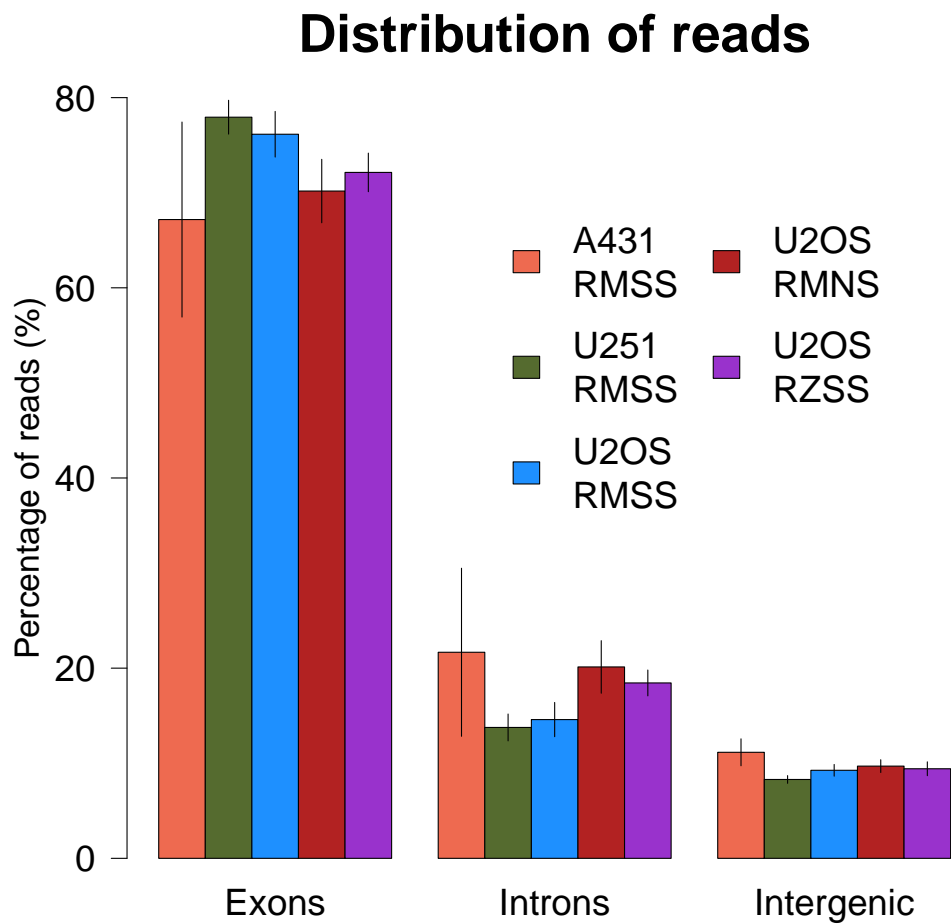


# Analysis of stranded information using an automated procedure for strand specific RNA sequencing

## Additional file 4



**Figure S2:** Distribution of mapped reads into exonic, intronic and intergenic regions. Shown are the averages for each of the five library groups and error bars denote standard error. The distribution is similar between groups and ANOVA revealed no significant difference between them. Noteworthy are the large error bars for the A431\_RMSS group. That group only contained two libraries, one of which showed unusually high mapping to intronic regions.