

Figure S1. ncRNA read size distribution. Y axis shows the number of the reads, while X-axis shows the size of the ncRNA reads in various regions of the brain in male and female rats.

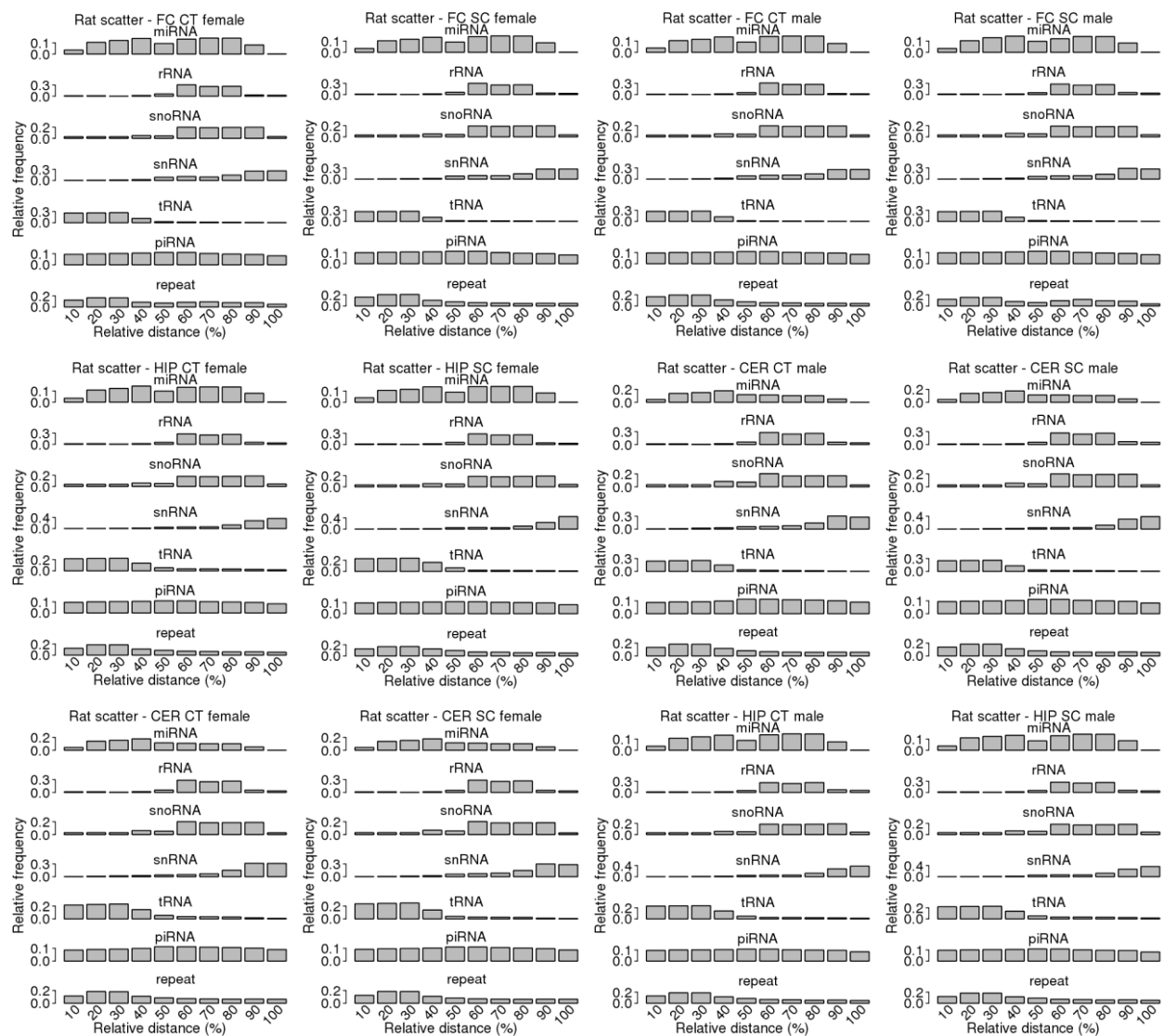


Figure S3. Analysis of reads distribution across the whole length of ncRNAs. The entire length of each ncRNA was taken as 100% and then divided into bins of 10% each, with 0 to 10% representing the first 10% of the ncRNA's length starting from the 5' end. The data are shown as the relative frequency of reads (calculated from three biological replicates) in a specific bin calculated by dividing the frequency of reads in a specific bin by all reads mapping to the entire length of ncRNA.

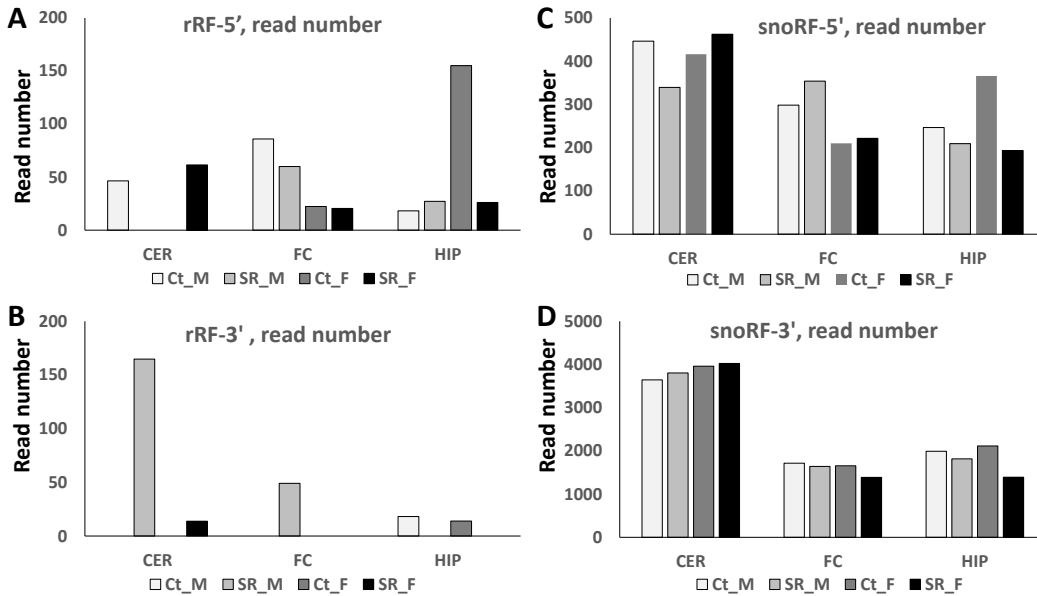


Figure S4. Number of rRF and snoRF reads mapping to the 5' or 3' ends of rRNA or snoRNAs. A. Number of rRF-5' reads in various brain regions of male and female rats. B. Number of rRF-3' reads in various brain regions of male and female rats. C. Number of snoRF-5' reads in various brain regions of male and female rats. D. Number of snoRF-3' reads in various brain regions of male and female rats.

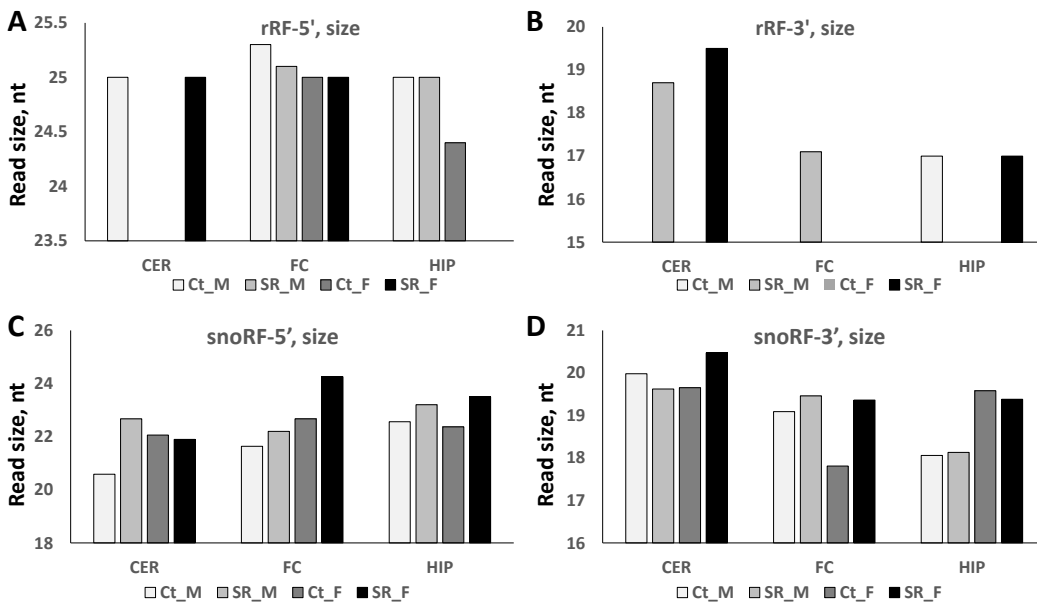


Figure S5. Size of rRF and snoRF reads mapping to the 5' or 3' ends of rRNA or snoRNAs. A. Size of rRF-5' reads in various brain regions of male and female rats. B. Size of rRF-3' reads in various brain regions of male and female rats. C. Size of snoRF-5' reads in various brain regions of male and female rats. D. Size of snoRF-3' reads in various brain regions of male and female rats.

