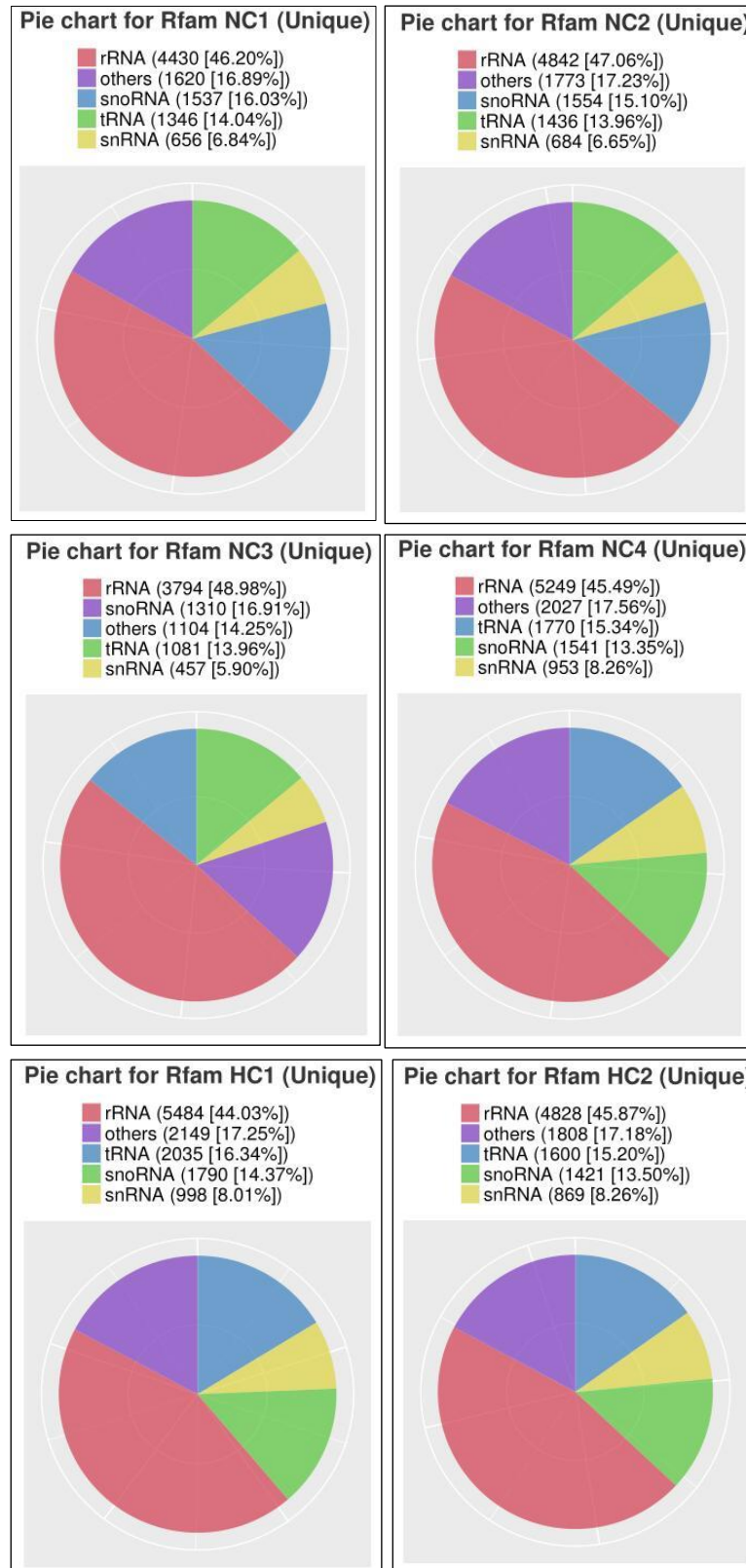
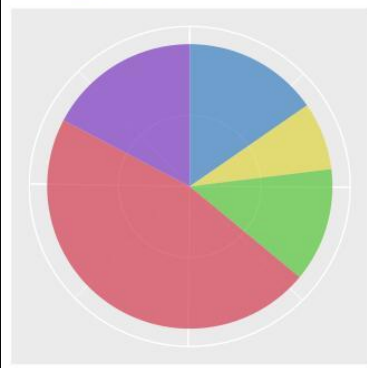


**Figure S1** Small RNA reads from NC group and HC group were blasted against the Rfam database non-coding RNA to annotate rRNA, snRNA, tRNA, snoRNA and others RNAs.



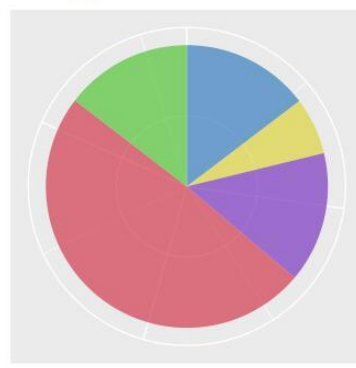
**Pie chart for Rfam HC3 (Unique)**

■ rRNA (5585 [46.70%])  
■ others (2068 [17.29%])  
■ tRNA (1836 [15.35%])  
■ snoRNA (1550 [12.96%])  
■ snRNA (921 [7.70%])



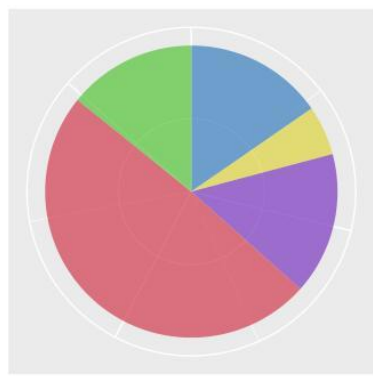
**Pie chart for Rfam HC4 (Unique)**

■ rRNA (4524 [49.24%])  
■ snoRNA (1375 [14.97%])  
■ tRNA (1348 [14.67%])  
■ others (1340 [14.59%])  
■ snRNA (600 [6.53%])



**Pie chart for Rfam HC5 (Unique)**

■ rRNA (3412 [49.19%])  
■ snoRNA (1093 [15.76%])  
■ tRNA (1066 [15.37%])  
■ others (985 [14.20%])  
■ snRNA (381 [5.49%])



**Pie chart for Rfam HC6 (Unique)**

■ rRNA (4226 [47.41%])  
■ others (1484 [16.65%])  
■ tRNA (1310 [14.70%])  
■ snoRNA (1216 [13.64%])  
■ snRNA (677 [7.60%])

