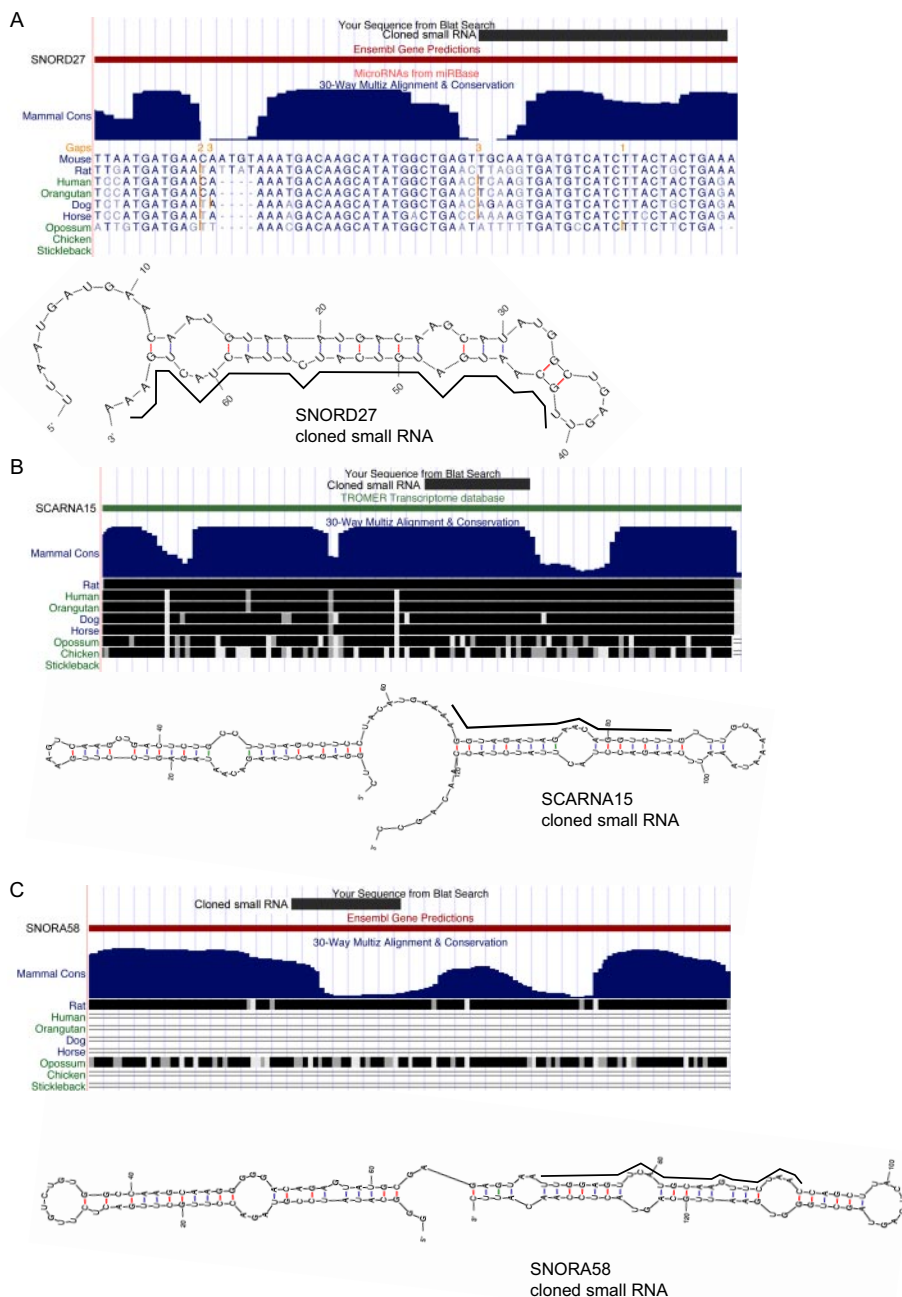


# Supporting Information

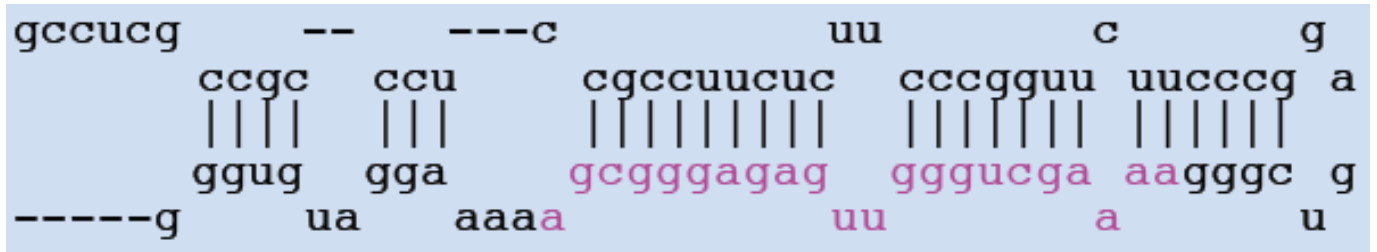
Yi et al. 10.1073/pnas.0810766105



**Fig. S1.** Genomic organization and predicted secondary structures for top three most abundantly expressed sn/snoRNA-derived small RNAs. (A) SNORD27 is a C/D box, small nucleolar RNA. The cloned small RNA is located at the 3' arm of the predicted hairpin. (B) SCARNA15 is a H/ACA box, small Cajal body-specific RNA. The cloned small RNA is located at the 5' arm of the right hairpin. Note the conservation is restricted to the stem-forming bases but not the loop region. (C) SNORA58 is a H/ACA box, small nucleolar RNA. The cloned small RNA is located at the 5' arm of the right hairpin. Lines mark the positions of cloned small RNAs in each hairpin.

A

Pre-miR-320 (extracted from miRBASE)



B

Pre-miR-484 (extracted from miRBASE)

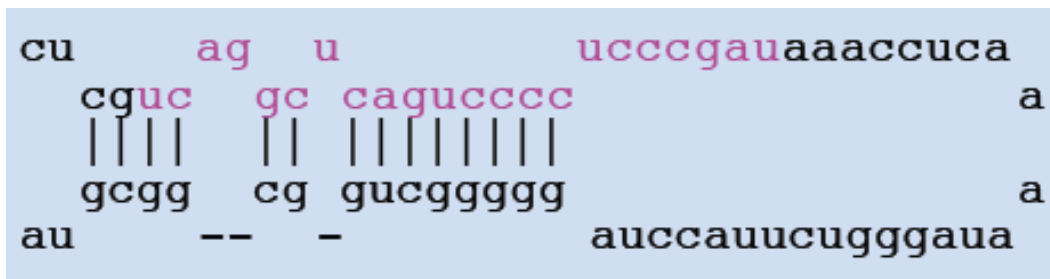
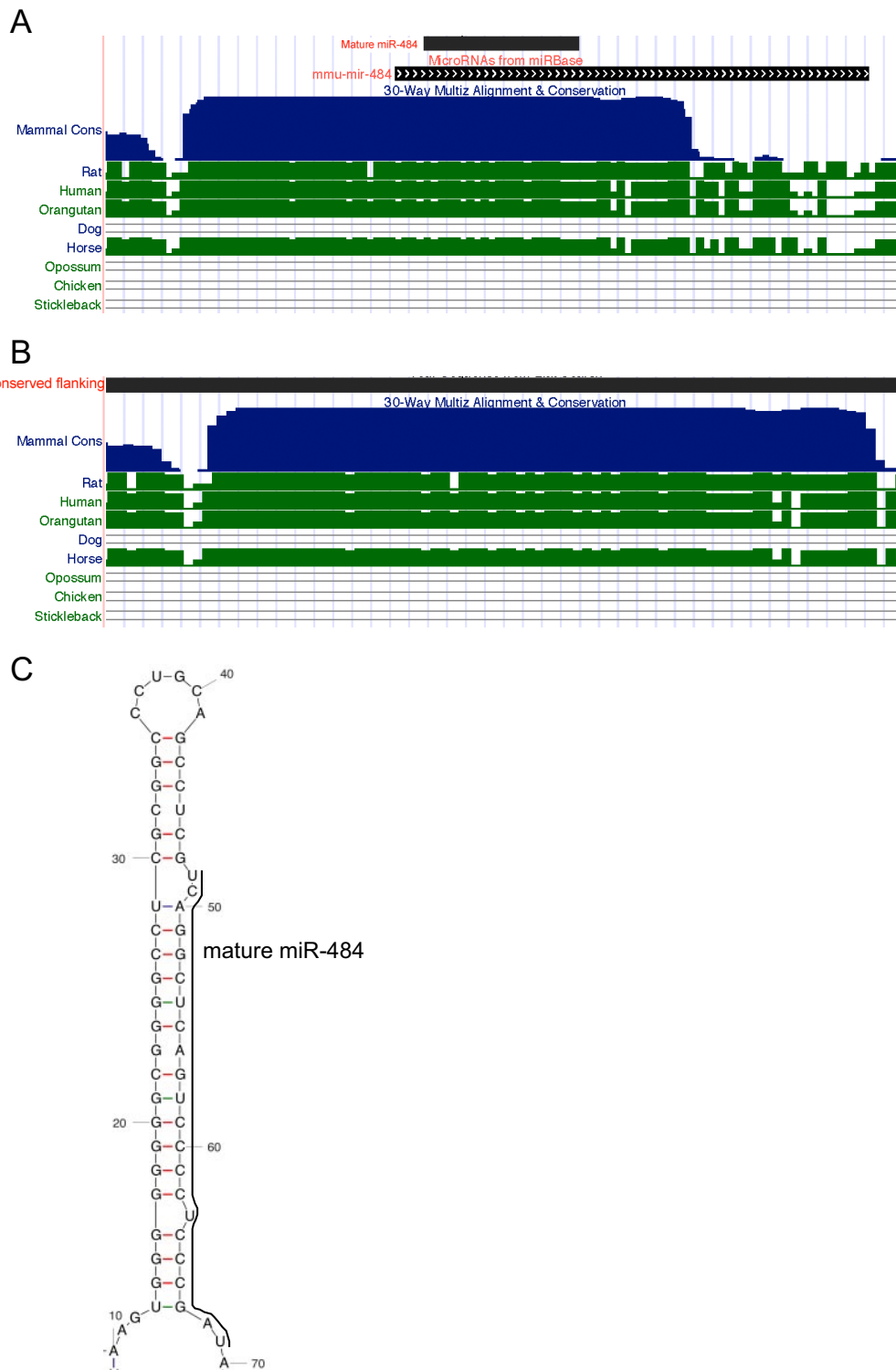


Fig. S2. Secondary structure of premiR-320 and premiR-484 was predicted by miRBase. Whereas premiR-320 (A) folded into a prototypical hairpin, premiR-484 (B) was predicted to fold into a structure uncharacteristic of microRNA precursor. Highlighted sequences are mature microRNA.



**Fig. S3.** Evolutionarily conserved flanking sequences of miR-484 are predicted to fold into a hairpin structure characteristic of prototypical microRNAs. (A) The annotated sequences of miR-484 precursor only partially overlap with the conserved sequences flanking mature miR-484. (B) Conserved sequences that flank mature miR-484. (C) The conserved flanking sequences are predicted to fold into a hairpin structure characteristic of prototypical microRNAs. The line marks mature miR-484 in 3' arm of the hairpin.

## Other Supporting Information Files

[Table S1 \(PDF\)](#)

[Table S2 \(PDF\)](#)

[Table S3 \(PDF\)](#)