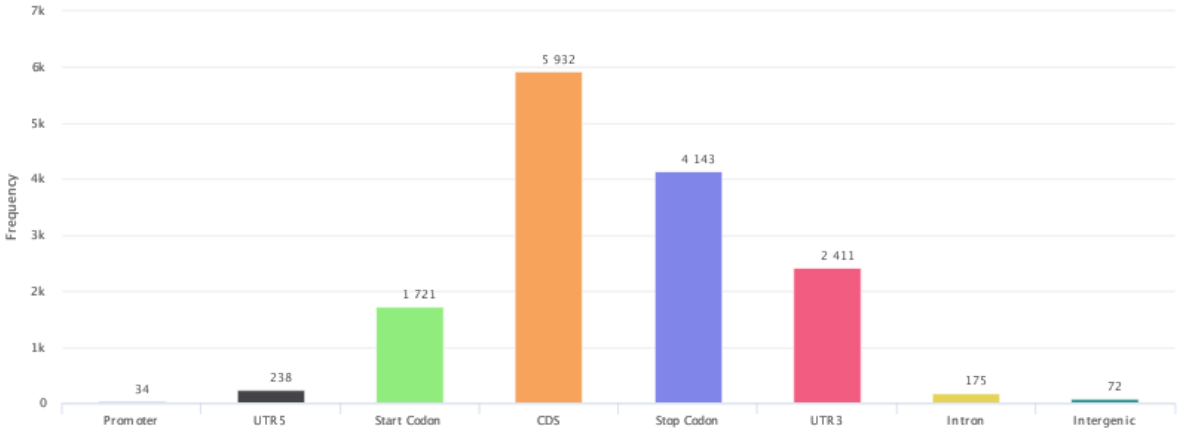
RNA Annotation (RNAmod)

RNAmod is a convenient web-based platform for the meta-analysis and functional annotation of modifications on mRNAs [14].

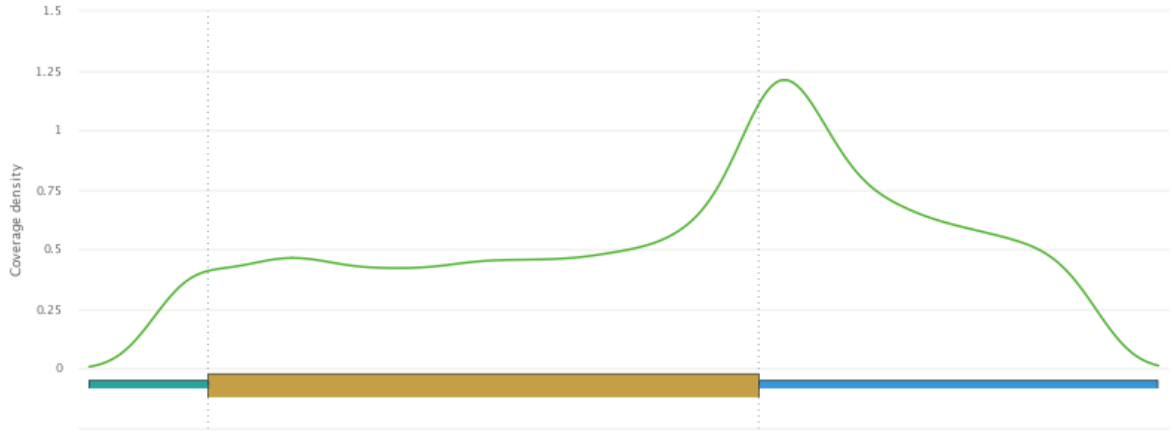
To obtain modification site information, click on "Single case" in the Home page, upload the BED file generated from exomePeak2 package, and submit the job. Then you will receive a job ID and will use it to query the job status and get the results in the result page. You can either view the results on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

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

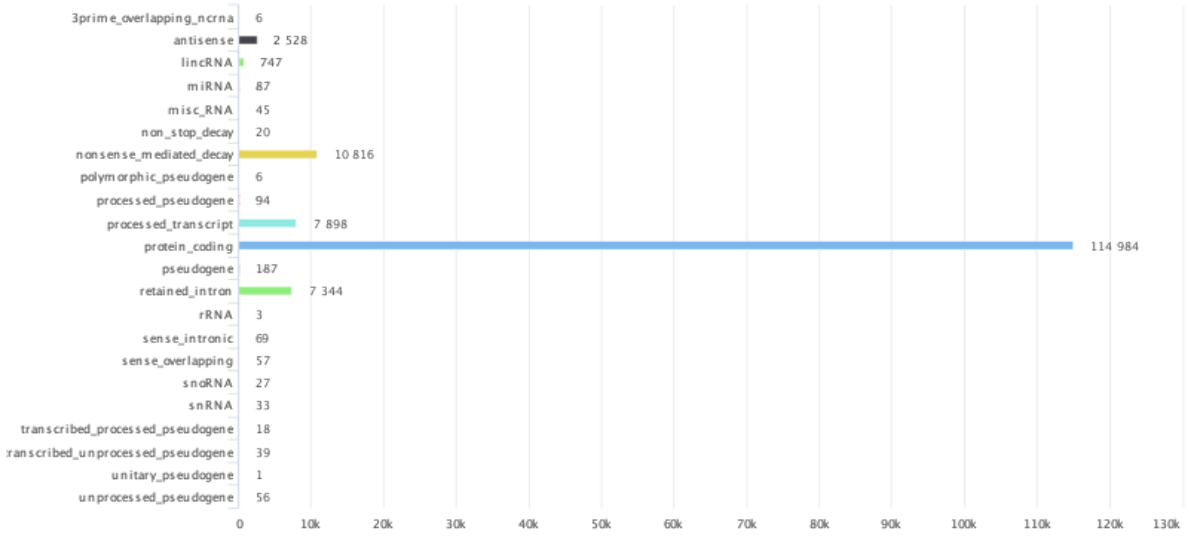
- Peaks gene features distribution:



- mRNA metagene plot



- Gene types distribution


3prime_overlapping_ncrna 6
antisense 2 528
lincRNA 747
miRNA 87
misc_RNA 45
non_stop_decay 20
nonsense_mediated_decay 10 816
polymorphic_pseudogene 6
processed_pseudogene 94
processed_transcript 7 898
protein_coding 114 984
pseudogene 187
retained_intron 7 344
rRNA 3
sense_intronic 69
sense_overlapping 57
snoRNA 27
snRNA 33
transcribed_processed_pseudogene 18
transcribed_unprocessed_pseudogene 39
unitary_pseudogene 1
unprocessed_pseudogene 56
0
10k
20k
30k
40k
50k
60k
70k
80k
90k
100k
110k
120k
130k