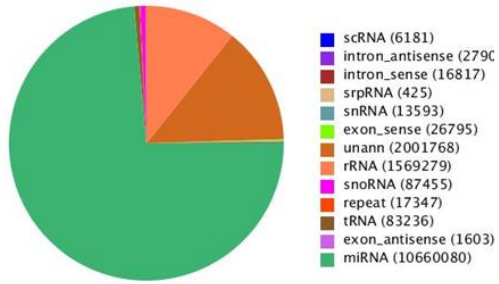
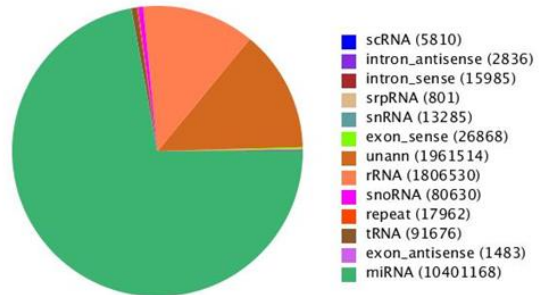


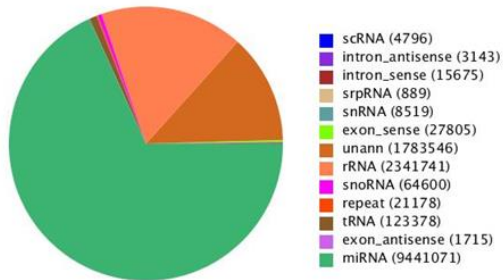
Pie chart for annotation_Ctl-1-total



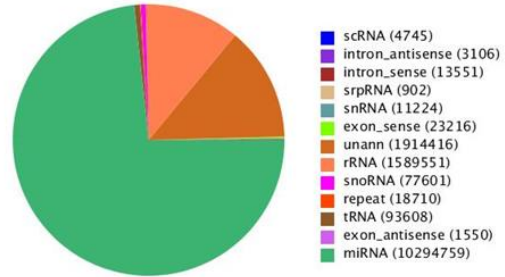
Pie chart for annotation_Ctl-2-total



Pie chart for annotation_CUMS-1-total



Pie chart for annotation_CUMS-2-total



S2 Fig. Small RNA categories annotation for control and CUMS groups. All of the high-quality clean reads larger than 18 nucleotides were mapped to the mouse genome and these genome-matched reads were divided into different categories of small RNAs according to their biogenesis and annotation. The most abundant RNA category from each library was miRNA.