# SUPPLEMENTARY INFORMATION

## Targeting mammalian intron-encoded box C/D 2'-O-methylation guide RNAs into the Cajal body

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### Results

To identify evolutionarily conserved and therefore, functionally important sequences in vertebrate box C/D scaRNAs, the coding genes of the intron-encoded mgU2-47, U90, mgU2-19/30, and the independently transcribed mgU2-25/61 and mgU12-22/U4-8 scaRNAs were identified in mammalian, bird, lizard, turtle, frog and/or fish genomes by BLAT search (UCSC Genome Browser). The predicted RNA sequences were aligned to maximum homology by using the ClustalW2 algorithm developed for multiple sequence alignment (EMBL-EBI). In addition to the conserved C/D and C'/D' boxes and the RNA-specific target recognition sequences, we detected long GU- and AU-rich internal repeat sequences in the intronic mgU2-47, U90 and mgU2-19/30 scaRNAs (Figures S1, S2 and S3). The 5'-terminal regions of the independently transcribed mgU2-25/61 scaRNAs are also enriched in GU dinucleotide repeat sequences (Figure S4). In contrast, compilation and comparison of the Pol II-transcribed mgU12-22-U4-8 box C/D scaRNA sequences failed to identify GU-rich internal sequences (Figure S5).

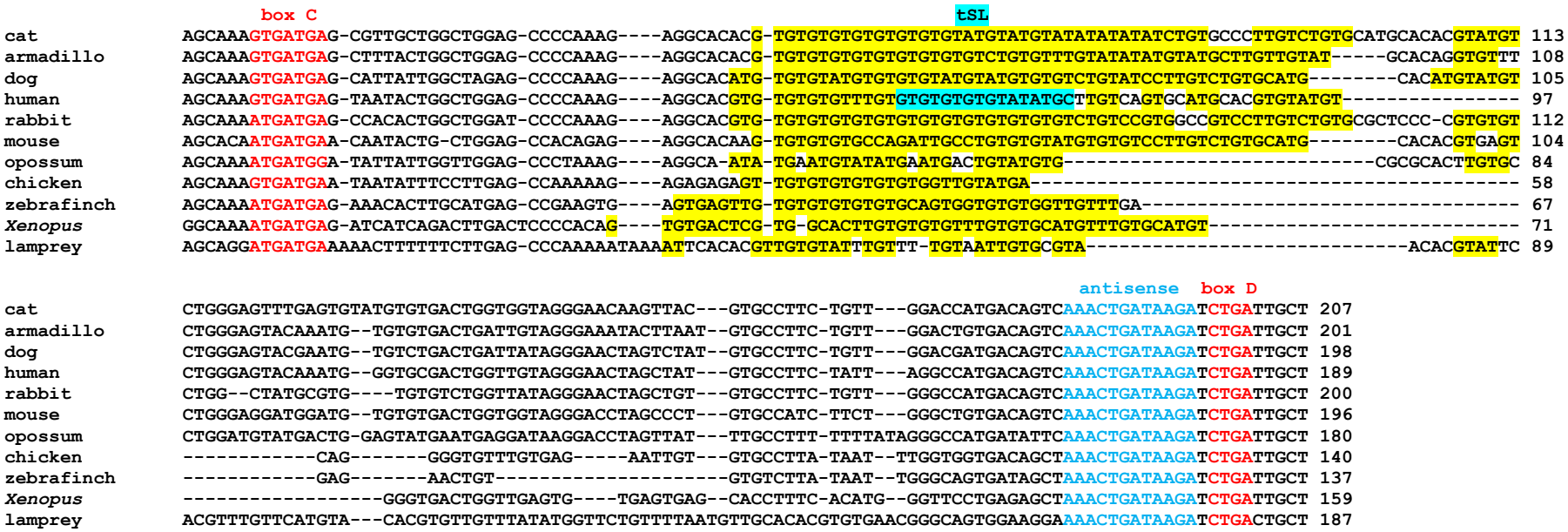


**Figure S1.** Sequence alignment of vertebrate mgU2-47 RNAs. The conserved box C and D motifs and the antisense sequences are indicated in red and blue respectively. The RU-rich internal sequences are highlighted in yellow. The experimentally defined CB-localization stem-loop (tSL) of human mgU2-47 is shaded in blue.


**Figure S2.** Sequence alignment of vertebrate U90 RNAs. The conserved 5'-terminal C and 3'-terminal D boxes and the putative internal box C' and D' motifs are indicated in red. The predicted antisense sequences are in blue. The RU-rich internal sequences are highlighted in yellow. The experimentally defined CB-localization stem-loop (tSL) of human U90 is shaded in blue.


**Figure S3.** Alignment of vertebrate mgU2-19/30 RNAs. Details are identical to Figure S2.

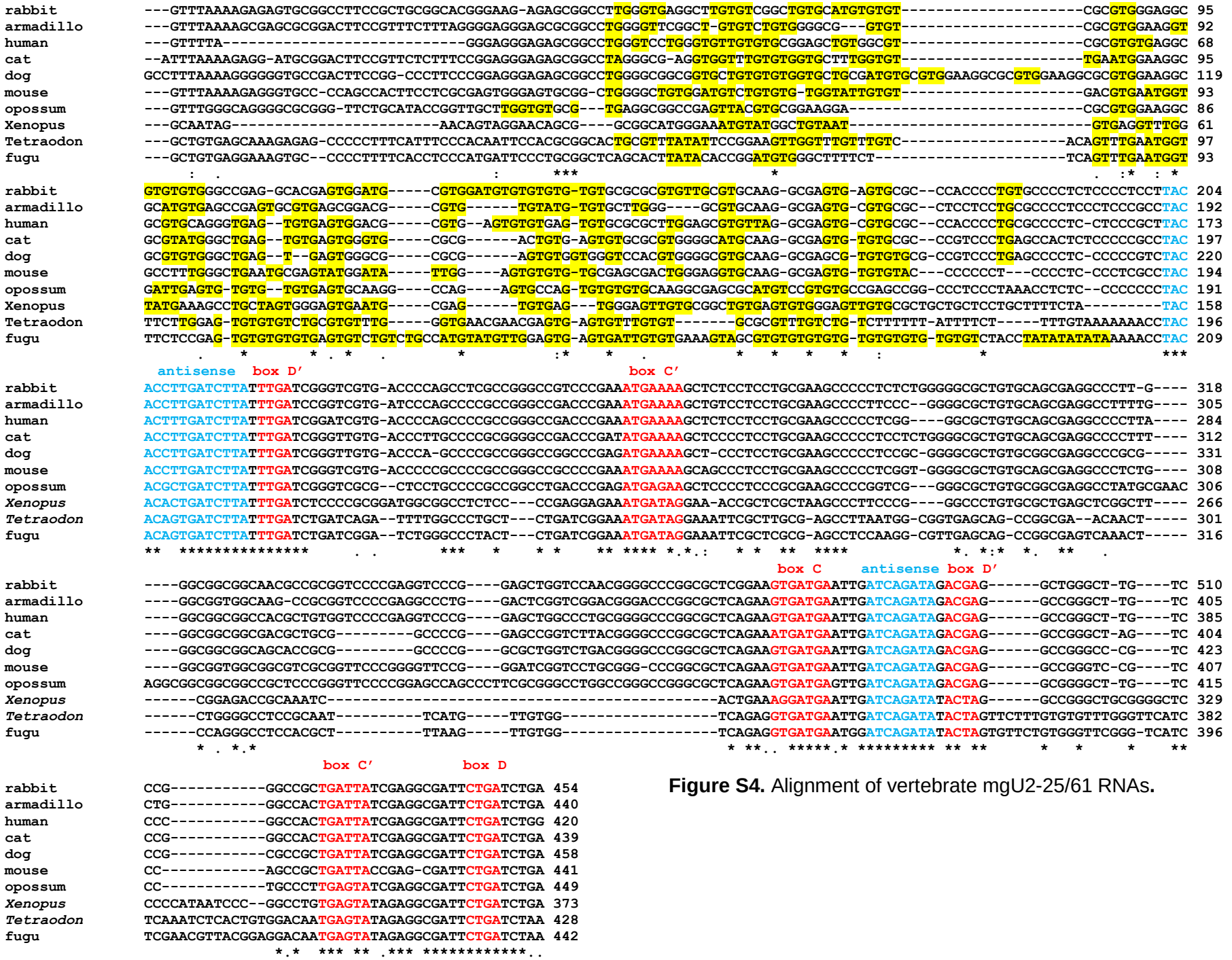


**Figure S4.** Alignment of vertebrate mgU2-25/61 RNAs.

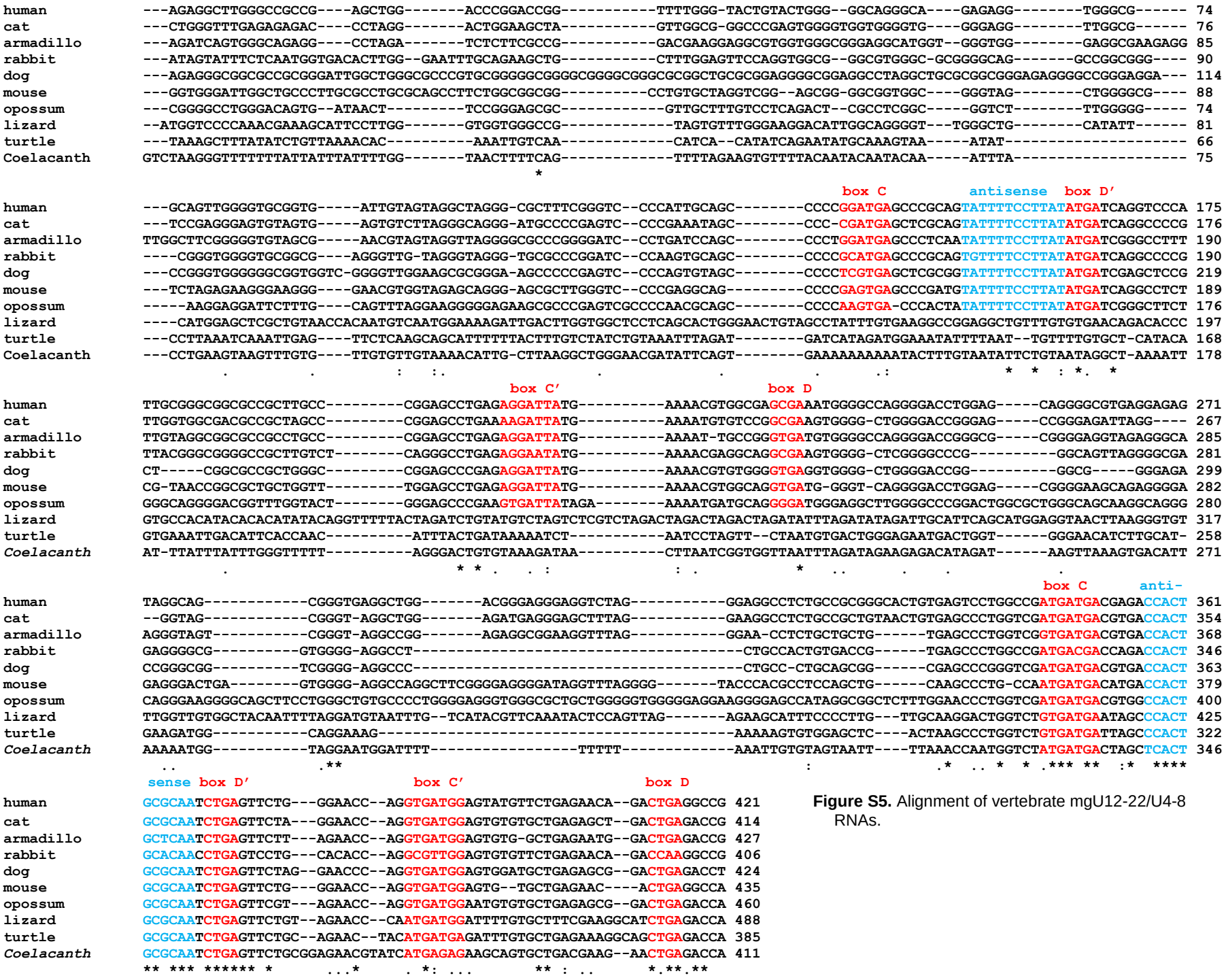


**Figure S5.** Alignment of vertebrate mgU12-22/U4-8 RNAs.