



Figure.S1 The histogram of *mature_seq_sim* of all the known animal miRNA pairs that are in the same family. The family information, which was clustered according to the pre-miRNA sequences, was downloaded from MicroRNA Registry. We pair-wise aligned each of the animal miRNAs to their homologs in the same family. For the precursors that produce mature miRNAs from its both arms (E.g. hsa-miR-142-3p and hsa-miR-142-5p are derived from the same precursor's (hsa-mir-142) 3' and 5' arm respectively), we just count the 3' to 3' and 5' to 5' product's alignment result respectively. There are totally ~4040 such homologue miRNA pairs were aligned, and 98.14% of them have *mature_seq_sim* over than 70. Thus, mature miRNA sequence similarity 70 is selected as our default criterion for homologue search, but we also have to point out that, as some of the miRNAs in MicroRNA Registry are computational predicted as close homologs of experiment verified ones, this statistic result may be favorable for relatively close miRNAs homologs.