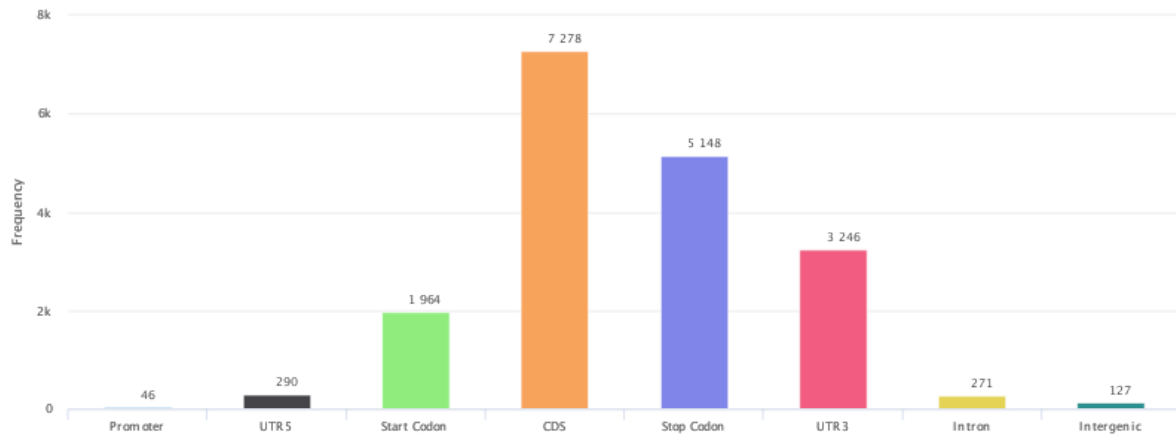# RNA Annotation (RNAmod)
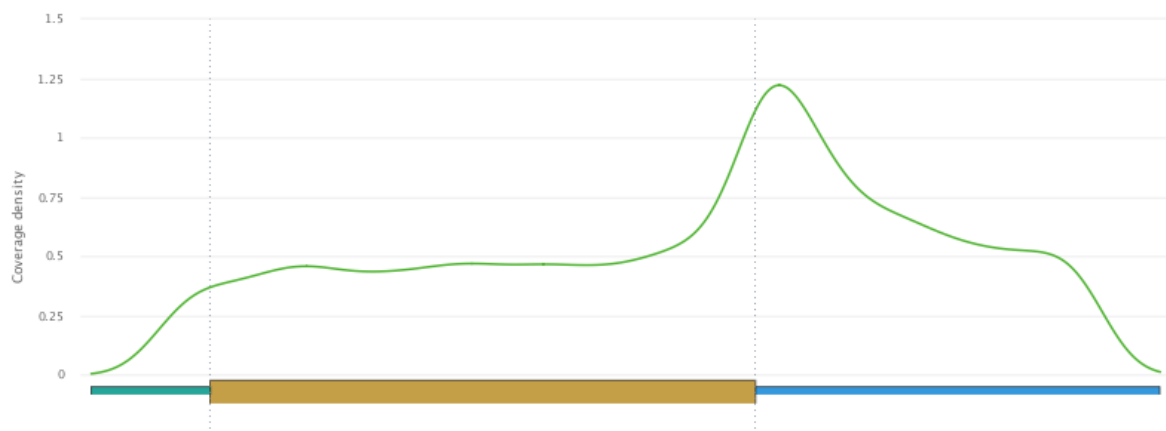
To obtain modification site information, click on "Single case" in the RNAmod Home page, upload the BED file generated from exomePeak2 package, and submit the job. Then you will receive a job ID and will use it to query the job status and get the results in the result page. You can either view the results on browser or download the zip file to the local place.

Some of the figures about modification site information are displayed below:

- Peaks gene features distribution:

- mRNA metagene plot

- Gene types distribution

Category	Value
3prime_overlapping_ncrna	8
antisense	3 239
IG_V_gene	4
lincRNA	948
miRNA	134
misc_RNA	54
non_stop_decay	35
nonsense_mediated_decay	14 140
polymorphic_pseudogene	1
processed_pseudogene	147
processed_transcript	10 110
protein_coding	143 461
pseudogene	313
retained_intron	8 828
rRNA	18
sense_intronic	101
sense_overlapping	98
snoRNA	36
snRNA	57
transcribed_processed_pseudogene	36
transcribed_unprocessed_pseudogene	135
unitary_pseudogene	5
unprocessed_pseudogene	97