

Supplementary Information

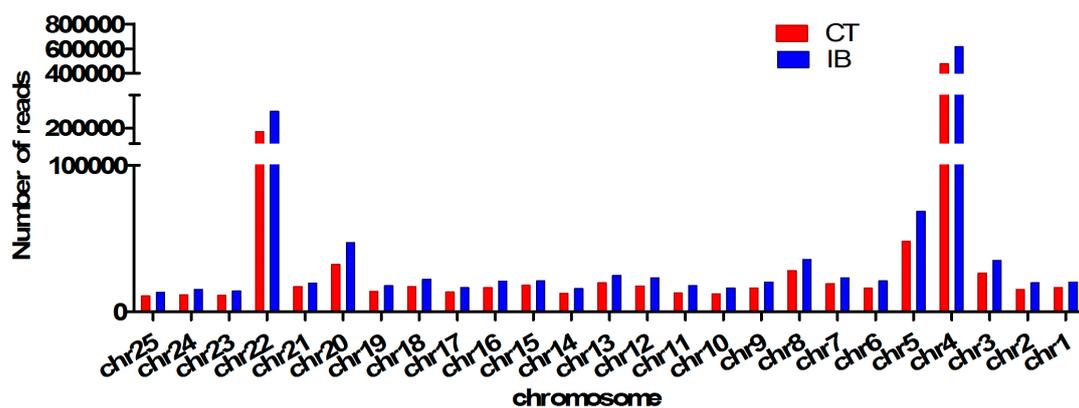


Figure S1. Number and distribution of clean reads mapped to the genome sequence of zebrafish.

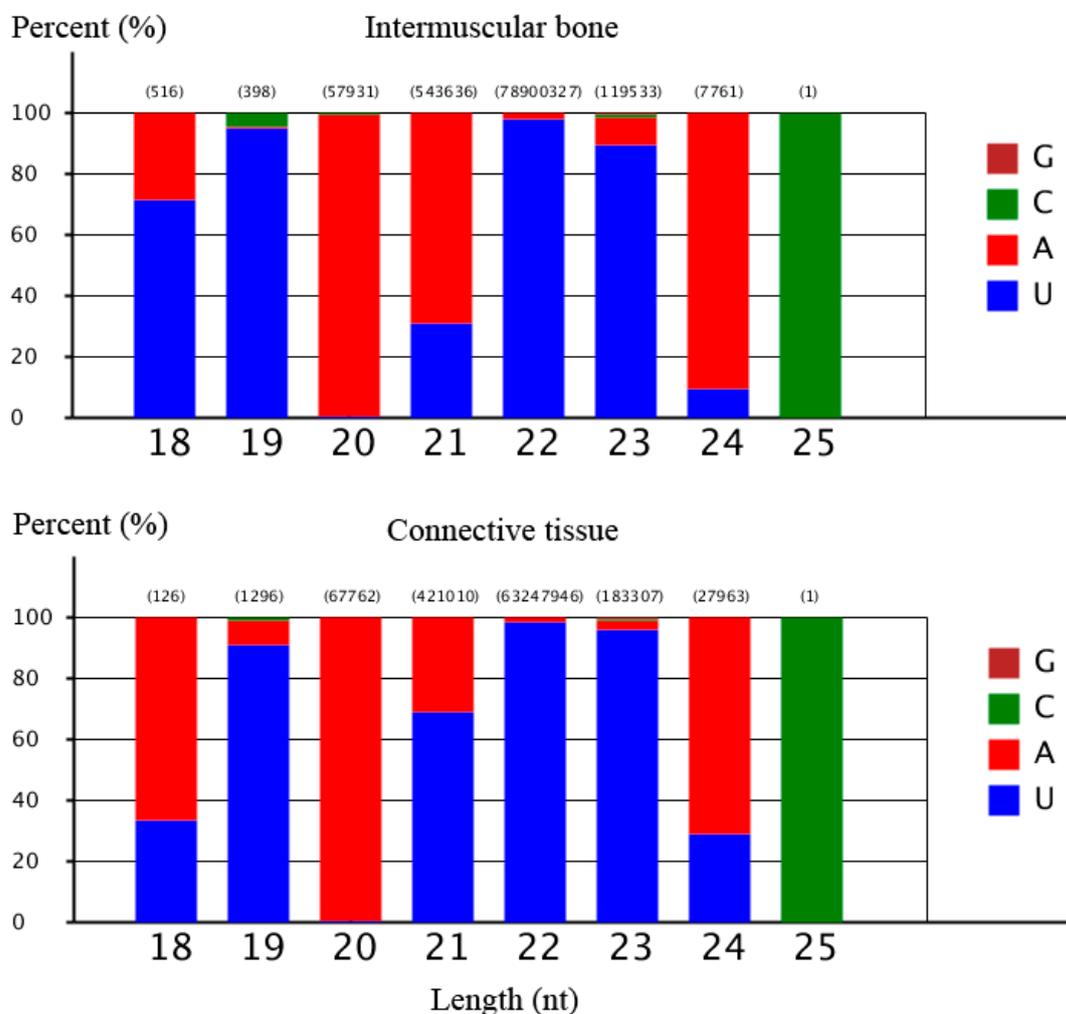


Figure S2. First nucleotide bias of 18~25 nt sRNA tags. The numbers above the histogram stand for the tags count in total. Each color in the figure shows the sRNA tags whose first base is a certain base.

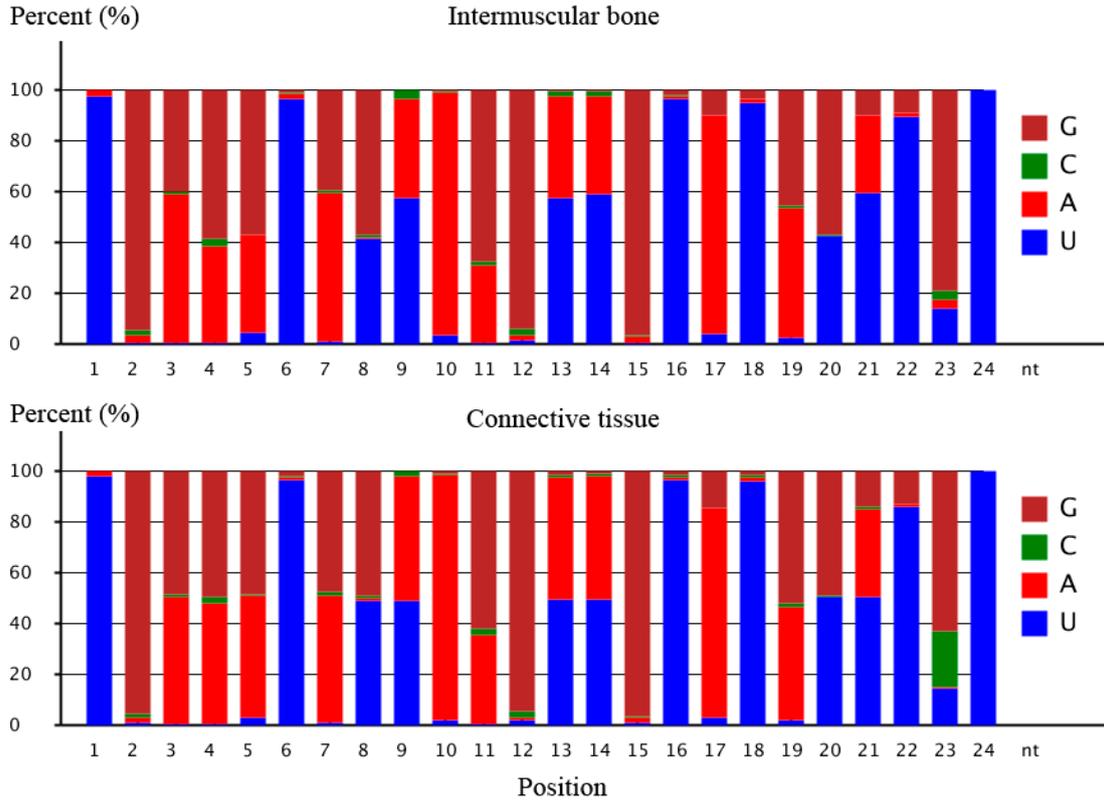


Figure S3. Base bias of the known miRNAs of intermuscular bone and connective tissue in *M. amblycephala* at each position.