Evolutionary analysis of 5S ribosomal DNA in metazoans

(first results)

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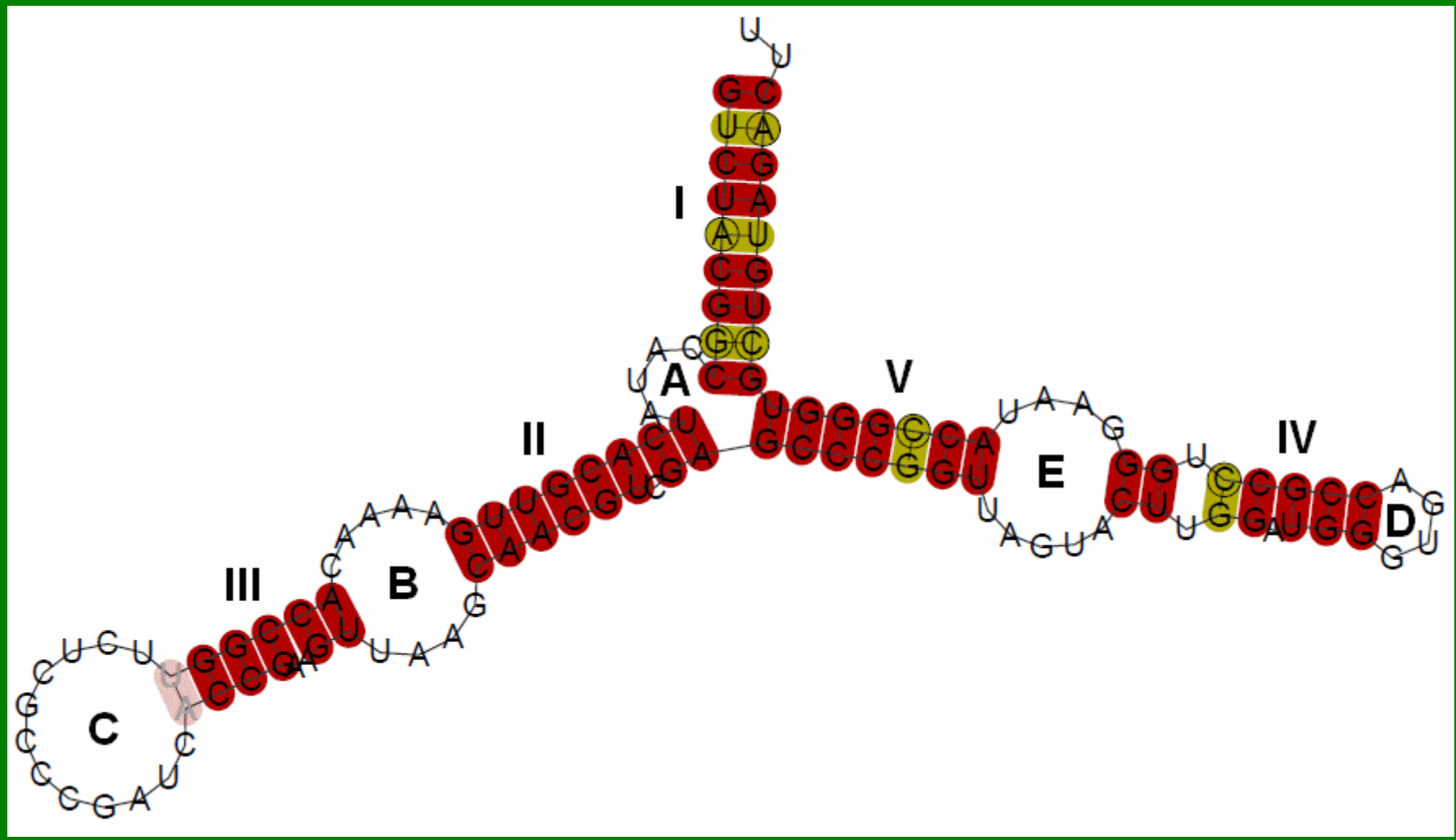
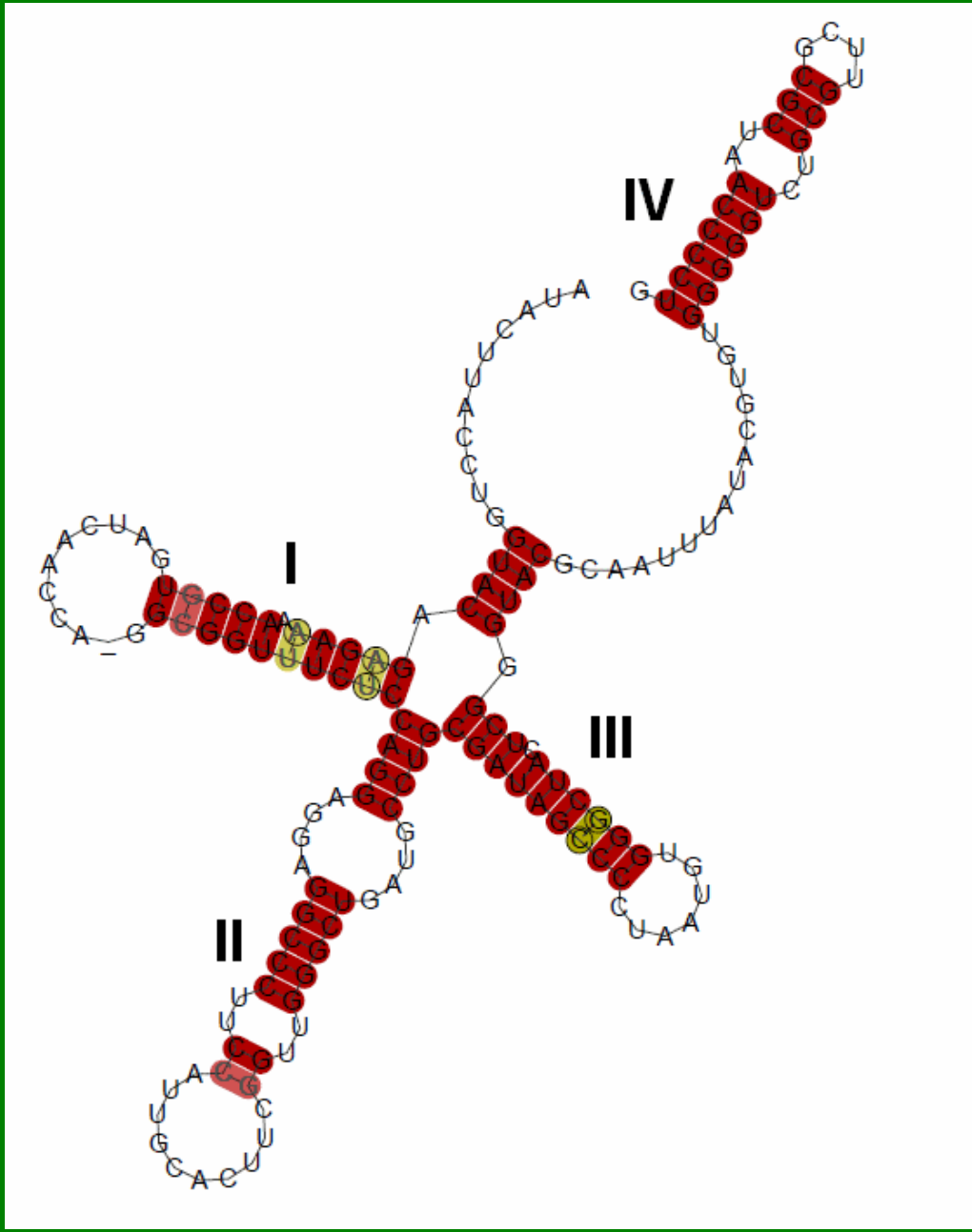
(Universidade da Coruña, Spain; Philipps Universität Marburg, Germany)

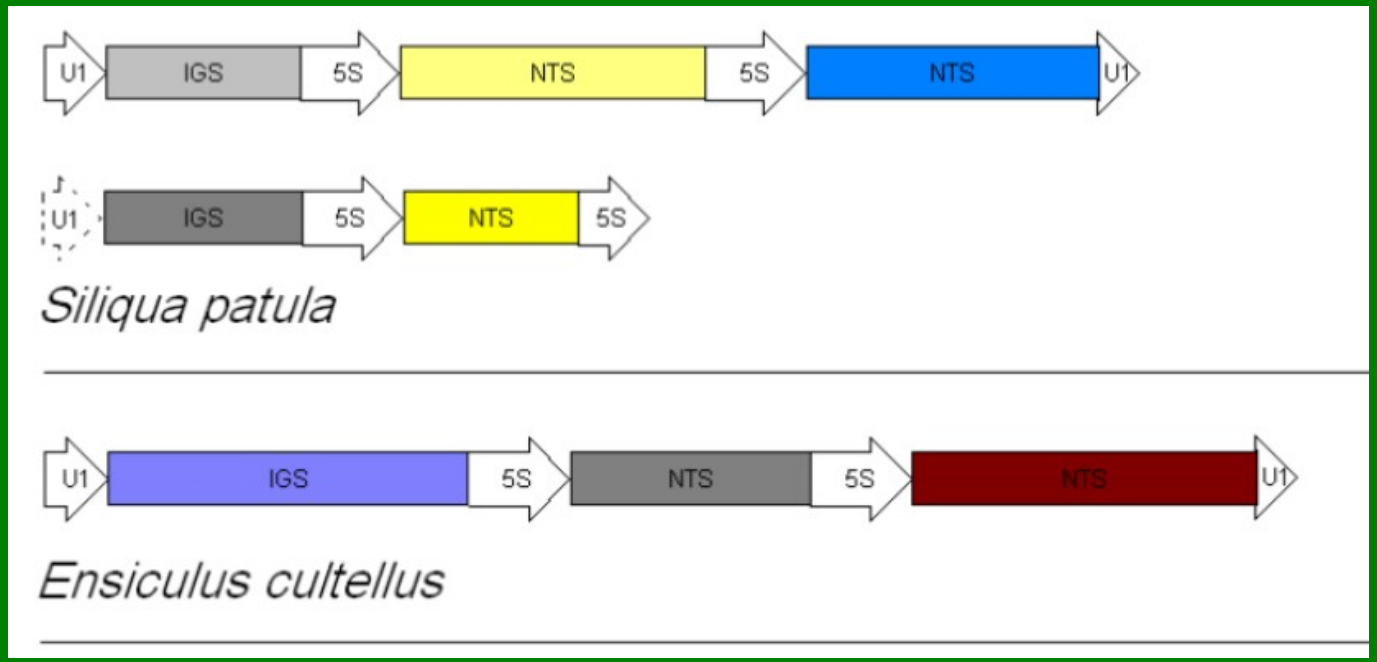
5S ribosomal RNA



U1 small nuclear RNA



Background



Heredity (2011), 1–16

www.nature.com/hdy

ORIGINAL ARTICLE

The linked units of 5S rDNA and U1 snDNA of razor shells (Mollusca: Bivalvia: Pharidae)

J Vierna[1], KT Jensen[2], A Martínez-Lage[1] and AM González-Tizón[1]

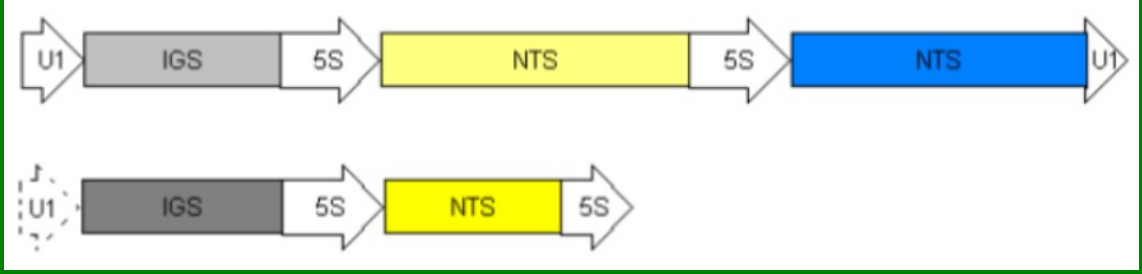
Background: linkage with other non-coding RNAs

5S ribosomal DNA – found linked to:
SL1
U1 snDNA
U2 snDNA
U5 snDNA
tRNAs
major ribosomal genes

Goals

Study 5S in metazoans using genome-project data

1 – linkage between 5S copies?
2 – linkage between 5S and U1 in other metazoans?
3 – linkage between 5S with other non-coding RNAs



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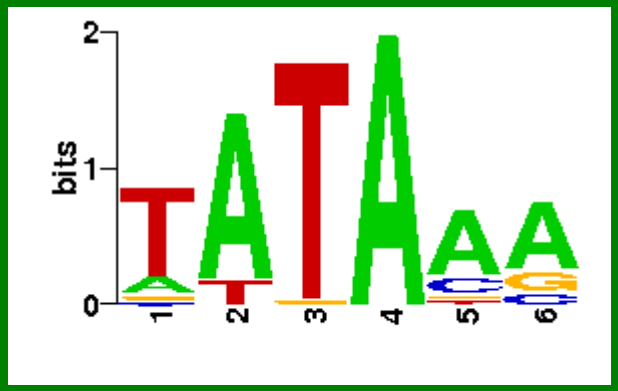
Goals

Study 5S in metazoans using genome-project data

1 – linkage between 5S copies?
2 – linkage between 5S and U1 in other metazoans?
3 – linkage between 5S with other non-coding RNAs
4 – conservation of the upstream region
5 – conservation of the RNA coding region



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Methods

For both 5S and U1:

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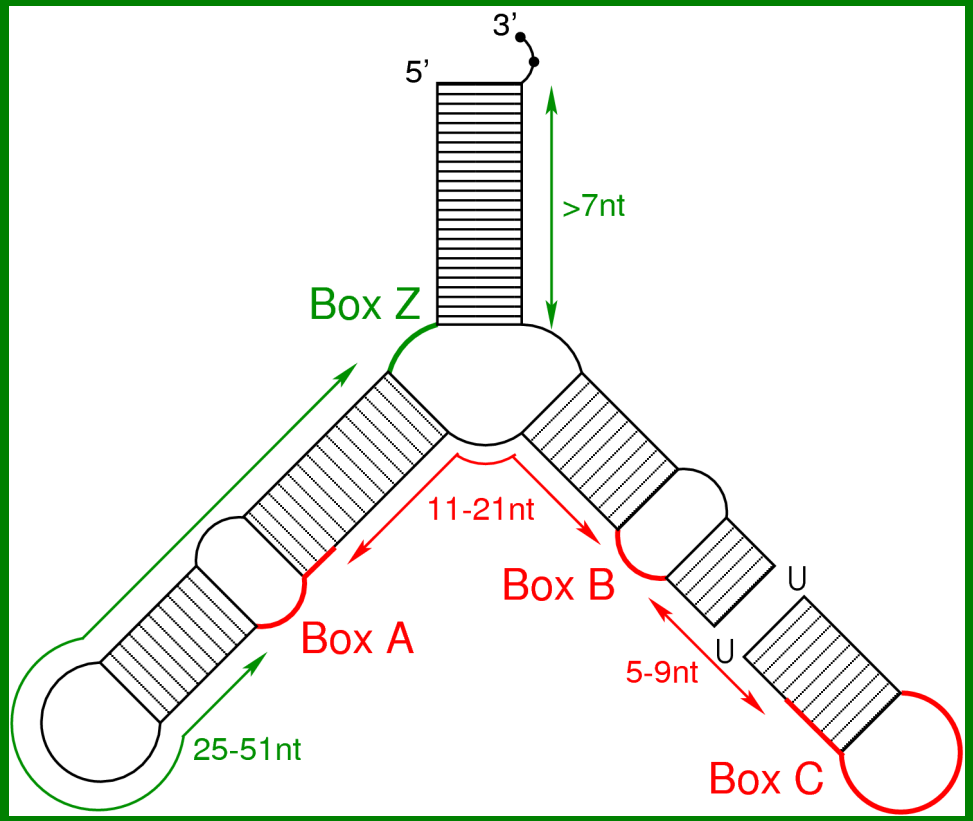
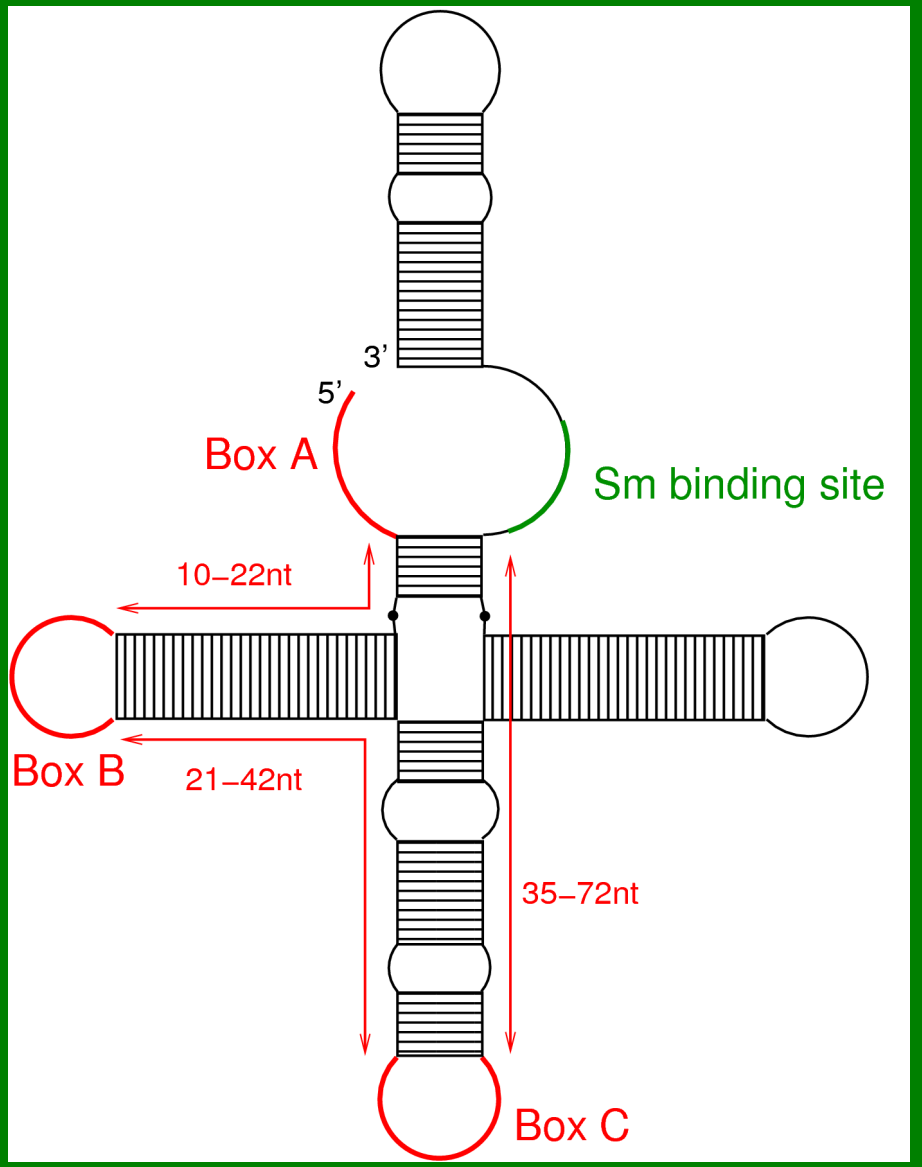
Methods


3'
5'
>7nt
Box Z
11-21nt
Box B
U
U
Box A
5-9nt
25-51nt
Box C


3'
5'
Box A
Sm binding site
10–22nt
Box B
21–42nt
35–72nt
Box C

Methods

For both 5S and U1:

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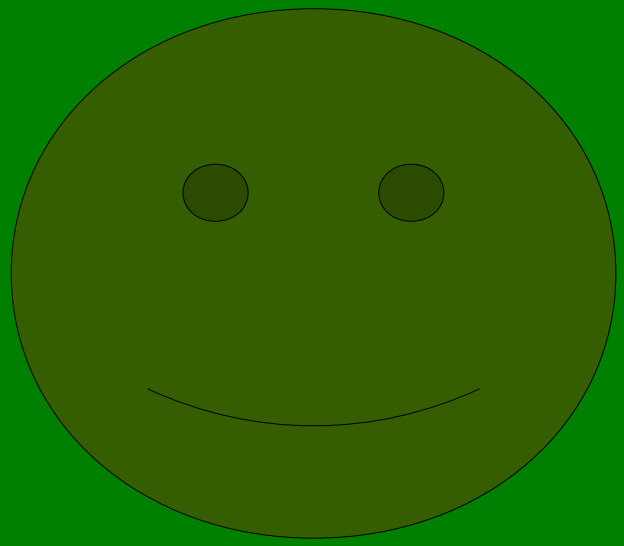
2- re-blasted using initial query + “first Blast” output + consensus sequence for each species
3- extended the sequences
4- filtered the Blast results using conserved motifs from the literature
5- folded and scored all candidate sequences and cleaned alignments according to secondary structures / scores

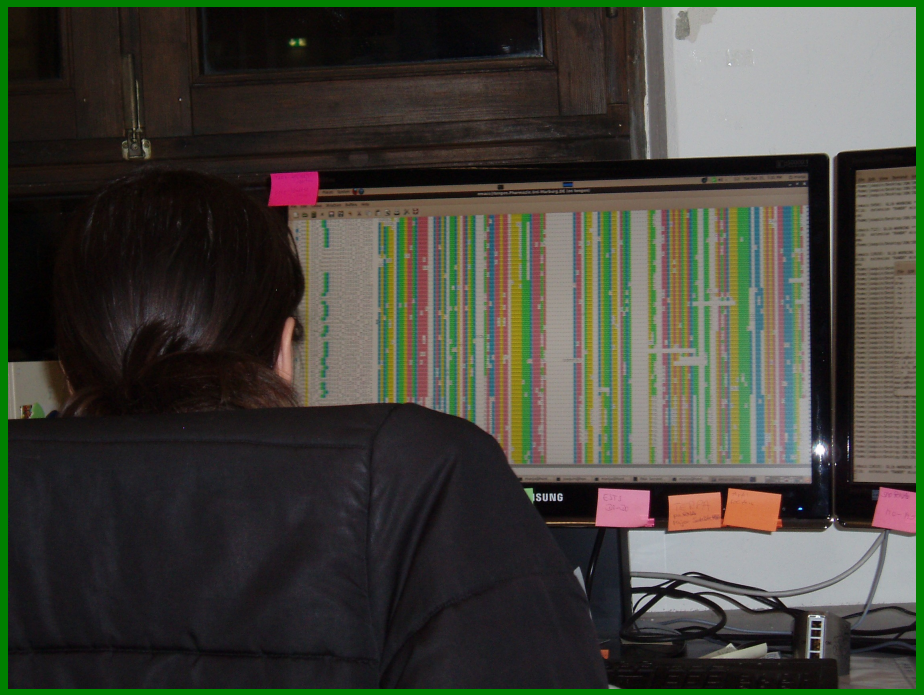
NOW WE HAVE THE 5S (AND U1) ALIGNMENTS FOR 104 METAZOANS!

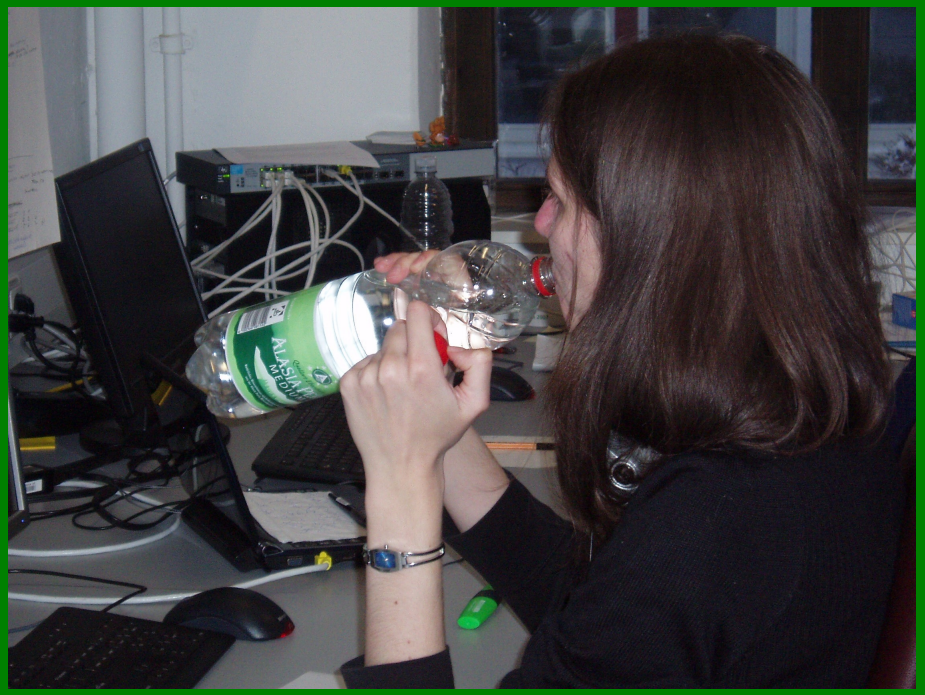
(putative functional sequences)



Methods

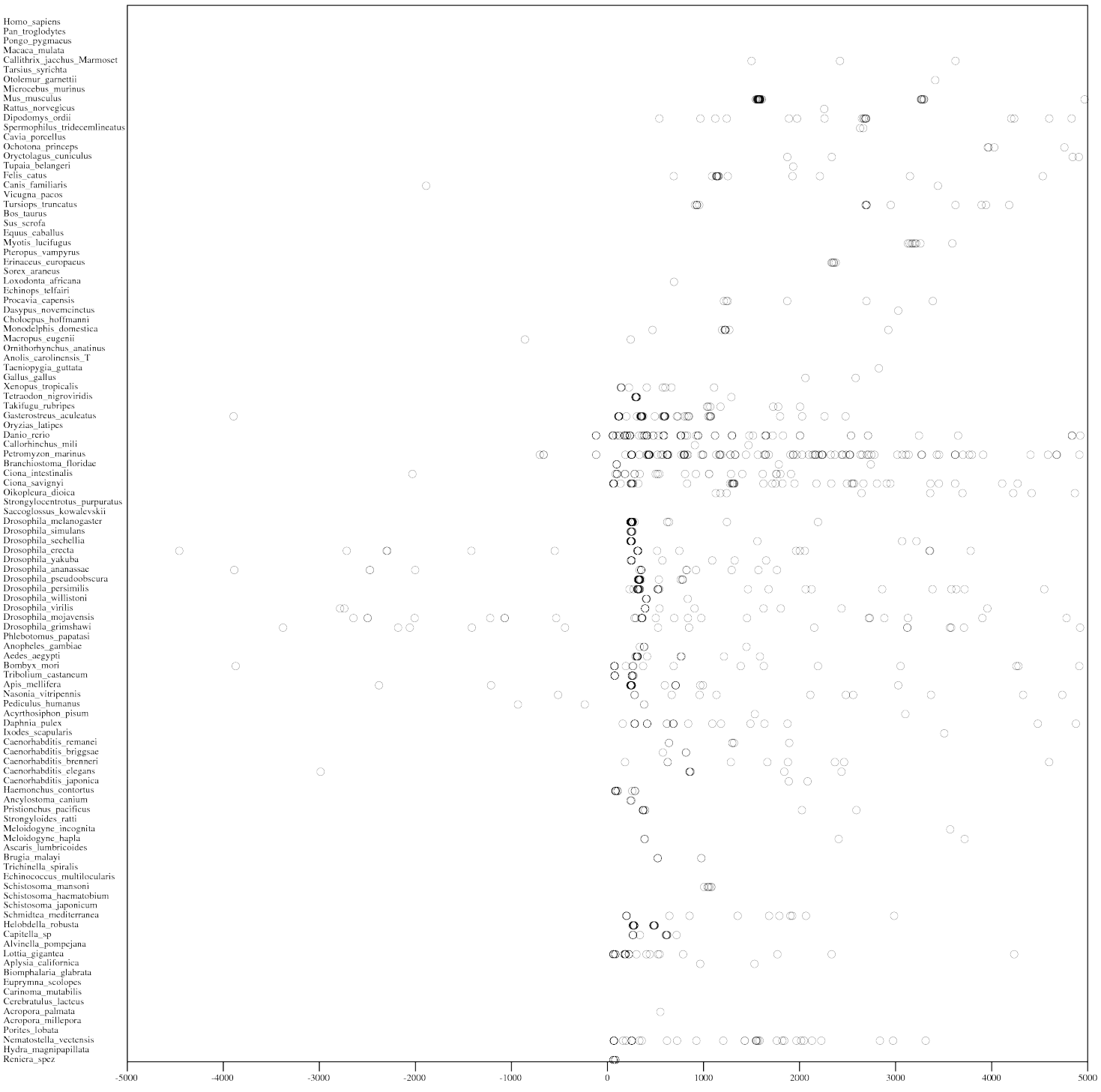
Once we had our alignments ready...



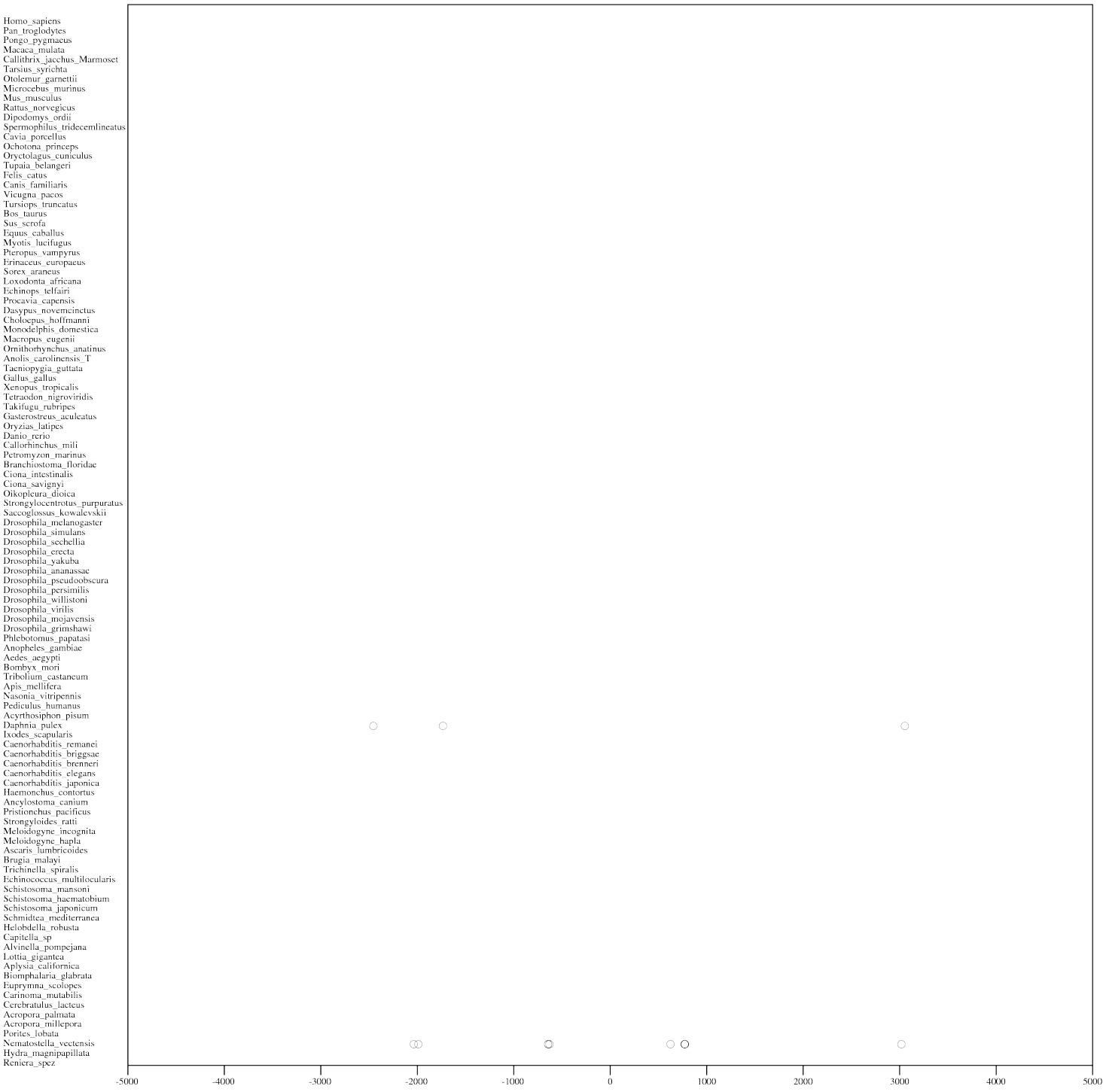


We looked for our goals...

Results: 5S-5S linkage



Results: 5S-U1 linkage

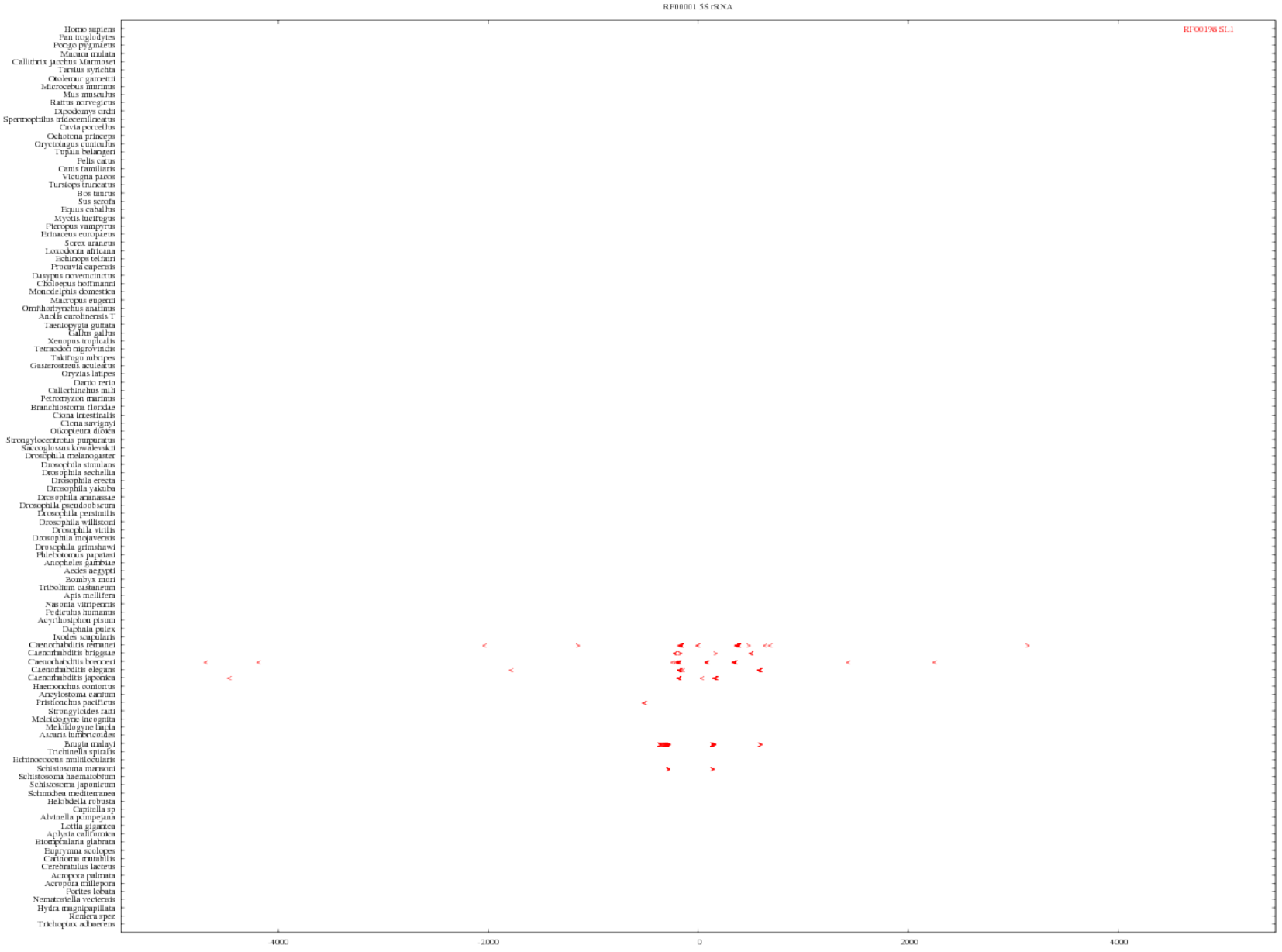


Results: linkage

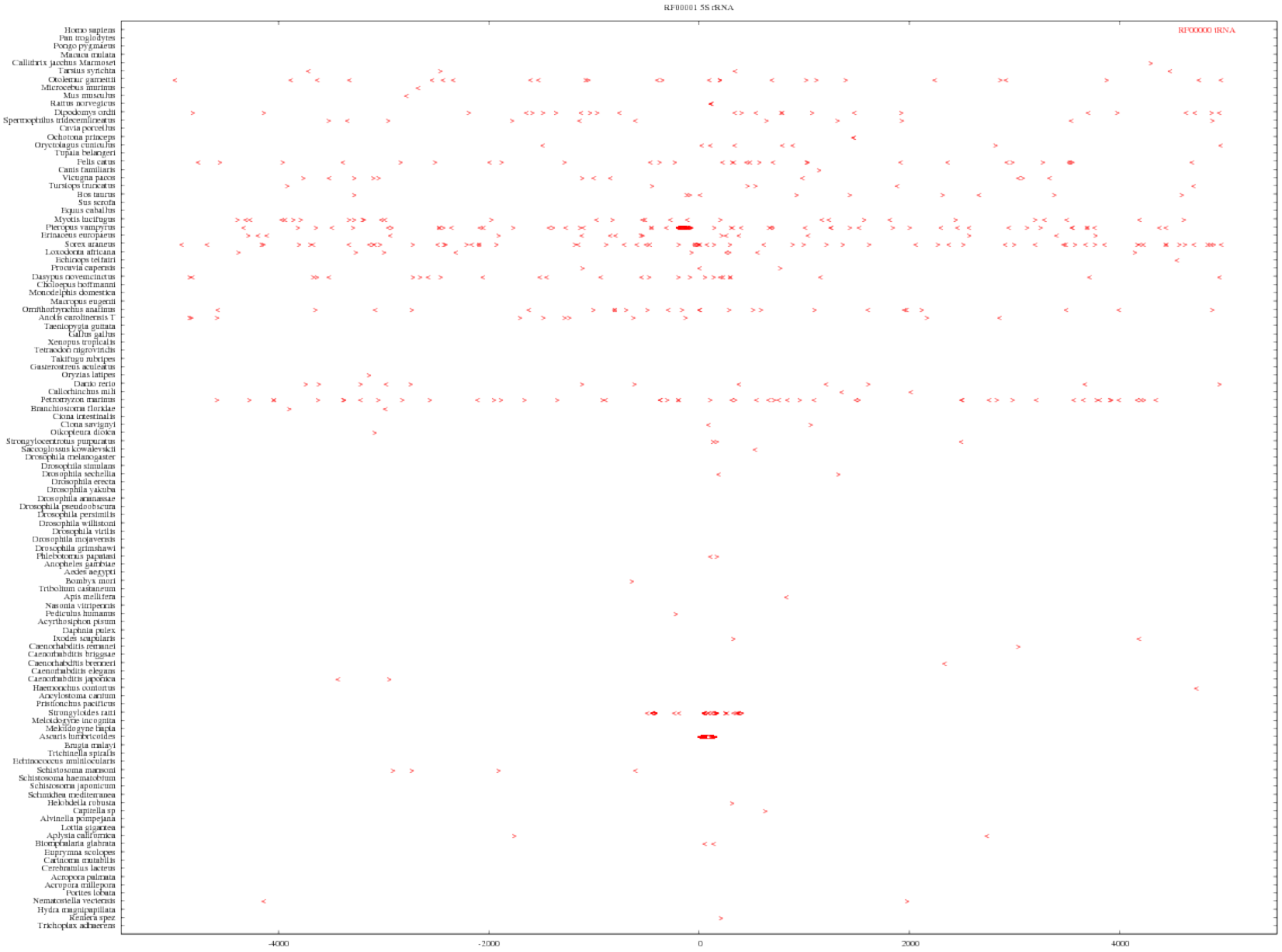
Rfam --> 1025 non-coding RNA classes

We found 23 ncRNAs that were linked to 5S in at least one species

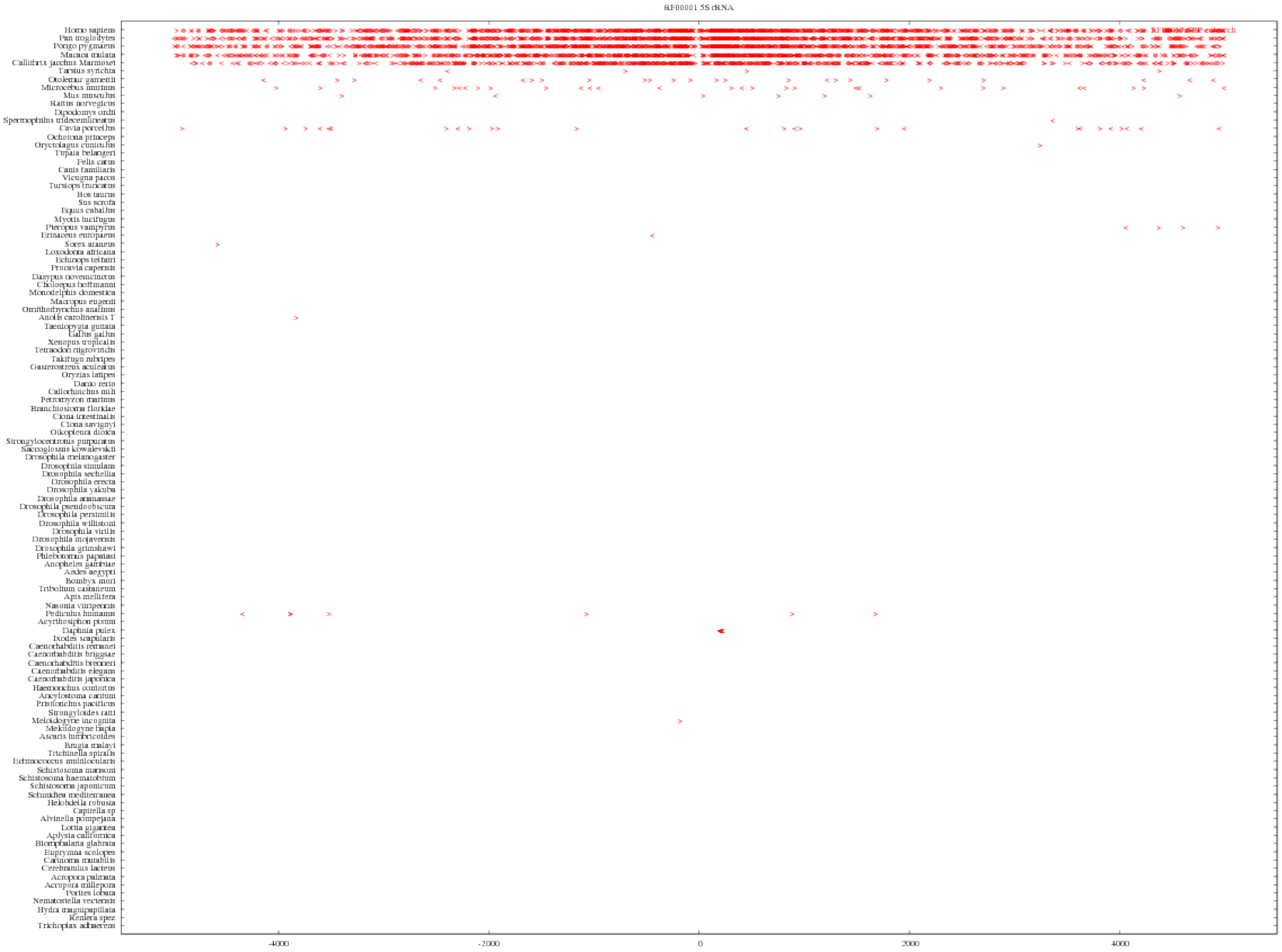
Results: linkage SL1



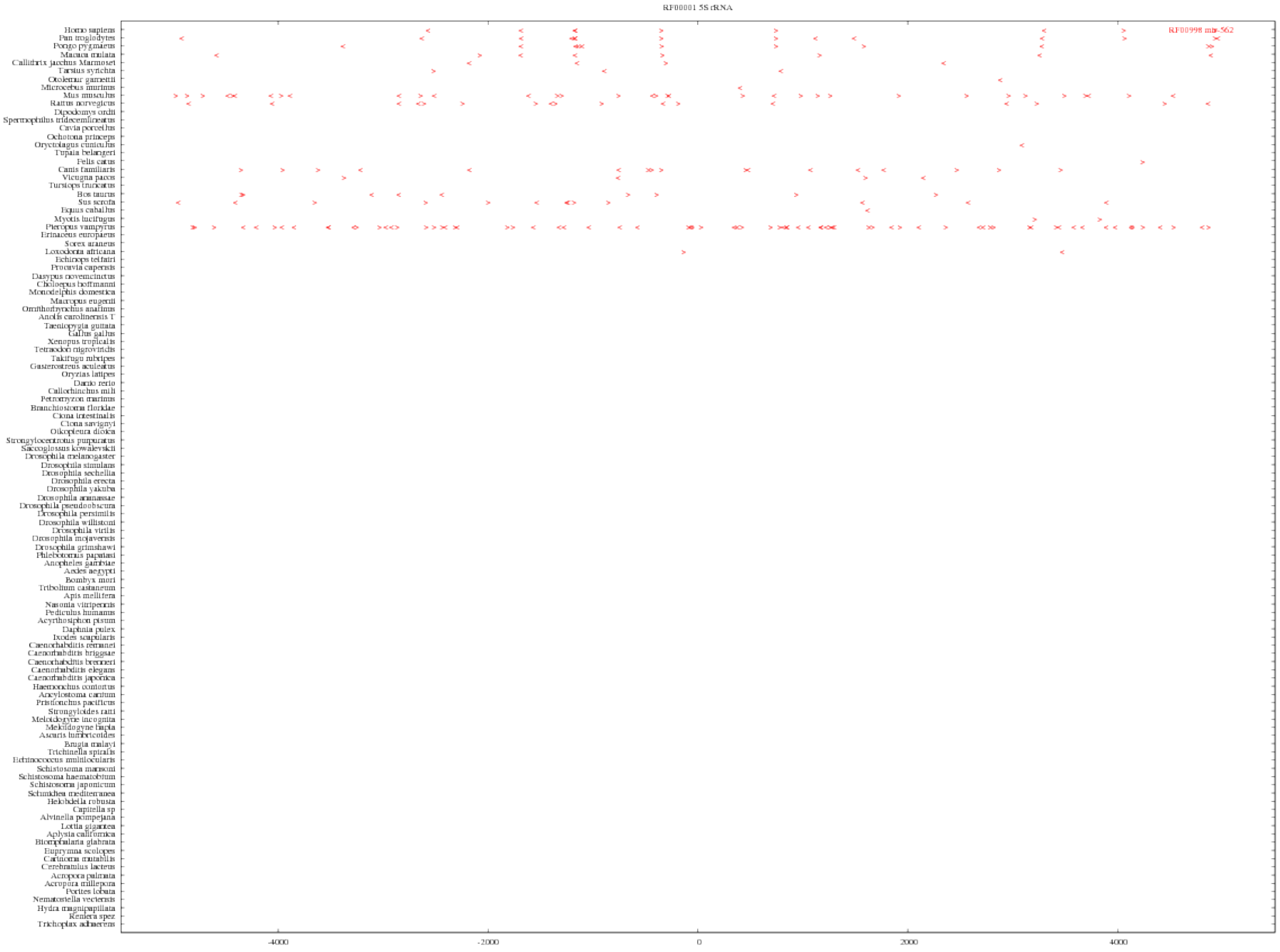
Results: linkage tRNA



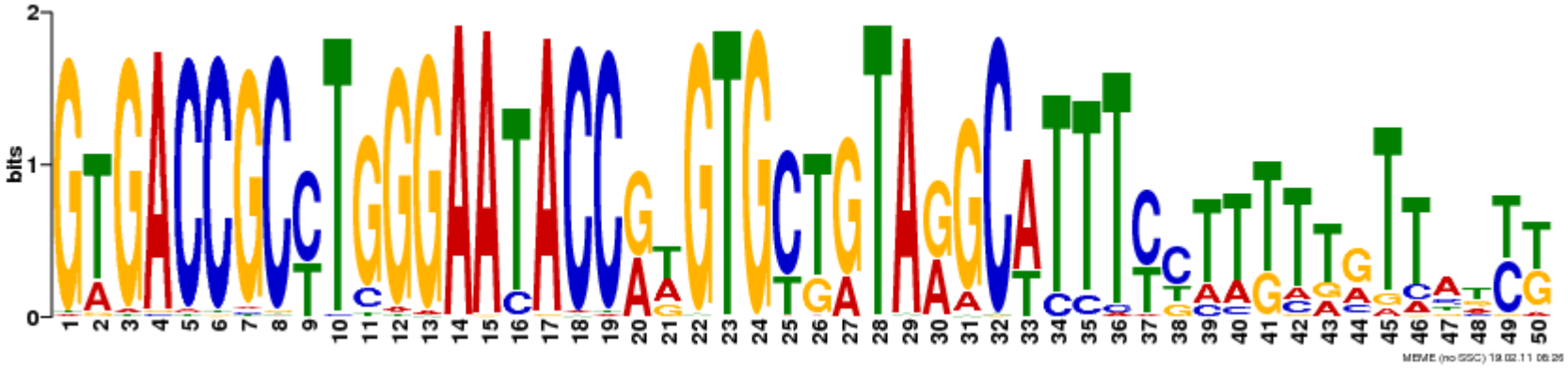
Results: linkage Signal recog. particle



Results: linkage mir-562



Results: conservation of upstream region (100 nts)



Results: conservation of RNA coding region (120 nts)

We have found three main classes of RNA coding regions:

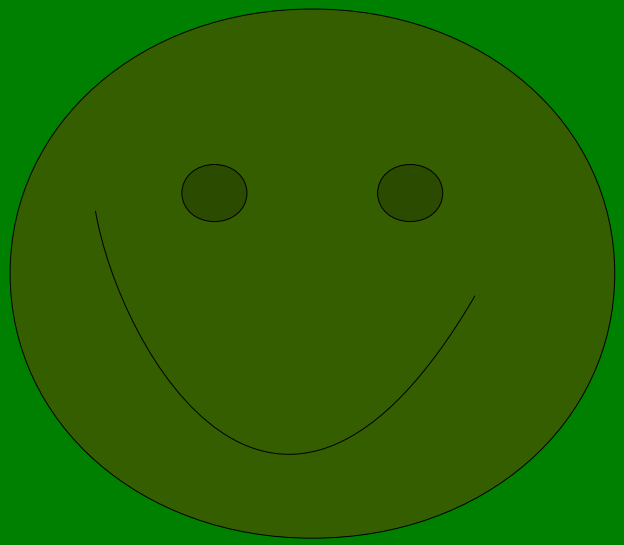
- **basal deuterostomes**
- **protostomes**
- **mammals**

First conclusions

5S ribosomal DNA appears to be linked to several different genes – are these linkages stochastic or do they provide any advantage?

First conclusions

Conservation:
- conserved upstream region in metazoans
- three main clases of RNA coding regions for basal deuterostoms, protostoms, and mammals



THANKS!