

Supplementary Data:

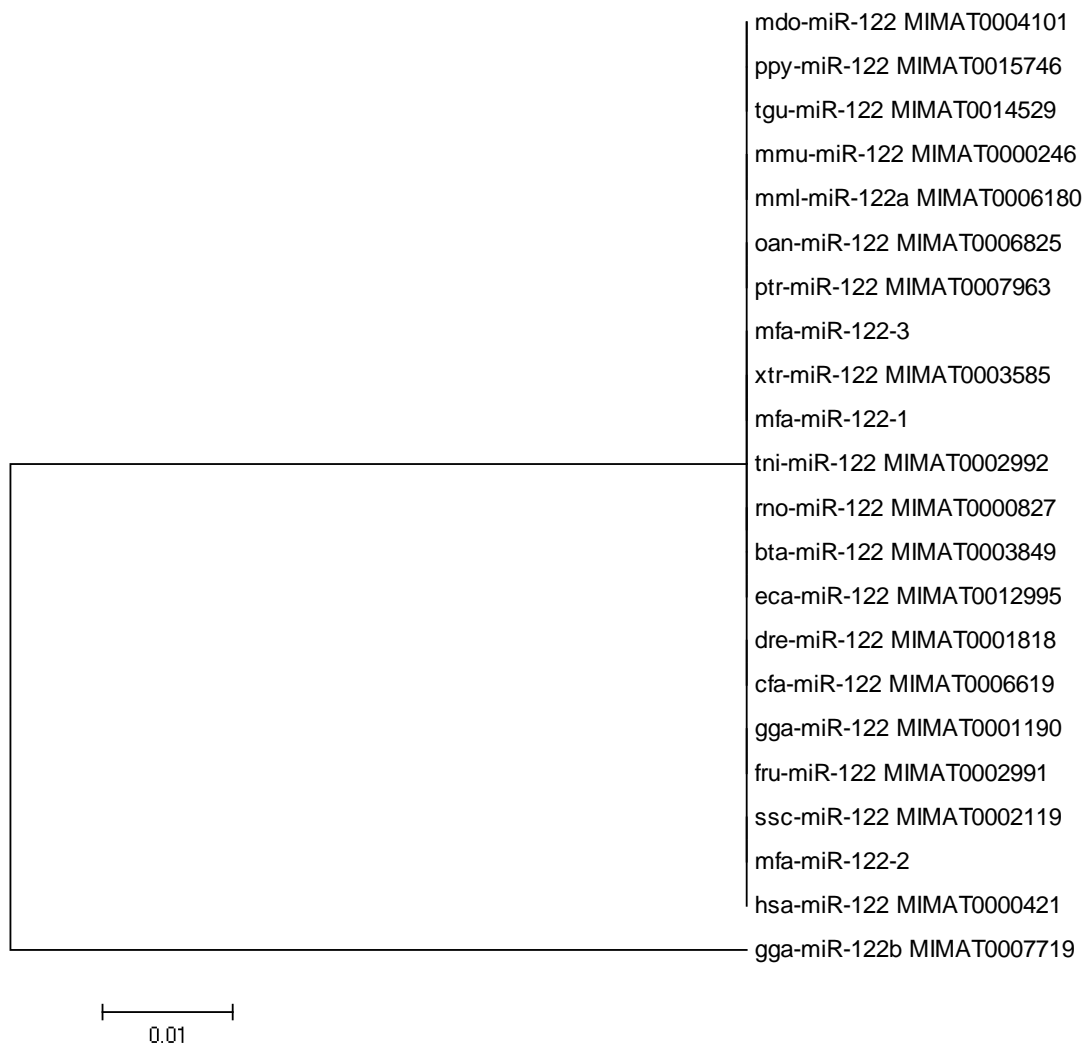
Table. Percentage of human miRNAs represented in the *Macaca mulatta* miRNAs database, and vice versa.

Species	Number of homologs	Percent(Homologs/Total miRNAs)
mml-miRNA	468	95.90%(468/488)
hsa-miRNA	589	30.66%(589/1921)

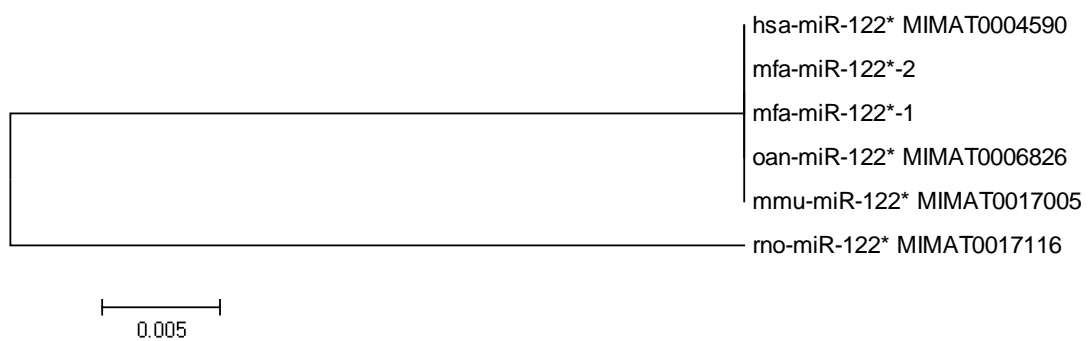
Phylogenetic analysis of mature miRNAs sequences in different families. (A) miR-

122(B) miR-122*(C) miR-548aa (D) miR-548d (E) miR-675

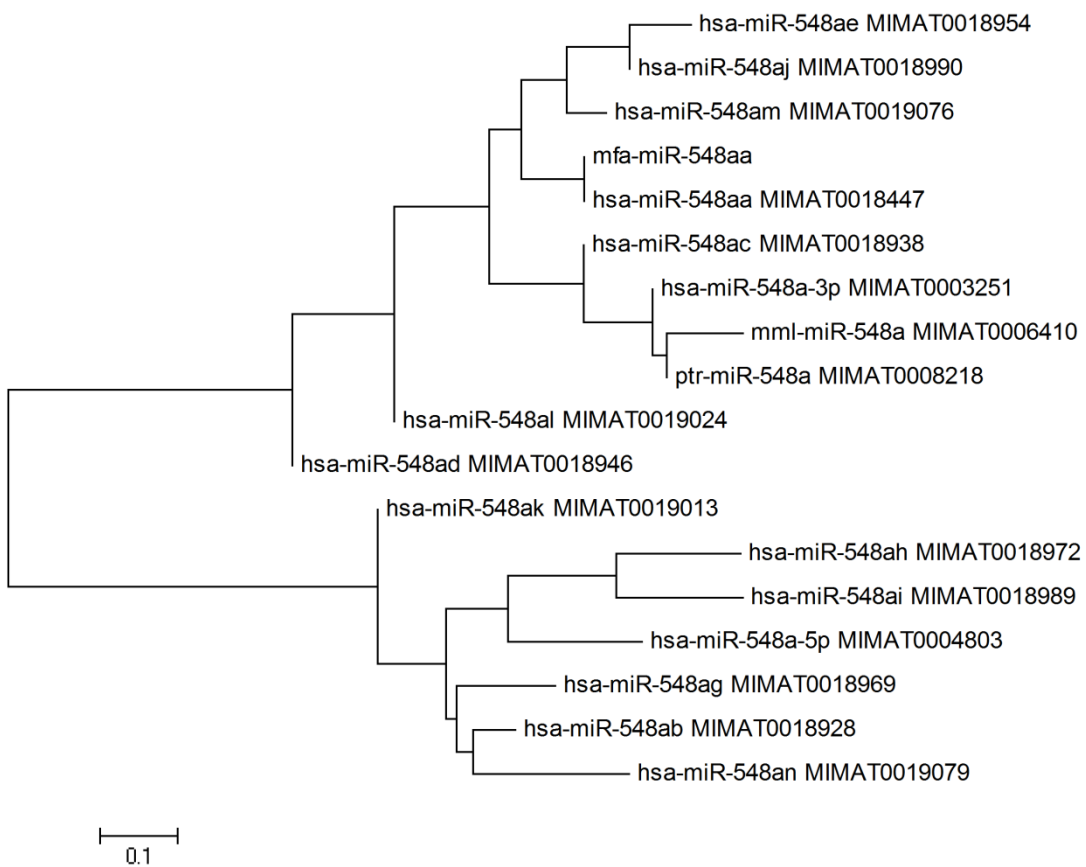
(A) miR-122



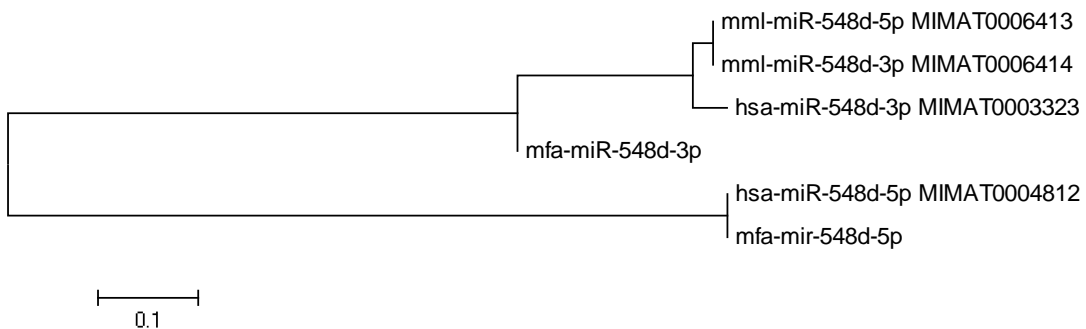
(B) miR-122*



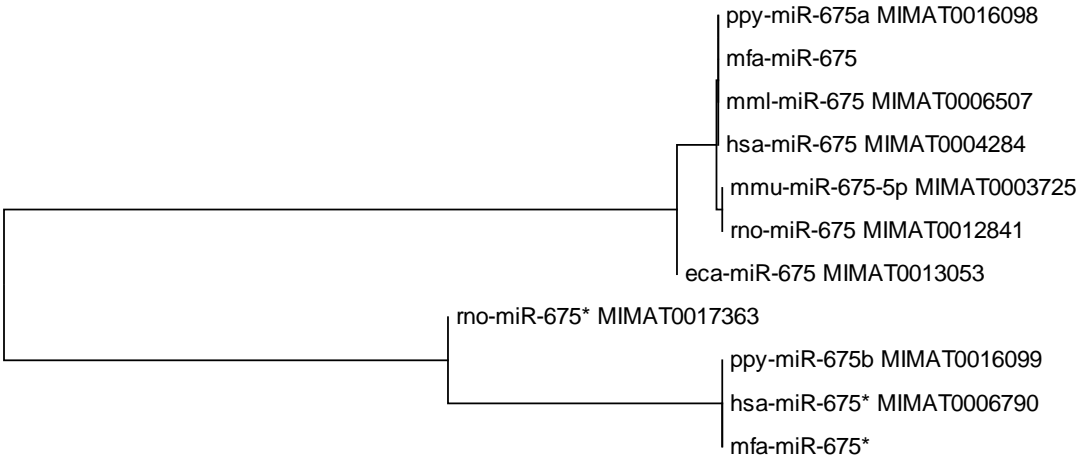
(C) miR-548aa



(D) miR-548d



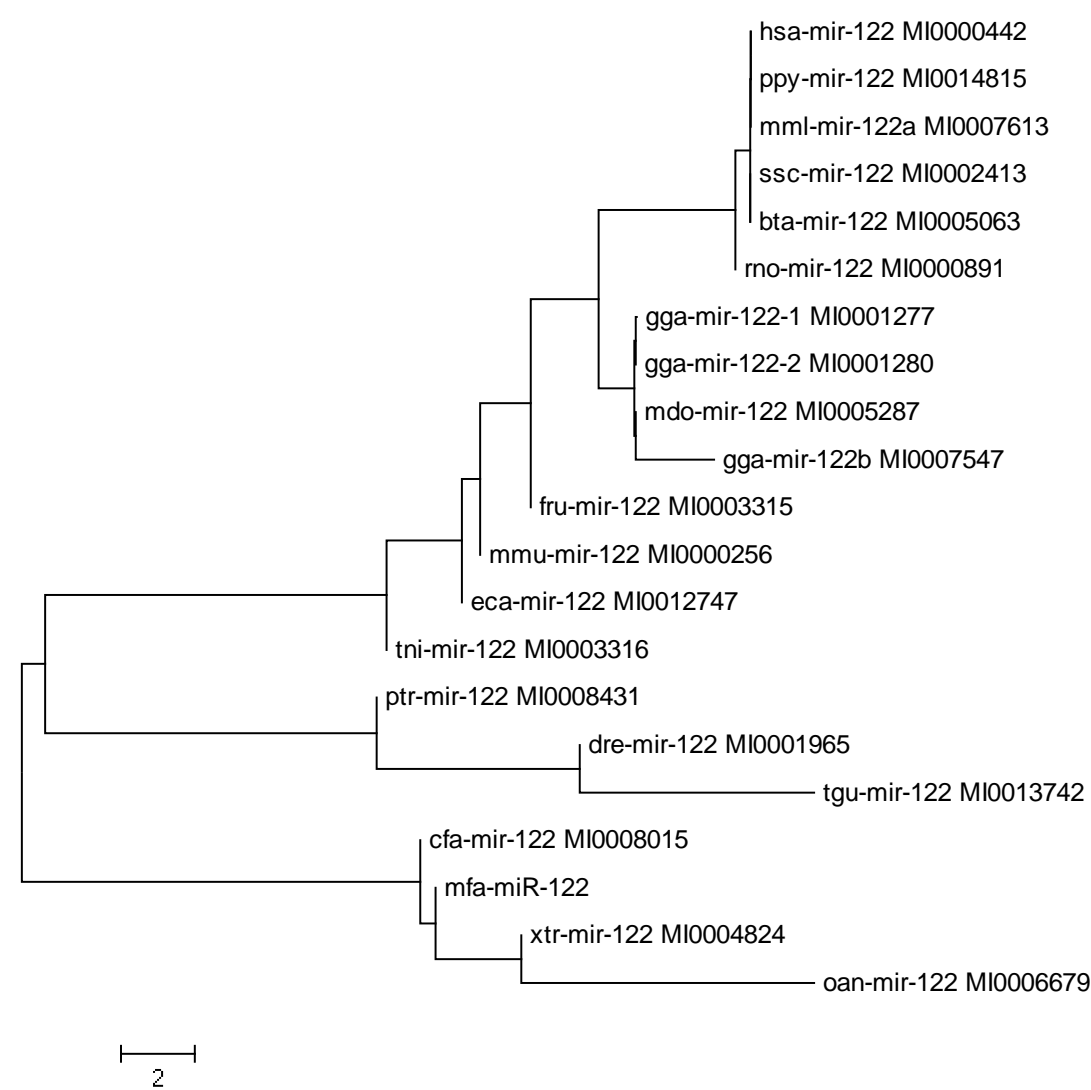
(E) miR-675



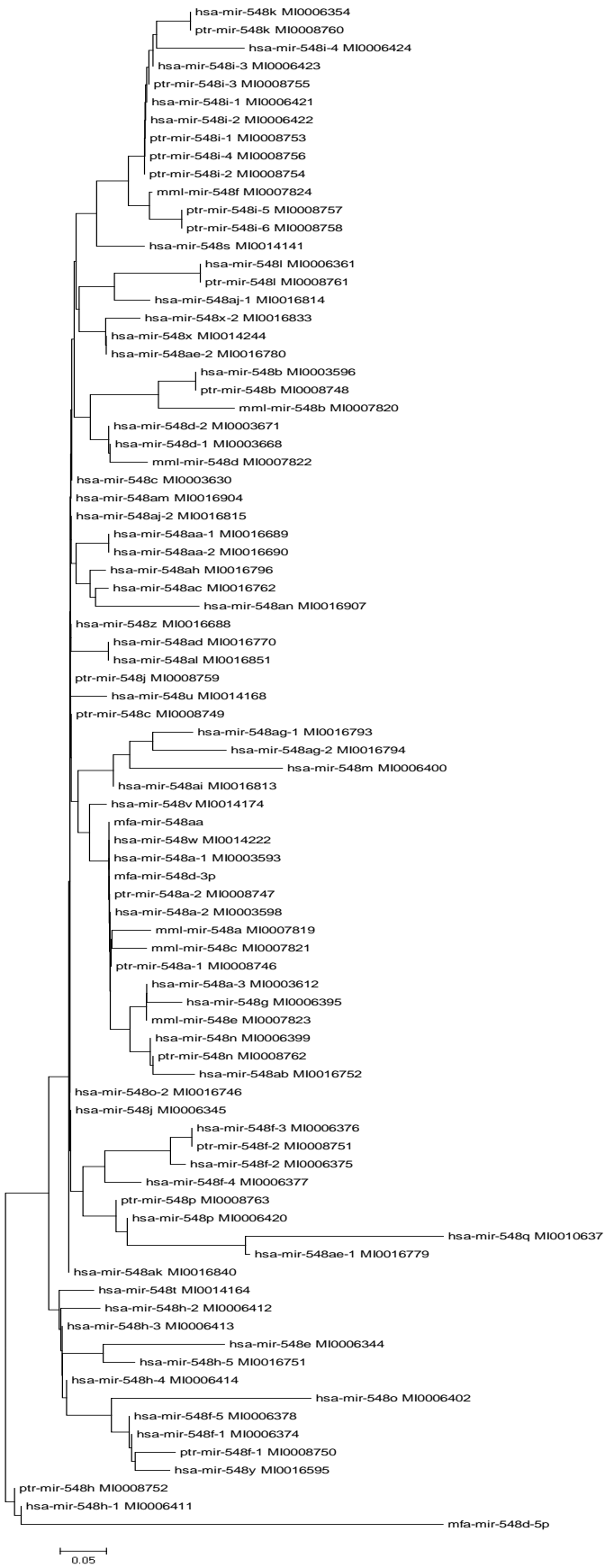
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Phylogenetic analysis of precursor miRNAs sequences in different families. (A) pre-miR-122 family (B) pre-miR-548 family (C)pre-miR-675 family

(A) pre-miR-122 family



(B) pre-miR-548 family



(C) pre-miR-675 family

