Ce11f (CeN1-2)	38	U1	C15F1.9	AC006608 (12788-12952)	aaacttacctGGCTGGGGGTATCTCGTGATCAT GAAGACGGGATCCCCATGGTGAGGCCTA CCCATTGCACTTTTGGGCGGGCTGACCTG TGTGGCAGTCTCGAGTTGAGATTCGCCAA CAGCTTAATTTTTGCGTATCGGGGCTGCG TGCGCGGGCCCTGaa
Ce79 (CeN4)	21	U6-2		X51388 (158-259)	gttctccgagAACATATACTAAAATTGGAACA ATACAGAGAAGATTAGCATGGCCCCCTGC GCAAGGATGACACGCAAATTCGTGAAGC GTTCCAAATTTTT
Ce117 (CeN3-3)	6	U5-1		X51385 (155-276)	aactctggttctctgcatttaaccgtgaaAATCTTTCGCT TTTACTAAAGATTTCCGTGCAAAGGAGCA TTTACTGAGTATTACATACAATTTTTGGA GACTCCTTGAGAAAGCGGGTca
Ce119a	6	U5-5	F07C6.5	Z69659 (6668-6789)	aactctggttctctgcatttaaccgtgaaatcttctgctttactaA AGATTTCCGTGCAAAGGAGCATAACATTGA GTATTATATAACAATTTTTGGAGTCCCCTC GAAAGAGCGGGACA
Ce119b	9	U5-7	F38E11.10	Z68342	aactctggttctctgCATTTAACCGTGAAAATCTT

(CeN3-2)				(1320-1441)	TCGCCTTTTACTAAAGATTTCCGTGCAAA GGAGCATACATTGAGTATTATATAACAATT TTTGGAGTCCCCTTGAGAAAGCGGGACa
Ce307a (CeN2-1)	35	U4-3		X51384 (287-430)	ctttgcgctggGGCGATAACGTGACCAATGAGG CTTTGCCGAGGTGCGTTTATTGCTGGTTG AAAACTTTTCCAATTGCCCGCGATGTCC CCTGAAACATGGGTGGCATAACGAATTTT TGAACGCCTCTAGGAGGCAGaa
Ce310a	1	U2-8		X51380 (303-489)	atcgcttctcggcttATTAGCTAAGATCAAAGTGT AGTATCTGTTCTTATCGTATTAACCTACG GTATACACTCGAATGAGTGTAATAAAGGT TATATGATTTTTGGAACCCAGGGAAGACT CGGGGCTTGCTCCGACTTCCAAGGGTCTG TCCTGGCGTTGCACTGCTGCCGGGCTCGG CCCAgt
Ce310b (CeN18)	49	U2-5	W07G1.8	Z82076 (18363-18549)	atcgcttctcggcttattagctAAGATCAAAGTGTAGT ATCTGTTCTTATCGTATTAACCTACGGTAT ACACTCGAATGAGTGTAATAAAGGTTATA TGATTTTTGGAACCTAGGGAAGACTCGGG GCTTGCTCCGACTTCCAAGGGTCTGCTCT GGCGTTGCACTGCTGCCGGGCTCGGCCCA Gt
Ce310c	2	U2-9		X51381 (239-425)	atcgcttctcggcttattagctaaGATCAAAGTGTAGT ATCTGTTCTTATCGTATTAACCTACGGTAT ACACTCGAATGAGTGTAATAAAGGTTATA TGATTTTTGGAACCTAGGGAAGACTCGGG GCTTGCTCCGCTTTCCAAGGGTCTGCTCC GGCGTTGCACTGCTGCCGGGCTCGGCCCA Gt
Ce310d	6	U2-14	F15H9.6	Z81504 (7105-7291)	atcgcttctcggcttattagctaagaTCAAAGTGTAGTA TCTGTTCTTATCGTATTAACCTACGGTATA CACTCGAATGAGTGTAATAAAGGTTATAA GATTTTTGGAACCTAGGGAAGACTCGGGG CTTGCTCCGACTTCCAAGGGTCTGCTCTG GCGTTGCACTGCTGCCGGGCTCGGCCCA gt

The number of clones describes their frequency in the sequenced cDNAs. Annotated sequences are available at Wormbase or NCBI GenBank. Accession numbers and locations are given in the fourth and fifth columns. Capital letters represent cDNA sequences. The additional sequences are completed by previously known RNA sequences (Thomas et al. 1990). Designations given in parentheses refer to Deng et al. 2006.

Literature

Thomas, J., Lea, K., Zucker-Aprison, E., and Blumenthal, T. 1990. The spliceosomal snRNAs of *Caenorhabditis elegans*. *Nucleic Acids Res.* **18**: 2633-2642.

Table S22: Experimentally found, previously annotated full-length *C. elegans* splice leader RNAs

name	number of seq. clones	NCBI (Wormbase)	sequence
Ce20 (CeN8-2)	5	Z82078 25296-25407 sls-2.14 (W09D6.7)	ggtttttaccagtaaCGAAGGTTAGCATTAAATTTTCGACCTTTCGC AAGAACGCGTTGAAATGCAAATCAATTTTTGGAACCGCTTC TTCGGGGAATCCGTTGAGGCAAA
Ce74	36	NR_000674 1-98 rrs-1.2 (ZK218.13)	ggtttaattacCCAAGTTTGAGGTAAACATTGAAACTGACCCAAA GAAATTTGGCGTTAGCTATAAATTTTGGAACGTCTCCTCTC GGGGAGACAAAa
Ce103a (CeN16-1)	8	U41279 13489-13598 sls-2.2 (C17C3.16)	ggtttaaccagttactCAAGGTACGCTGGAGTTCTGACCTTTCGAA AGAGAGTGTCAAACAACTTTAACTTTGGAACCGCTCTGCT GGGGTTATCCGGTAGAGCAAA(c)
Ce103b (CeN16-4)	3	AF067219 24613-24722 sls-2.4 (R12E2.16)	ggtttaaccagttactCAAGGTACGCTGGAGTTCTGACCTTTCGAA AGAAAGTGTCAAACGACTTTAATTTTTTGGAACCGCTCTGCT GGGGTCATCCGGTAGAGCAAA
Ce133 (CeN16-2)	3	U29244 35344-35453 sls-2.1 (ZK1248.18)	ggtttaaccagttactAAGGTACGCTGGAGTTCTGACCTTTCGAAA GAGAGTGTCAAACAACTTTAATTTTTTGGAAAAGCTTCGCTG GGGTTATCCGGCGAAGCAAA
Ce224	2	U10438 39357-39465 sls2.16 (B0280.15)	ggtttaaccacaAGTTAACCAAGGTTAGCATGGAATTCGATCTTTC GAAAGAAATGTGTCGAACACAAAAATTTTTGGAACAGCTTC CTCGGGGTTTCCGTGGAGGCAAA
Ce226 (CeN7)	2	AL033514 181360-181470 sls-2.8 (Y75B8A.38)	ggtttaaccacaGTTTAACCAAGGTTAGCTGTCGTTTCGATCTCTC GAGAGAGTGTGTCGAATAAAAAATAATTTTTGGAATCGCTT CATCGGGGAATCCGTTGAAGCAAA

The number of clones describes their frequency in the sequenced cDNAs. Annotated sequences are available at Wormbase or NCBI GenBank. Accession numbers and locations are given in the third column. Capital letters represent cDNA sequences. The additional sequences completed by Wormbase or GenBank information are in lower case letters. Designations given in parentheses refer to Deng et al. 2006.

Table S23: Experimentally found, previously predicted *C. elegans* full-length SRP-RNAs

name	SRP	number of seq. clones	NCBI	sequence
Ce121a (CeN107-3)	SRP-C	195	Z34533 38793-39085	accgagcGTCGTGGCGGGCGCTTGTGAGTCAGCTTCTT GACGGTAGATGAGTGTGGATGGAGTGAGAGGAGGA GTCCTGTGTATGTCGTTGTCAACGTCGACCGAGCGT CCGTGCCAAGCGCTGCGTCACCAAGGGGATGACTGT CGGAAGATGGTCAGTCCCGGGTGCATAAAGGAGTGG TGGATGGTTCAGGACCGAAAAGGTAGCAGACAAAAG CCACCGCGCGGTGCAGTGGCCGGACAGCGCTTGTG AGTTGACACGTATACACAGCCTTCTCAATACCTTCA GACCACTTGCACCT
Ce121b (CeN107-2)	SRP-D	157	U23515 33855-33564	accgagcGTCGTGGCGGGCGCTTGTGAGTCAGCTTCTT GACGGTAGATAAGTGTGGATGGAGTGAGAGGAGGA GTCCTGTGTATGTCGTCGTCTACGTCGACCGAGCGT CCGTGCCAAGCGCTACGTCACCAAGGGGATAACTGT CGGAAGGCGGTTAGTCCCGGGTGCATAAAGGAGTGC TGGATGGTTCAGGACCGAAAAGGTAGCAGACAAAAG CGACCGCGTGGTGCAGTGGCCGGACCGCGCTTGTG AGTTGACACACATACACAGCCTTCTCGATACCTTCA GACCACTTATCATT
Ce121c (CeN107-1)	SRP-A	384	U00064 12857-13148	accgagcGTCGTGGCGGGCGCTTGTGAGTCAGCTTCTT GACGGTAGATAAGTGTGGATGGAGTGAGAGGAGGA GTCCTGTGTATGTCGTTGTCTACGTCGACCGAGCGT CCGTGCCAAGCGCTACGTCACCAAGGGGATAACTGT CGGAAGGCGGTTAGTCCCGGGTGCATAAAGGAGTGC TGGATGGTTCAGGACCGAAAAGGTAGCAGACAAAAG CGACCGCGTGGTGCAGTGGCCGGACCGCGCTTGTG AGTTGACACACATACGACGCTTCTCGATACCTTCA GACCACTTATCATT

The number of clones describes their frequency in the sequenced cDNAs. The NCBI GenBank accession number and coordinates are given in column four. Capital letters represent cDNA sequences. The additional sequences completed by GenBank information are in lower case letters. Definition of the 5'-ends of the sequences refers to previously predicted SRP-RNA sequences (<http://psyche.uthct.edu/dbs/SRPDB/rna/srprnaalphalist.html>). A fourth locus exists in the *C.elegans* genome. None of our cDNAs match this fourth locus. Designations in parentheses refer to Deng et al. 2006.

Table S24: Compilation of all computationally (com) derived “possible” C/D box snoRNA candidates that did not fulfill the criteria described in results

1. C/D sno RNA-candidates from neighboring H/ACA-introns

F17C11.9a – Int1

ttaattgattaaattgagtggttaagaatagtaacgtgattccggtcgttcattgaaaaatgattag
 Gm703/26S; guidebox D'(11nt)
 Gm49/tRNA-Arg; guidebox D'(10nt)
 Gm3005/26S; guidebox D'(9nt)

T08B2.9a – Int8

atattgtaaatgcatgagatattgattacggtgatgtgctgtaaaactagatattagaggttgttctaaaaagt
 Um613/26S; guidebox D'(9nt)
 Am3113/26S; guidebox D(10nt)
 Am459/26S; guidebox D(9nt)

ZK546.13-Int3

ggaaaactgtgaaatgtaactcctacctgaafatggaataatgcatfataatgcatattataatgcaatacttctaatgttttc
 Um 2894/26S; guidebox D(10nt)

C10C6.6 – Int3-sno1

actctgtgactaaaaaggcatttcaatcaacgaaacacgcgtgataaattgccaaatactcctccgcgactgtacacaaaattgagatttccctggaagt
 Um1834/26S guidebox D'(9nt)
 Am3264/26S; guidebox D(11nt)
 Am95/5.8S; guidebox D(11nt)
 Am1058/18S; guidebox D(10nt)

C10C6.6 – Int3-sno2

ttttttcatcaaatcttgaaccgccatttgaacctaatgaagcctgtgaccacaaattctgtactccatgtaagaaaatgagaaaaag
 Gm3194/26S; guidebox D'(9nt)

C10C6.6 - Int4

atattgatttccagaaaaccataagaaaacatataatttctcaataaaaaaaatgaaaaatggccaaaatttgagcraatttgaaaaat
 Um94/U2 guidebox D'(11nt)
 Um3217/26s; guidebox D'(9nt)
 Um1705/26S; guidebox D'(10nt)
 Um1810/26S; guidebox D(11nt)
 Um8/tRNA-Lys; guidebox D(10nt)

C10C6.6- Int5

gtttttaatgaataatttttaacgaaaaactatgaaactccgcagcaaaaaatgttttaaaactacagactcctcaaggc
 Am1512/18S; guidebox D(10nt)

Y43F4B.6 - Int4-sno1

gtattaatgagacggacgatttgattcaacattcacgaaactgttaacatttgacattccaatatgacgatg
 Gm96/U1; guidebox D(9nt)

Y43F4B.6 - Int4-sno2

cagtgtgtgaaagtccccctcgtgatgtttgtggttttttaagtgtgtgtcagaatgtttatgcaattctctgtctg
 Um73/5.8S; guidebox D(9nt)
 Um47/tRNA-Arg; guidebox D(10nt)

Y43F8C.7 – Int4

gaaatgatgaggaaaattgacgtttgccccggaaaattcggaaaaaacggacaaaaatcgatgaaatgattttgctgaaaaatgatttt
Am2814/26S; guidebox D' (10nt)

K02C4.4 – Int8-sno1

tttaaagaagagatacttctacatcactaaaggactttataaagtatttctgccaacaaaaacagagggg
Gm867/26S; guidebox D' (9nt)
Gm52/U1; guidebox D' (9nt)

K02C4.4 - Int 8-sno2

gtcttctgctgtgttctgatggcgaagagagagacgacgacgcaagcaaatgacgaatcgacacctgccccactcaaccctggggcg
Gm 273/26S; guidebox D (11nt)

2. C/D sno RNA-candidates from neighboring C/D-introns

2.1 C/D snoRNA-candidates from same intron/intergenic region in which a library-C/D was found

Y116A8C.35 – Int1

gaaaatgatgaaaaaacacaattctggggcaaaaaagtatatattttgtccagaaatcgatgttttccgcttttcctgatt
Am 36/U1; guidebox D (12nt)

F54C9.1 – Int2

taaatatgaagaactatataatgattataaaactttcaactagtttttacaacaaactgaaagcttaccaaatgataatattccaaaaacaaaactctgaattat
Am314/18S; guidebox D' (10nt)
Um3505/26S; guidebox D (10nt)

Intergenic region; neighbourhood of Contig138

ttgattgattcgaagaaaaaattaaagttcaagctgtatataccctatagggaacatctctgtttacaatcgaagagtagtattggaaaataattctgacaa
Am1096/18S; guidebox D' (10nt)
Am12/tRNA-Cys; guidebox D (10nt)

Intergenic region; neighbourhood of Contig246

aaaatgatgtatttagtactgctaaagcctttattgaaaaatgagaaagcggagaaaatgggtctctctcatt
Um718/26S; guidebox D' (9nt)
Gm1377/26S; guidebox D (9nt)

2.2 C/D sno RNA-candidates from neighbouring C/D-introns

C27H6.1 – Int-1sno1

aaattgattgtaaaatttttcacaactgaaaaagctattataagttttcaaaaatttaaattagccattctcttcattgaatt
Cm2019/26S; guidebox D' (11nt)
Um388/26S; guidebox D' (10nt)
Cm3011/26S; guidebox D (11nt)

C27H6.1 - 1sno2

ctgtgctcatttttcggacacagcttaacagtttataatatttgacatcaaatcttactatcgttcaactgaaag
Gm305/26S; guidebox D (10nt)

C27H6.1 – Int2-sno1

ttaacgaagcacctgcctattctattctcaagctcactctgtgtaattttaattttcggaacttcaactgaaa

Gm685/26S; guidebox D'(9nt)
Gm2552/26S; guidebox D (10nt)

C27H6.1 - Int2-sno2

ttcgatattgtagtatttacaatgacataagaatcttggatggtatf~~ta~~acttctgaaa
Um73/5S; guidebox D (9nt)
Cm1300/26S guidebox D (11nt)
Cm1492/26S; guidebox D (9nt)
Cm65/tRNA-Gly; guidebox D (10nt)
Cm21/tRNA-Thyr; guidebox D (9nt)
Um17/tRNA-His; guidebox D (9nt)

C27H6.1 -Int2-sno3

aaatgagtc~~atcattt~~taaccgggacgggaagtagaggaa~~gcctg~~ccccgtaatt
Cm506/18S; guidebox D'(10nt)
Um1565/18S; guidebox D (9nt)

C27H6.1 - Int5

gtttttgagta~~ttttagtt~~ctactatctcgaattaatacag~~atgag~~cgcgtattcc~~aa~~aa~~gaaa~~atgagac
Am65/26S; guidebox D'(11nt)
Um368/18S; guidebox D (11nt)

C27H6.1 - Int8

aaaattaag~~taact~~aaatta~~at~~act~~ccgact~~gcttggacacatacat~~gttgg~~caaatgggagatttaacttagaatactgat~~ga~~ataatttcag
Um500/18S; guidebox D'-1(9nt)
Gm845/26S; guidebox D'-2(9nt)
Gm1575/26S; guidebox D'-2(10nt)
Gm2042/26S; guidebox D'-2(11nt)
Gm613/18S; guidebox D'-2(9nt)
Gm15/tRNA-Phe; guidebox D'-2(10nt)

C27H6.1 - Int9

tttagaaa~~ttttc~~caactctttcgaatt~~aaact~~tcagctgtataaaa~~taataa~~atcc~~aaa~~ag~~act~~ctggaaa
Gm2720/26S; guidebox D'(10nt)
Gm17/U1; guidebox D'(10nt)
Um2971/26S; guidebox D (9nt)

C27H6.1 - Int10-sno1

tatagtt~~ccac~~tattcaga~~atttt~~tagtaccatc~~faaa~~atag~~ctaa~~att
Gm2565/26S; guidebox D'(10 nt)
Um130/U1; guidebox D (9nt)
Um130/U2; guidebox D (9nt)

C27H6.1 - Int10-sno2

aatgtgtgattttcaaatgttttcaaaaa~~ctca~~ctaatgtcgaattacattttaaaga~~ctgtt~~gaagttcta~~ttaca~~gagattgaatt
Um3503/26S; guidebox D'(10nt)
Um32/tRNA-Thr; guidebox D (9nt)

R166.5b -Int2-sno1

gagaaaaatgaaaa~~tattt~~gatc~~ctaa~~attttagttgatattcatca~~ca~~attagac~~gatcct~~tctagtgattctc
Am30/U2; guidebox D (10nt)
Am734/18S; guidebox D'(9nt)
Am1017/26S; guidebox D'(9nt)
Am911/18S; guidebox D (9nt)
Am3288/26S; guidebox D (10nt)
Am572/26S; guidebox D (10nt)

R166.5b – Int2-sno2

aaattgataccggaagcaattgatgatgtgagatgacggcacgtagattgacattgattgatta

Um675/18S; guidebox D'(9nt)

Am1408; guidebox D(9nt)

ZK994.3 - Int1

gatactgaaatttaaatatcatctaggctttcctgaattccttatttttcattttaagaaccgtttttaataaaaataactgatatt

Gm3317/26S; guidebox D'(9nt)

Gm45/tRNA-Ala; guidebox D'(9nt)

ZK994.3 - Int4-var1

aagtagttgacaaattttgaatttgagttcgaaattagaataaagcaataacctaccataaagaaatgaaactt

Am3157/26S; guidebox D'(10nt)

Cm2969/26S; guidebox D(10nt)

Cm1873/26S; guidebox D(9nt)

ZK994.3 - Int4-var2

aaagtagttgacaaattttgaatttgagttcgaaattagaataaagcaataacctaccataaagagtaattgaaacttctggttt

Am3157/26S; guidebox D'(10nt)

Am218/18S; guidebox D-2(9nt)

ZK994.3 - Int6

gtaagttattttactttc atgacttttctaatttttgttca/cacaaagaarcttatac

Gm872/18S; guidebox D'-1(12nt)

Am741/26S; guidebox D'-1(10nt)

Gm3115/26S; guidebox D'-2(10nt)

Gm1702/26S; guidebox D'-2(10nt)

Gm42/18S; guidebox D'-2(9nt)

Cm1858/26S; guidebox D(12nt)

ZK994.3 - Int8

ttttggtacttgatcatgcaatgtgactgtttcaatgtaactgtgtttccatgtacatgcatattttatgacaaatctatcaacaatctctctcaaaaa

Am1201/26S; guidebox D'(11nt)

Am1348/18S; guidebox D(9nt)

Am23/tRNA-Gly; guidebox D(9nt)

ZK994.3 - Int9

ggttgatgattggaaaatcatttcaaatctgaatgatgaacattttaaaccggaaatgaaatgaaatt

Gm 492/18S; guidebox D'(10nt)

Um 1174/26S; guidebox D(10nt)

ZK994.3 - Int14-sno1

aattacagttgctcagattttcagaaactgaataaataagaatgtgtaggtgtaattatgaaaaattatgcaccgaaactgaaatt

Um104/U2; guidebox D'(9nt)

tRNA-Cys; guidebox D'(10nt)

Um2150/26S; guidebox D(10nt)

ZK994.3 - Int14-sno2

ataattatgcattaaccatttttctcactgagcccgatgtttcgaaaaaaactctataatcaataactgaga

Am2487/26S; guidebox D'(10nt)

ZK994.3 - Int14-sno3

tttatgaataactctctcattgattgtaattccgggacaaaataaccagacaagaacaataaaggttttaactgataag

Am221/26S; guidebox D'-1(9nt)

Um684/26S; guidebox D'-2(9nt)

Um344/26S; guidebox D'-2(9nt)

Um1514/18S; guidebox D`-2(9nt)
Am721/26S; guidebox D (12nt)

ZK994.3 - Int14-sno4

tttgatggaacgtagtacaatctgaattgtctcctgaatttat/ta/cttgga

Um1317/26S; guidebox D` (9nt)
Am1356/26S; guidebox D (10nt)
Am736/26S; guidebox D (9nt)

F46F11.9b - Int4

taalcgataattttagaar/cac/taaaataggtctaaaaaaactctcaaa/ctct/taaa/gatattg

Um334/18S; guidebox D` (9nt)
Um2890/26S; guidebox D` (9nt)
Am833/18S; guidebox D (9nt)
Gm1434/26S; guidebox D (9nt)

F01D5.10 - Int1-var1

aatttatgctaaacctctcgaaa/caaa/ccc/gatgattgatcaagccgtattaggcgaaatcgaa/cttctcaaat

Am2721/26S; guidebox D` (9nt)
Um 97/5.8S; guidebox D (9 nt)

F01D5.10 - Int1-var2

aatttatgctaaacctctcgaaa/caaa/ccc/gatgattgatcaagccgtattaggcgaaatcgaaatttctcaaa/cttagctgaaatt

Am2721/26S; guidebox D` (9nt)
Um2529/26S; guidebox D (9nt)
Um 1151/18S; guidebox D (9nt)

F01D5.10 - Int2

tttaaatcgcatatctcggcggagattaaaggtaacaaaat/ctcaac/gacaaa

Cm1200/18S; guidebox D (9nt)

F48A11.5 - Int2

ggtagggctctctcctcccctg/cagtggtcccgctgacatattgattcgtctca/ctcc/teacgc

Am1115/26S; guidebox D (10nt)

F48A11.5 - Int3

tcgtgacgtgctctt/taaa/ccgaccaatagccccatttcacatggatt/ctct/cagattgacga

Am602/18S; guidebox D` (10nt)
Am833/18S; guidebox D` (10nt)
Am390/26S; guidebox D` (10nt)
Cm40/tRNA-Pro; guidbox D (9nt)

F48A11.5 - Int5

aaaaatagattgcttggggca/cttt/ccagctcagatcaattatttccgattttgttataaaaa/teggc/attctg/catttt

Gm1841/26S; guidebox D` (10nt)
Gm887/26S; guidebox D` (10nt)
Am402/26S; guidebox D` (9nt)
Am402/18S; guidebox D` (9nt)
Um20/5S; guidebox D (10nt)
Um2431/26S; guidebox D (9nt)
Um168/26S; guidebox D (10nt)
Um55/U5; guidebox D (9nt)

F47G9.3 - Int4

ctggataaaaa/taaa/tgagttatgtaaa/aattagaagaata/ctaac

Um 129/U1; guidebox D` (9 nt)

C08D8.1 - Int2

atttttataacteggggatcgttcaagacc**catc****tcac**atgagcgtgtaccttgaatga**cgttga****gtttc**ggaaat
Um31/U1; guidebox D' (9nt)
Um 98/5.8S; guidebox D (12nt)

C07A9.11 - Int11-sno1-var1

tttaaaaaatttaa**aatcc****ttctcaga**gagatggattttgcaaactttgatgattttaagcatgctagattat**tata****tattc**gaaa
Gm2417/26S; guidebox D' (9nt)
Um83/U5; guidebox D (9nt)
Cm5/tRNA-His; guidebox D (9nt)

C07A9.11 -Int11-sno1-var2

tttgatgattttaagcatgctagattat**tata****tattc**gaaaagagttttggaacatttttagaat**tgatta**aattggatt**ttctca****acggc**taaaa
Um83/U5; guidebox D' (9nt)
Cm5/tRNA-His; guidebox D' (9nt)
Cm12/tRNA-Pro; guidebox D (9nt)
Cm64/tRNA-Thr; guidebox D (9nt)

C07A9.11 -Int11-sno2

tattaggactatgaaaaat**tcattt****tagt**ctaaaaagtagtctaaaaaat**actg**aactttttca**aagtc****ttcgc**taaat
Cm506/18S; guidebox D' (9nt)
Am912/18S; guidebox D (13nt)

C07A9.11 -Int11-sno3

aactctagatcaacattttatt**ctaa****cca**ctggaccggttttacaatttctca**tgaaa**tttcccattgtcacgtaataat**ttcaa****taata**ctgagtt
Gm18/U2; guidebox D' (9nt)
Um121/U4; guidebox D (9nt)
Um104/U2+U5; guidebox D (9nt)
Um95/U2+U5; guidebox D (9nt)

C04G6.1a - Int2

ttttacacatctttt**gaa**ccaa**gttt**ttcaattggaccagtact**gaaaa**atggctcacaaaaat**atg**cc**g**aa**ct**taagaaa
Tm3162/26S; guidebox D' (14nt)
Um133/U1 guidebox D (10nt)

C04G6.1a - Int4-sno1

aacgtgagaatggagaca**l**atttctaa**caat**gtattgctgactct**g**aagg**ctgagg****ccag**ctgaagt
Gm1318/26S; guidebox D' (10nt)
Um367/26S; guidebox D (11nt)
Um781/26S; guidebox D (10nt)
Um1710/26S; guidebox D (10nt)

C04G6.1a - Int4-sno2

attgaaaaattatataa**ttt**ctgattttta**atg**attttttcaattttgcaacaata**atta****aagg**ctgattta
Gm93/U2; guidebox D' (13nt)
Am3216/26S; guidebox D' (11nt)
Am1703/26S; guidebox D' (11nt)
Um2879/26S; guidebox D (9nt)

C27H5.1-Int1-Var1-Sno1

tttcaccagtacaaa**attg****aagt**ctgttaattttataaaaaacactgtat**tgtaa**aatctcacagcaat**tttga****atta**ctcaaaa
Um1106/26S; guidebox D' (10nt)
Um2837/26S; guidebox D' (10nt)
Um98/5.8S; guidebox D (11nt)

C27H5.1-Int1-Var1-Sno2

aat**tttga**attttgccaat**ttacca****aac**ctgactgatataaaaaat**tgatta**cgactactggtcatgtttacctaaactattaa**ggtttca****l**gtttctgtt

Um1176/26S; guidebox D'(9nt)
Um933/26S; guidebox D (12nt)

C27H5.1-Int1-Var2-Sno1

tgtatggtaaatacctacagcaatgttgaattacccaacccaattttgaattttgccaattacaaaacgctgacigataaaa
Um98/5.8S; guidebox D'(11nt)

C16D9.2a - Int7

ttttttgattcgctcatggctgacaaaagattggttcaaaaatgttctgtagaga
Um1316/18S; guidebox D'(11nt)
Um1110/18S; guidebox D'(9nt)
Um22/tRNA-Cys; guidebox D (9nt)

C16D9.2a - Int27-sno1

gttcaagaatggggatcggaatattgaatttcgaaccattcctatagttattatgagaaaggctaaaggc
Um2293/26S; guidebox D'(9nt)
Um103/U2; guidebox D'(10nt)
Um130/U1; guidebox D'(9nt)
Um120/U4; guidebox D'(9nt)
Um28/tRNA-Cys; guidebox D (9nt)

U11029-Int7

tttttatttaaaatccttcagtaaacgggttagtaattcaaccaccatccaatccaatacaccatccaattataaaaacttagattcattgaaatcaaaaatctgactaa
aaaa

C05H8.1 - Int5

ttattatagcgaatcttccgagcgcgttttaaacgattgaaagtgtactcaalcctgctgaga
Um1511/18S; guidebox D'(10nt)
Um 3441/26S; guidebox D'(10nt)
Am201/26S; guidebox D (10nt)

C05H8.1 - Int6

ttggattgattgattactgtatattggtattactcagtgaaatttaaatttctctgaaaattgaaattttaacaagtggtgaagtctcgcttaactaaa
Um1676/26S; guidebox D'(11nt)
Am 1636/26S; guidebox D (10nt)

3. C/Ds in RPG-introns

rpl-12 - Int1-var1

tttaattaggatattgacgtatargcagattttcaattgtcaagattcatcatcgtgatttgaaa
Gm105/5S; guidebox D'(9nt)
Am37/U2; guidebox D'(9nt)
Cm2547/26S; guidebox D (9nt)

rpl-12 - Int1-var2

aagtgcctcattttgtgcacatttaattacgtatgacgtattatgcgtgatttcaattgtcaagatttcaatcactcgtgattt
Cm2240/26S; guidebox D'(12nt)
Gm91/5.8S; guidebox D (11nt)
Gm868/26S; guidebox D (9nt)

rpl-13 - Int3

atttaattaagttcaaglatfagaacttagtcgataacagttgttaaatattctgcat
Am2099/26S; guideboxD'-1(11nt)
Gm144/18S; guideboxD'-2(10nt)
Am456/18S; guideboxD'-2(9nt)
Am923/18S; guideboxD'-2(9nt)

Um11/tRNA-Cys; guidebox D (9nt)

rpl-14 - Int1-sno1-var1

tattaataagaaaaaaaaaatgtaagcagatttatgaattttacttaaactttttaaaaagttagattatcaatcgatcagaaatg
Um675/18S; guidebox D'(9nt)
Cm1695/18S; guidebox D (11nt)

rpl-14 - Int1-sno1-var2

atgttgtaaaatgcaaaatcgaaaagcatagctctgaacattaaatagtgaaatcatcctgaaatat
Um132/U1; guidebox D'(10nt)

rpl-14 - Int1-sno1-var3

gtttagattatcaatcgatcagaaatgtttgtaaaatgcaaaatcgaaaagc
Cm1695/18S; guidebox D (11nt)
Um132/U1; guidebox D (10nt)

rpl-14 - Int1-sno1-var4

aaatcatcactgaaatatgctcglta aatcatttactgaacaattagtaattagattgatattatgatt
Am1427/26S; guidebox D'-1(9nt)
Um3408/26S; guidebox D'-2(10nt)
Um1110/18S; guidebox D (10nt)
Um47/U6; guidebox D (9nt)
Um2422/26S; guidebox D (10nt)

rpl-14 - Int1-sno2

aagtgatttactgaaacaattagtaattagttgtaatttatgaatcaacaactccctttgaaattgttcgaatataatcgatataaaattagctgagcgttt
Um2422/26S; guidebox D'(10nt)
Um1110/18S; guidebox D'(9nt)
Um47/U6; guidebox D'(9nt)
Gm3064/26S; guidebox D (9nt)

rpl-18 - Int3

aaaatgtaaaaaattattcttggtttatgaaaccagtatctgaaataatacgaaaacatcgagtactccggaatt
Am43/18S; guidebox D'-1(10nt)
Am843/18S; guidebox D'-1(9nt)
Am1762/26S; guidebox D'-1(10nt)
Am6626S; guidebox D'-1(9nt)
Am97226S; guidebox D'-1(9nt)
Gm1620/18S; guidebox D'-2(9nt)
Um21/U1; guidebox D (11nt)
Um487/18S; guidebox D (9nt)
Um28226S; guidebox D (9nt)

rpl-19 - Int1-var1

agtttttaaatcatttccaattgaagatcagccaagcgtctttgaagatatgactttcgttaatgagaatt
Am 1053/18S; guidebox D (11nt)

rpl-19 - Int1-var2

gaaagatcatgccaagcgtcttttgagatatgactttcgtttaatgagaattgcaaaaattgcatttttattatgatt
Um2656/26S; guidebox D'(9nt)
Um785/26S; guidebox D'(9nt)
Um1713/26S; guidebox D'(9nt)
Um1326/18S; guidebox D'(9nt)
Um2245/26S; guidebox D (9nt)

rpl-19 - Int3

taaatgattgtttttccaaattgagaagcttttcaatcaattattcatattaaaatcctgatgattt

rpl-21 - Int1-var1

gaaagtaattatgtagtcttttcaatttgaaaaacaactcaatccaactcatttgactgaaatgactgatttt

Gm1206/18S; guidebox D'-1(9nt)
Cm2969/26S; guidebox D'-2(12nt)
Um2894/26S; guidebox D (9nt)

rpl-21 - Int1-var2

ttgaaatgacacctaataacatgctagcatgctgacaatttcatttcgaaagtaattatgatagctcttttcaatttgaaaa

Gm1206/18S; guidebox D (9nt)

rpl-26 - Int2-var1

gactcatcaacaactgtcaacttttgacttccaatgattcttaattgttcattcggactaggaaaaagttattatatttgaaatgaccgagtt

Um3176/26S; guidebox D'-1(9nt)
Um2519/26S; guidebox D'-1(9nt)
Um2530/26S; guidebox D'-1(9nt)
Am772/18S; guidebox D'-2(10nt)
Am146/26S; guidebox D (11nt)

rpl-26 - Int2-var2

gactcatcaacaactgtcaggttttgacttccaatgattcttaattgttcattcggactaggaaaaagttattattatatttgaaatgaccgagtt

Um 638/18S; guidebox D'(9nt)
Um1651/18S; guidebox D (10nt)
Um141/26S; guidebox D(11nt)
Um490/18S; guidebox D (9nt)

rpl-26 - Int2-var3

gtgagttccatgattcttaattgttcactggaactaggaaaaagttattattatatttgaaatgaccgagttcgt

Um2558/26S; guidebox D'(9nt)
Cm793/26S; guidebox D'(9nt)
Um85/U2; guidebox D'(9nt)
Um1651/18S; guidebox D (10nt)
Um490/18S; guidebox D (9nt)
Um141/26S; guidebox D (10nt)

rpl-26 - Int2-var4

ggtttgacttccaatgattcttaattgttcattcggactaggaaaaagttattattatttgaaatgacc

Am782/18S; guidebox D'(10nt)
Am145/18S; guidebox D (11nt)

rpl-32 - Int1

ttttgaaacacctactcattagaattgaaaaagcagagaataaataatgatgtaacaaa

Cm1669/18S; guidebox D (9nt)

rpl-33 - Int1-var1

ccgctggataatttgactctctgtaaaaaatcagaactgcaaatctcatatagctttaaaaaatgatagtacattatcctaactatttctatctaaatccgagg

Gm398/26S; guidebox D'-1(12nt)
Gm2775/26S; guidebox D'-1(11nt)
Gm3153/26S; guidebox D'-1(9nt)
Am2310/26S; guidebox D'-2(10nt)
Gm1674/26S; guidebox D (9nt)

rpl-33 - Int1-var2

ggatattttgactctgctgaaaaatattcagactgcaaatctcatatagctttaaaaaatgatagtagcaatctaaatctattt

Am2310/26S; guidebox D'(10nt)
Am443/26S; guidebox D (10nt)

rpl-33 - Int1-var3

tttaatacagtgaccgctggaattttgagctctgctgaaaaatatcagactgcaaa
Am2310/26S; guidebox D (10nt)
Am172126S; guidebox D (9nt)

rpl-37 - Int1

aattggaagaataaacatcagacggctctaaattgtcttattactttctgctccatgtgttctactcaaat
Gm1265/26S; guidebox D (11nt)
Gm 61/U4; guidebox D (9nt)
Gm2408/26S; guidebox D(11nt)

rpl-38 - Int1-sno1-var1

gcacaaatctttataagatacgtagattcaacgctcaagctcttcggaaaagtgtgaagattcacctgattttg
Gm616/18S; guidebox D (10nt)
Um95/5.8S; guidebox D (9nt)
Gm773/26S; guidebox D (9nt)

rpl-38 - Int1-sno1-var2

tctttataagatacgttagattcaacgctcaagctttcggaaaagttgtgaagattccacctgattttccagttcttgaagaa
Gm616/18S; guidebox D (10nt)
Am951/26S; guidebox D (10nt)
Am972/26S; guidebox D (9nt)
Am25/U6; guidebox D (13nt)

rpl-38 - Int1-sno1-var3

ggaaaagtgtgaagattcacctcaattgttccagttttcggaaaacaattcattggagttttctgattttct
Um95/5.8S; guidebox D (9nt)
Gm 773/26S; guidebox D (9nt)
Um1104/26S guidebox D (15nt)

rpl-38 - Int1-sno2

gaaagaaaaacaattcattggagttttctgaattttcctaattgttgagtcagcacattgtatctgttctg
Um1104/26S; guidebox D (15nt)
Gm1117/26S; guidebox D (10nt)

rpl-42 - Int2

tgtttataaaaaa/raattcaaatgaagtgtttgtctgatttttaaaagctgtttggaatttcaatt/aaaaatatacctga
Am1808/26S; guidebox D (9nt)
Gm100/U2; guidebox D (13nt)

rpa-2 - Int2-var1

gttatgaagtcctaaaaaagtgactgacttggtaaattcagcagatgcttaactcggaat
Am54/5S; guidebox D(9nt)

rpa-2 - Int2-var2

gttatgaagtcctaaaaaagtgaagcactggtaaattcagcagatgcttaactcggaattttgagaaaaaaccttga
Gm598/26S; guidebox D (9nt)
Cm2650/26S; guidebox D (10nt)

rpa-2 - Int2-var3

ttatgaagtcctaaaaaagtgaagcactggtaaattcagcagatgcttaactcggaattttgagaaaaaaccttga
Gm598/26S; guidebox D (9nt)
Um1454/26S; guidebox D (11nt)
Um3254/26S; guidebox D (10nt)

rps-7 - Int1

gtttgttttaaacatttaacttgaattttgatttttgaagaaagctttgaaat

Um20/5S; guidebox D´(10nt)
Um2315/26S; guidebox D´(9nt)
Um1577/26S; guidebox D´(9nt)
Cm1213/18S; guidebox D (10nt)
Um2652/26S; guidebox D (11nt)

rps-8 - Int1

gctgtttaattttattttattaccaggaatggaatcagtaaaattaatttaaaaagatgacg
Am123/18S; guidebox D´(9nt)

rps-9 - Int2-var1

ttttacaaatgttttcgattaaaccagtaggatttcctgcgctattttaaagactgactccagtagtcaattgtccggaatttcattataaaaatttattcactgaaga
Gm1541/18S; guidebox D´-1(11nt)
Gm1226/26S; guidebox D´-1(10nt)
Cm143/26S; guidebox D´-2(10nt)
Am2416/26S; guidebox D (9nt)
Am1202/26S; guidebox D (9nt)
Gm1548/26S; guidebox D (9nt)

rps-9 - Int2-var2

atttgaagaactgactccagtagtcaatttcctgcggaatatttcattataaaaatttattcactgaaga
Gm449/18S; guidebox D´(11nt)
Am826/18S; guidebox D´(9nt)
Am1057/26S; guidebox D´(9nt)
Am2416/26S; guidebox D (9nt)
Am1202/26S; guidebox D (9nt)
Gm1548/26S; guidebox D (9nt)

rps-19 - Int2

aaaataaattataaaaatttcataaatatgcgctgaaattaacatgcaaaattagatgttatattaaaatttaatttcgcatgttt

rps-18 - Int2

agtgaaaataggcctgttttttttaaatctgatacagggccaccagtttaatttttgagagaccatttgact
Am2628/26S; guidebox D´(11nt)
Am1102/18S; guidebox D´(9nt)
Gm3211/26S; guidebox D´(10nt)
Gm389/26S; guidebox D´(10nt)
Um676/18S; guidebox D (9nt)

rps-20 - Int1-sno1-Var 1

gggtgtggaattttttcaaaaatttcgaatttcagcggatttttgattttatgaggaaatttgaattc
Um104/U2; guidebox D´-1(11nt)
Um120/U4; guidebox D´-1(10nt)
Am646/26S; guidebox D´-2(10nt)
Um131/U1; guidebox D (12nt)

rps-20 - Int1-sno1-Var 2

gggtgtggaattttttcaaaaatttcgaatttcagcggatttttgattttatgaggaaatttgaattc
Um104/U2; guidebox D´-1(11nt)
Um120/U4; guidebox D´-1(10nt)
Am646/26S; guidebox D´-2(10nt)
Cm162/18S; guidebox D (10nt)
Cm401/16S; guidebox D (10nt)
Cm3/tRNA-Cys; guidebox D (9nt)

rps-20 - Int1-sno1-Var 3

tttgggtgtggaattttttcaaaaatttcgaatttcagcggatttttgattttatgaggaaatttgaattc
taarcttaatttgaacttaaaa

Um104/U2; guidebox D'-1(11nt)
Um120/U4; guidebox D'-1(10nt)
Am646/26S; guidebox D'-2(10nt)
Um2061/26S; guidebox D (10nt)
Um1810/26S; guidebox D (9nt)

rps-20 - Int1-sno1-Var 4

ggatttttgatttttatgcggaattttgattcttaatacaatttttgacttaaattgatattttccttaataaaa
Um2293/26S; guidebox D (9nt)
Um131/U1; guidebox D (12nt)
Um 3267/26S; guidebox D (9nt)
Am925/18S; guidebox D (10nt)
Am458/18S; guidebox D (9nt)
Am2490/26S; guidebox D (9nt)

rps-20 - Int1-sno1-Var 5

ttttatgcggaatttttaattcttaatacaattttgacttaaattgatattttgcttaataaacctatttatgcccagaatt
Cm1629/18S; guidebox D (10nt)
Cm401/26S; guidebox D (10nt)
Gm38/tRNA-Ala; guidebox D (10nt)
Gm68/tRNA-Glu; guidebox D (9nt)

rps-20 - Int1-sno1-Var 6

aattttggaattctaaactaattttgacttaaattgatattttgcttaataaacctattttatgcccagaatt
Um2061/26S; D'(10nt)
Um1810/26S; D'(9nt)
Gm38/tRNA-Ala; guidebox D (10nt)
Gm68/tRNA-Glu; guidebox D (9nt)

rps-20 - Int1-sno1-Var 7

tattttgcttaataaacctattttatgcccagaattcatcaaaaatcatttttattattttcagcctcaaaatggaata
Gm38/tRNA-Ala; guidebox D (10nt)
Gm68/tRNA-Glu; guidebox D (9nt)
Am668/18S; guidebox D (11nt)

rps-20 - Int1-sno2

aaactggaaatagagcaccgaaggctaaatcaaaagatagcagacctcaaagctcttaaatctacatcgaaacaaacatggtgatt
Um1064/18S; guidebox D (9nt; IGT-Paar)
Um 1062/18S; guidebox D (11nt)
Gm1229/18S; guidebox D (9nt)
Gm333/18S; guidebox D (10nt)

rps-21 - Int1

gtgagatttatctaattatatgtatatagaacgtgaccaaactctacgtttaacgctttatataat
Um21/tRNA-Ile; guidebox D (10nt)
Um20/tRNA-Leu; guidebox D (10nt)

rps-24-Int1

tcttaaaatgtttttattttgatttgcgaattgcttgatcactaccgtttaacatgaatgg
Um1100/18S; guidebox D (9nt)
Gm2046/26S; guidebox D (11nt)
Am722/26S; guidebox D (9nt)

rps-24 - Int2-var1

ttttcgaataagaacggaatttttaataatgacttctagctaaattgatagacaaattctacgttcagcctttcgaagag
Um2910/26S; guidebox D'-1(9nt)
Am1312/26S; guidebox D'-2(10nt)

Am22/tRNA-Ser; guidebox D'-2(11nt)
Gm837/26S; guidebox D (11nt)
Gm45/tRNA-Trp; guidebox D (11nt)

rps-24 - Int2-var2

ggaattttgatagatgactcctactgtaaaatgatagacaaattcctacgctcagccttctgaagagtct
Am1312/26S; guidebox D'(10nt)
Am22/tRNA-Ser; guidebox D'(11nt)
Gm837/26S; guidebox D (11nt)
Gm45/tRNA-Trp; guidebox D (11nt)

rps-24 - Int3

attgttaacttcagtaaaacgatttactacagaattgttttcgtttttatgttgacttgagttggtatccctctcatat
Gm413/26S; guidebox D'(9nt)
Am1539/18S; guidebox D (9nt)

rps-24 - Int4

tgcttcatgctacgacaaatttttgaatttcaccacttggatgctcgaactcacttgaata
Am1703/26S; guidebox D'(9nt)
Um54/tRNA-Asn; guidebox D (10nt)
Um54/tRNA-Val; guidebox D (10nt)
Um682/18S; guidebox D (9nt)
Um1701/18S; guidebox D (9nt)

rps-25 - Int1

ttttgctgtctggaaaaatttcaactgatttgaataggaaatcacaaagtagcaaacacgattgaaaga
Um671/26S; guidebox D'(9nt)
Um227/18S; guidebox D (12nt)

rps-27 - Int1-var1

atgtgcttaaragccttcagaaattgtttttcaaaagtttttgctcgacaaaccgccccttttctgagat
Am1022/26S; guidebox D'(9nt)
Am2476/26S; guidebox D'(9nt)
Um309/26S; guidebox D (10nt)
Cm2477/26S; guidebox D (9nt)

rps-27 - Int1-var2

agtttttgcgacaaacgccccttttctgagattgacgattctgtattcaactgttaaatctctaacatctaaatgct
Um309/26S; guidebox D'-1(10nt)
Cm2477/26S; guidebox D'-1(9nt)
Am2225/26S; guidebox D'-2(10nt)
Am2779/26S; guidebox D'-2(9nt)
Um108/U1; guidebox D (9nt)

4. C/Ds in RPGs with different variants whereof all have orthologes in *C. briggsae*

rpl-3 - Int1-Var1

agtgttatgggtcggttttgggtcatttggtcttttcctgattacaagtctgtatttcagtcgctgttcttaagtcggttccctcccgact
Cm1683/18S; guidebox D'(9nt)
Cm3202/26S; guidebox D'(9nt)
Cm2462/26S; guidebox D'(9nt)
Am407/18S; guidebox D (10nt)

rpl-3 - Int1-Var2

gtttcgtgattacaagctctgtatttcgacgctccttcttaagtcggttccttcgctgtacttatgtacatgatggtaaacgaactgagtgctaaagc
Gm2863/26S; guidebox D'(9nt)

Gm1726/26S; guidebox D` (9nt)
Gm149/26S; guidebox D` (9nt)
Um3163/26S; guidebox D (10nt)
Um477/26S; guidebox D (10nt)

rpl-12 -Int2-var1

tttaatgcgttgggtcggg**gagtcgat**gctctcatcccctggctcttact**cataa**gtttgtaa**agtt****gtgact**aaa
Um920/26S; guidebox D`-1(11nt)
Am3172/26S; guidebox D (10nt)

rpl-12 -Int2-var2

aaaagt**ttgtga**cttaaagactagtaac**taagtga**tttcatgct**ccg****gagtt**gatttt
Gm682/18S; guidebox D (11nt)
Gm2138/26S; guidebox D (9nt)

rpl-12 -Int2-var3

gactaaagaactagtaacctaag**tgat**tttcatgct**ccg****gagtt**gat**tttcc**gggtt
Gm42/18S; guidebox D (11nt)
Am950/18S; guidebox D (10nt)
Am2917/26S; guidebox D (9nt)
Gm26/U4; guidebox D (9nt)

rpl-12 -Int2-var4

act**cataa**gtttgtaaagttt**gtgact**aa**agacaa****aaac**ctaa**gtgatt**tc**catg**ct**ccg****gagtt**gat**tttcc**gggt
Cm678/18S; guidebox D` (10nt)
Gm42/18S; guidebox D (11nt)
Am950/18S; guidebox D (10nt)
Am2917/26S; guidebox D (9nt)
Gm26/U4; guidebox D (9nt)

rpl-31 - Int1-sno2-Var1

ttctgtgag**tgct****ctc**cagaaacgccgttctgttctcattcgagaatcgga**eggag**atct**agga****catc**ctcaaa
Gm376/18S; guidebox D` (9nt)
Cm1401/18S; guidebox D (9nt)

rpl-31 - Int1-sno2-Var2

gtttcgg**tgag****tgct****ctc**cagaaacgccgttctgttctcattcgagaat**eggac****gag**atctcaggggc
Gm376/18S; guidebox D` (9nt)
Gm2086; guidebox D (9nt)

rps-6 - Int1-var1

gaagtgatg**ttct****gtct****aaat**ccca**ttgt**tcacg**tgct**ttttcttc**ctga****atgg**ctgactagacatacat**tgagag**tccag**ttttgttt****tgaa**ccgattct
Um2531/26S; guidebox D`-1(9nt)
Um2894/26S; guidebox D`-2(9nt)
Am942/18S; guidebox D (13nt)

>rps-6-Int1-var2

gaagtgatg**ttct**gtgtcaaatcctcattg**ttc**acgtgcttt**ttc**ctga**aat**ggctg**tgacta**gacatacattgagag**tccag****ttttgttt****tgaa**ccgattct
Gm57/26S; guidebox D` (13nt)
Gm2499/26S; guidebox D` (12nt)
Gm392/26S; guidebox D` (11nt)
Gm568/26S; guidebox D` (10nt)
Gm58/26S; guidebox D` (9nt)
Gm368/26S; guidebox D` (9nt)
Gm2022/26S; guidebox D` (9nt)
Gm528/18S; guidebox D` (9nt)

Am942/18S; guidebox D (13nt)

5. C/Ds in RPGs with different variants, some of which have orthologs in *C. briggsae*

rpl-7a - Int3-Var1

atttttatcagagtcagtactaaaagcagccttgagcttgcactgacgcatttactctataggtgaagt

Um755/18S; guidebox D' (9nt)

Um2133/26S; guidebox D' (9nt)

Um 2821/26S; guidebox D' (9nt)

Cm733/18S; guidebox D (9nt)

rpl-7a - Int3-Var2

agagtcagtactaaaagcagccttgagcttgcactgacgcattactctgagtagtgaagtaaggctttgacttt

Um755/18S; guidebox D'-1(9nt)

Um2133/26S; guidebox D'-1(9nt)

Um 2821/26S; guidebox D'-1(9nt)

Am1090/18S; guidebox D'-2(9nt)

rpl-7a - Int3-Var3

gagtcagtactaaaagcagccttgagcttgcactgacgcattactctgagtagtgaagtaaggcttgcactttacgctgttatgtttccagtgtatttctgttt

Um755/18S; guidebox D'-1(9nt)

Um2133/26S; guidebox D'-1(9nt)

Um 2821/26S; guidebox D'-1(9nt)

Am1090/18S; guidebox D'-2(9nt)

Um2918/26S; guidebox D (11nt)

rpl-7a - Int3-Var4

atgtactatagcaagccttgagcttgcactgacgcattactctgagtagtgaagtaaggcttttgactfacgctgtatgt

Am1090/18S; guidebox D'-2(9nt)

Am1549/18S; guidebox D'-2(10nt)

Am1151 guidebox D'-2(9nt)

Gm1216/26S; guidebox D (11nt)

Gm1440/18S; guidebox D (10nt)

rpl-7a - Int3-Var5

tgataggtgaagtaaggctttgactttacgctgttatgtttccagtgtatttctgtttca

Um2918/26S; guidebox D (11nt)

rpl-30 - Int1-Var1

taattgagaaggagtagcftccccctcattctgtcacgggcttcgggtgctcaatgtaagcgctcgcaaattccaatattcgaacgcctgatga

Gm1902/26S; guidebox D' (11nt)

rpl-30; - Int1-Var2

agcgatggagtaatccggagcctcgggtgatttaattgagaaggagtagcftccccctcatt

Gm1902/26S; guidebox D (11nt)

Gray = double stranded regions, yellow = C' and C boxes, green = D' and D boxes, red = the complementary nt at the target site is methylated. Bold and underlined letters represent the antisense elements, italic letters indicate G-U pairings corresponding to the target site. If more than one possible target site is given for a given box, the underlined antisense element belongs to the first target site in the list. If potential targets were found for two possible D'-boxes, the boxes are numbered by their position from the 5'-end (e.g., D'-1; D'-2). In those cases both antisense

elements are marked only if they do not overlap each other. Var denotes variants with different possible C or D boxes.

Table S25: Compilation of all computationally (com) derived “possible” H/ACA snoRNA candidates that did not fulfill the criteria described in results

Comp. found H/ACAs, which do not fulfill our stringent criteria

rps-22-Intron 1

aatagatgatgatgctggcagcctcggtcgcaaaaaatgaccaaggctctccgtgaatttagaatttagtgaagaaactcggtttatttccaa
acataacttgcggttctaattaacggagacccc

W08G11.3 - Intron 2

ctggcaaaaatggtgaaaagcaagaatttagccaaaaatgtgaaattttcgaaaaatgaattcttactctcctcggggagtacacga

Sequences marked in purple denote box H and ACA.

Table S25: Oligonucleotides used for pre-selection and sequencing

name	sequence 5' – 3'	Annealing °C
Oligonucleotide sequences used for preselection		
pSP0RT	CGTGCATGCGACGTCATAGCTCTTCTA	65
SNI	ACTAGTTCTAGATCGCGAGCGGCCGCTC	69
CeU1	CACGCAGCCCCGATACGCAAAAAT	64
CeU2	TTTTTGGAACCTAGGGAAGACTCG	60
CeU4	CCCGCGATGTCCCCTGAAAC	64
Ce5S/1	GCTTACGACCATATCACGTTGAATGCACGC	66
Ce5S/2	GATCTGGCAAGTTAAGCAACGTTGAGTCCA	65
Ce5S/3	TACTTGGATCGGAGSCGGCCTGGGAATCCT	69
Ce5.8S/1	CGATACTCGATGCAACCGATCCATCGCTGA	68
Ce5.8S/2	GCGTCTGCAATTCGTGGTAAGTAACGCAGC	68
Ce5.8S/3	CAACCAGACGTACCAACTGGAGGCCAGTT	69
Ce18S/1	GCAGACACCCTTCCGGATAGAGTCAGTCG	69
Ce18S/2	GATACACTAGGAGAGCTGGAATTACCGCGG	68
Ce18S/3	CTGTTGGGCGTCTCACTACGGTCCACGAAT	69
Ce18S/4	CGCCAACTATTTAGCAGGCTAGAGTCTCGC	68
Ce18S/5	CCCTATCCCGGACATGGAAGAATTTCAACG	66
Ce18S/6	CTCGAAGCGACAGTCCCCACTTCTCGAA	69
Ce28S/1	CAACCCGACTCCAAGGAGCAAGCGAACCAA	69
Ce28S/2	CGTAACTAAACGCTAGCCGCCACGAACCCA	69
Ce28S/3	CCCCTTGGACCTCGCATTACGTTGACAG	69
Ce28S/4	CCTTCCTACTCGTTACGACCTGGCGCTAGA	69
Ce28S/5	CGAGACACCACAGAAACCGCGGTGCTTTTC	69
Ce28S/6	GTCAACGTCCGCAAGGACCATCTGTACCT	69
Ce28S/7	CCTGTCTCACGACGGTCTAAACCCAGCTCA	69
Ce28S/8	GGCGTTGGCAAGCGTCGCAGAATTCCTAC	69
Oligonucleotides used for sequencing and colony PCR		
M13-FSP	GCTATTACGCCAGCTGGCGAAAGGGGGATGTG	71
M13-RSP	CCCCAGGCTTTACACTTTATGCTTCCGGCTCG	70

Table S26: Oligonucleotides used for Northern blots

name	sequence 5' – 3'	annealing °C
tRNA modifying snoRNAs		
Ce62	GCAAAGTACAGTGGCACGTTCTCTTCAC	62
Ce63	CCGCCCTAGTCGCAAACCTCATC	62
Ce94	CCCTGAAGTGGGAATAGGAATGATAACC	61
Ce245	GGTGTCTCGACATATTGGCATTCCG	62
Ce246	GCGCTCAGCAAATGGGTATGTTATCA	62
comCe3	GGTCTTGCGATAGAGACGGGAACTC	60
compensatory mutations in snoRNAs		
Ce138	CTTCACGGTTGGTGCAGATGTCC	60
Ce234.2	CATGATGAGAATCAACTGACTCGGCTAC	60
presence/absence of snoRNAs		
comCe14	CGAATATGACCGAGTGCAGCGAA(T)AAAA	64
comCe15	AGTTTAAAATGAGAGAAACCCAGCTAAAAAT	58
Ce356	TTGTGTGACAACCGTT(T)AAAAATCGAGA	61
Ce273	TGT(CATC)GTTACACCAGGAAAAATAGAA(T)A	62
Ce80	CTAAAACTAGAAGATATAGCACCAACACATACATAAGG	61
comCe7	GGACTTCACACGAGACATGCTTATTGATA	60
comCe12	CTAAACTAAACGTCGAAAAGCACAGGCA	62
Ce236	AACATGAGCATCAAAATATGAAGCACAT	58
transposon CELE45/PIGGYBAC		
Ce157	GACGATCCGTTCTTCAAGTGCTATGC	61
Ce268	GCAGCGCGCATAGGCACTGA	62
Ce293	TGTCTGAATACACCCAATTTCTAATGAA	59
C/D box snoRNAs		
Ce86	CTCTGGTTTACAGCCATGGTAGCGT	64
Ce96	CTGACCTCGAAAGGACAGGGTTCTC	65
Ce135	TGTACACTGGGTCTTTAGTAAGGCC	62
Ce139	GCATCATGGATTCAGCCGAAAGATG	62
Ce167	AAGCCTCAGCTAATGAAATCACCTC	60
Ce171	CAGCTCAGACGTTGCGCATATTTCC	64
Ce177	GCTCAGACGTCCAAGGAAGTTTAGC	64
Ce223	GCCATCATACTTTCTTGTTCATCATG	59
Ce243	GCTCTGATAGGGGCGAAATTTCTCA	62

Ce254a/b	CTCAGACAAATGCCTCATATCCGCA	62
Ce304	GTGCTCTGATAATGTAGGAAGACAT	59

comp found C/D box snoRNA

comCe4	GTTTTCGTCATCGGTAACAGATTCAGG	60
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known C/D box snoRNAs

Ce61	CTCAGACGGGGAAAGTTAATCTTCA	60
Ce81	GGATCAGACCCAAAATTCAGCCCG	64
Ce100	GAGCTCAGACTAAGGCGTACTATTT	60
Ce209	GAGCTCAGAGATCCTAGTGGACTCA	64
Ce230	TGTCCTCAGTTGGTGTTCATGGAT	62
Ce239	GTCTCAGAATTGTATAAGATTGATC	55

H/ACA box snoRNA

Ce23	CGGATGAACTTTTAAACGCACACCCT	62
Ce27	AATCGAAGGAGTGGACATCATTCCG	62
Ce48	GTCATGGGACGCGACGTTAGCGAAT	65
Ce57	AATTGTGCACGAAGATGGTGTGCAC	62
Ce58	GGAGCGGGAATAAAGGACATGTTTT	60
Ce176	CATCAGGTGATCATTAGCTCACAGG	62
Ce192	TGAAGTCGGGGAGCGCAAAGCAAG	65
Ce375	CCCGAGGAGAAAAGGAACCATATTG	62
Ce375/2	TATTGCATTAAGCAAACCGGCAC	59

new U5 isoform

Ce13	TGCCTTGCTCTTTCGAGAAGGCTCC	65
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others

Ce228-2	GCTCACATCGGCGGTGCTCAG	63
Ce228-1	TATAGCGAGATCAATCTAGACCGAAATACG	60
Ce142	CCGGTAGTCAAGTTAGTTCGTATGGGG	61
Ce220+129	GGTCAAGTTGATGCCGATGGGA	61
Ce1+5	GGCTCCGTGCGGTCATCAAG	60
Ce1+5rev	CTTGATGACCGCACGGAGCC	60
Ce26	CGATCAGAGTAGGCCCTATGCTGTTCTAAG	63
Ce87	GCTGATTGGCAATGGCGGAG	60
Ce104	CCTGCTCTAACCCAATTCAACTCGTC	60
Ce106	GTGTCGCGATGAACATTTATGACCAT	60
Ce118	GAAGCATCTGAGTTAAAAAGCTCATTTCG	60
Ce148	GCCAATTCGCATCATTTCCCTTC	62
Ce244	CAATCTATAAACAAACAGCATCACATCTACGG	61
Ce296	TTGTTCCAAAGGTCAAGCTAACTACATCC	61
Ce347	CCCGTTCGTTCCGCTTTATCTGC	63
Ce121	AAGTGGTCTGAAGGTATTGAGAAGGCTG	60
Ce150	CCGGTCAAGGGATGTCTATGGGG	62
Ce342	GTCCTAGGTCCATATAGATAACAACAAGAATGC	60
Ce9a/b	AGAATCGGGCTGGCAGGCGGGTATT	67

Ce210	TGCATGGTTTGGTCCTAACCGTCACG	64
Ce376	TTTCAAATGAAGAGAGTACAAATG	64
