

Unusual Novel SnoRNA-Like RNAs in *Drosophila melanogaster*

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Supplemental Material

Supplemental Table 1. Target predictions for snoRNA in ribosomal and spliceosomal RNAs. The interactions are shown with the snoRNA guide sequence in 3'→5' orientation on top and the target RNA sequence in 5'→3' orientation on the bottom. The predicted methylation site is indicated by a ^-character.

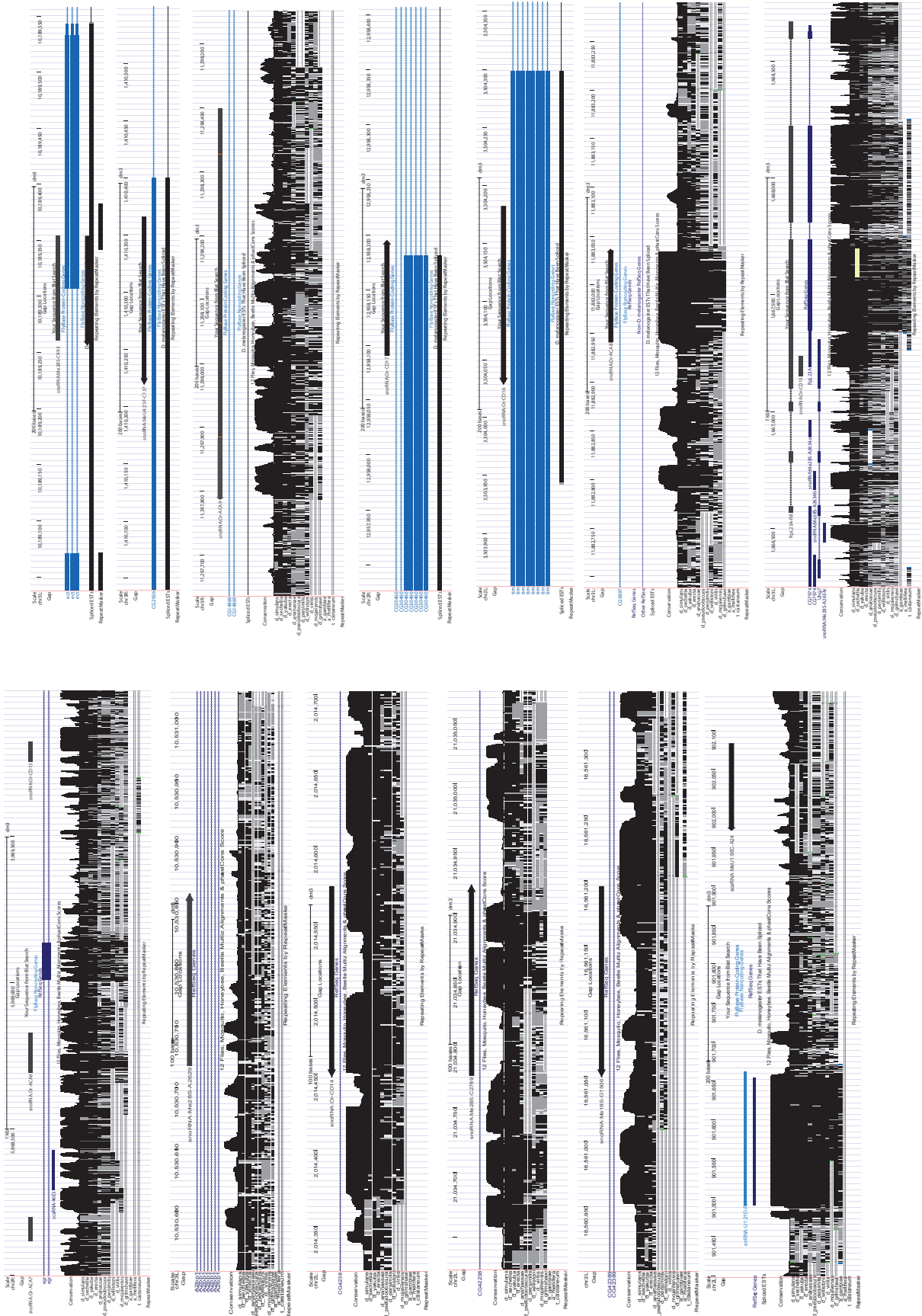
snoRNA	type	target	position	base pairing
<i>snoRNA:Me28S-A2629</i>	C/D	28S rRNA	A2629	AGAUUGCUCGAA : AUUAACGAGAUU ^
<i>snoRNA:Me28S-C2789</i>	C/D	28S rRNA	C2789	AGGAGCCAACUU : ACCUCGGUUUGG ^
<i>snoRNA:Me18S-G1506</i>	C/D	18S rRNA	G1506	GACACAAAGUUA : UUGUGUUUGAAU ^
<i>scaRNA:MeU1:95C-A24</i>	C/D	U1 snRNA	A24	CAAUUGGUUAAG : : GUUAACCGUGAUC ^
<i>scaRNA:MeU4:25F-C137</i>	C/D	U4 snRNA	C137	CGGGGUUCCGUUAC : : GCCCAAGUGGCUG ^
<i>snoRNA:Me28S-C993</i>	C/D	28S rRNA	C993	ACUUGAUCUUAACGAG UGAACUAUACUUGAUC ^
Box D'		18S rRNA	C1686	UAGAGGAUCUAGU : : AUUCCUAGACCG ^

scaRNA:MeU1:95C-A24 is predicted to recognize all *Drosophila* U1 snRNA isoforms at a sequence conserved in all of them.

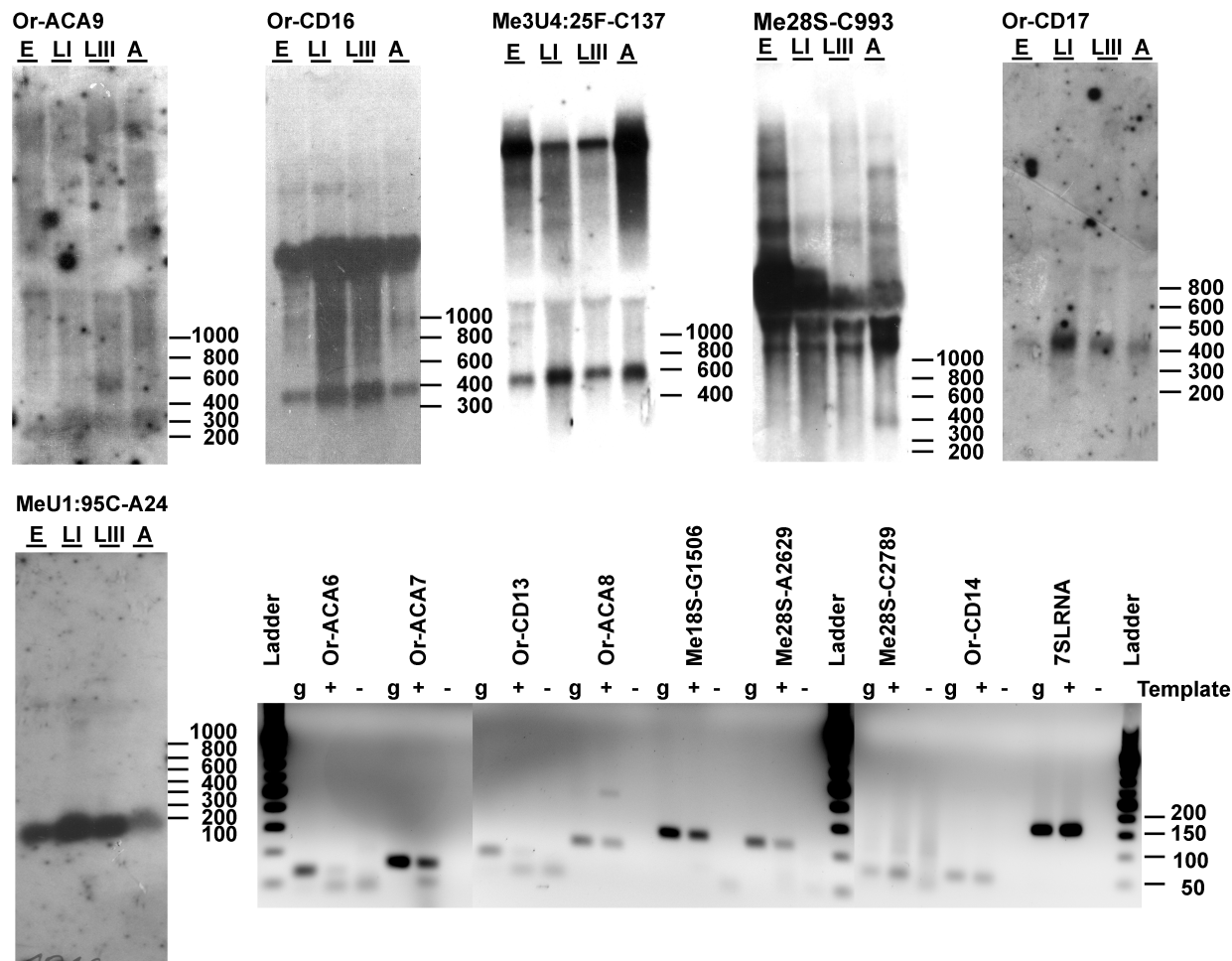
Supplemental Table 2. Summary of the best putative targets for the orphan Box C/D snoRNAs. The binding energy in the ΔG column is given in kcal/mol.

Name	ΔG	Gene	Function
<i>snoRNA:Or-CD13</i>	-30.20	dlg1 (intron)	protein-binding
<i>snoRNA:Or-CD14</i>	-24.80	EC 3.1.1.3 (exon)	lipid catabolic process
<i>snoRNA:Or-CD15</i>	-31.50	Hel89B (intron)	immune response
<i>snoRNA:Or-CD16</i>	-34.40	cadN (exon)	axon extension
<i>snoRNA:Or-CD17</i>	-39.20	CG-34380 (intron)	signal transduction

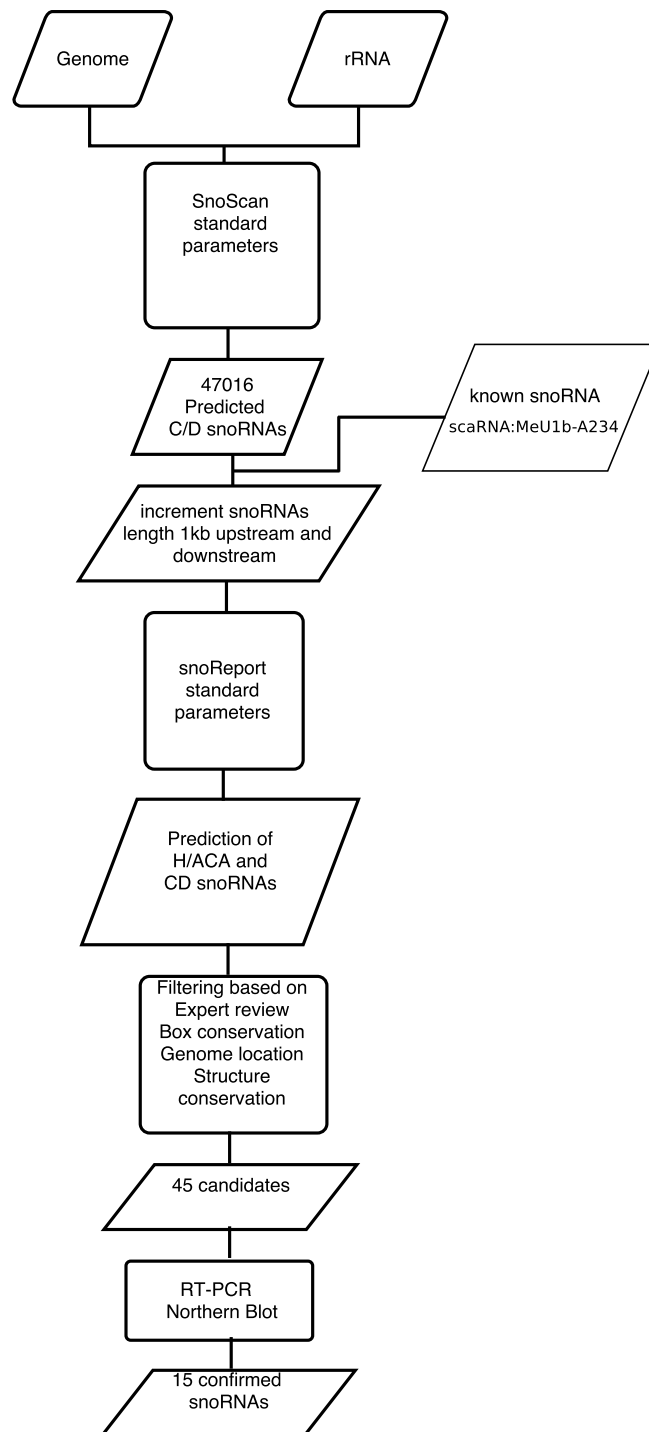
Supplemental Figure 1. UCSC genome browser maps of the new snoRNAs and snoRNA-like RNAs reported in this contributions (thick black arrows). Gene annotation and conservation tracks are shown.



Supplemental Figure 2. Northern blots and RT-PCR of novel snoRNAs and snoRNA-like RNAs. Upper panel expression of snoRNAs derived from HG exons and/or characterized by uncommon length. Lower panel, Northern blot and RT-PCR expression of snoRNAs characterized by common length. In Northern blot Low range RNA Molecular Weight Markers (Fermentas), in RT-PCR DNA Molecular Weight Marker XIII (Roche) were used. Template for PCR: (g) gDNA, (+) RT+, (-) RT-; 7SL-RNA was used as positive control.



Supplemental Figure 3. Graphical representation of the analysis workflow leading to the identification of the 15 new snoRNAs.



Supplemental Data File 1. Sequences of the four snoRNA-like RNAs not deposited in GenBank as identified by SnoScan and SnoReport. C/C' boxes are shown in italics, D/D' boxes in boldface.

> *snoRNA:Or-CD16*

ATGCCAAGGATGATGCGGTCCTGGAGTCGGTCATCCGGATACTCGTCAAT**CTGAC**GGT
GCCGGTGGAGTGCTCTTCTCCGTGGAC*GTGATGTACCGCACGGATGTGGGT*CGCCACA
CCATCTTCGAG**CTGA**ACAAGCTGCTGTACACCAG

> *scaRNA:MeU4:25F-C137*

TAGATGATGATGATGAGGATACGGATATAACCATTGCCTTTGGGGC**CTGAG**CCCCGAACCC
GTTCCCGAAAAAGTCCCGAAAAAGTAGTGATGATGACCTCTACGAGCCAGAGAATCCAAC
CGAAGAACC**CTGA**AGAACCCGAAATG

> *snoRNA:Me28S-C993* box D *Me18S-C1686* box D'

CGACGATGATGAGCCTGATCTAGGAGAT**CTGAT**CGATGACGATGATGGTAGGTTTAG
AGCAATTCTAGTTCA**CTGA**ATGCACCCAGGCCGCAC

> *snoRNA:Or-CD17*

TGACGCACTAGGGTTGCTGATGATTGGTGCTTGGAGACCAGACTACCGATTCCCTGCT
CATCCATTTCCACATTGCAAATGGGCGTGCCGC**CTGAT**GTGGAAC