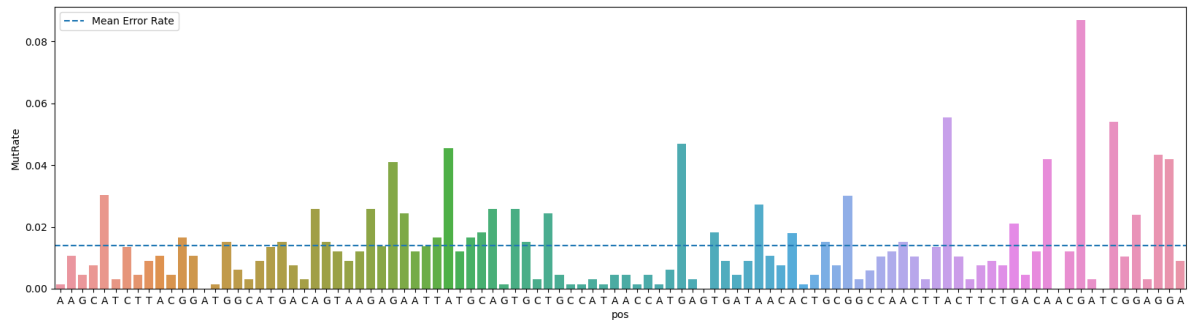


Libraries Analysis using plasmidsaurus sequencing

With the stats file you can check the mutation rate per position.

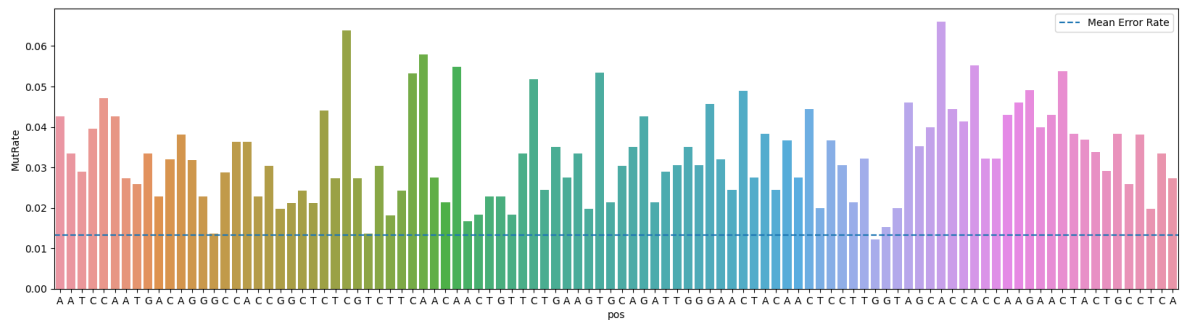
In the control region the mutation rate should be very low:



And in your region of interest you can check how's the coverage of your library and to check if there's some positional bias.

Good coverage:

In almost all the positions the mutation rate is above the Mean Error Rate. Meaning that the mutations are spread all along your region of interest.



Positional bias:

In this case you have some positions where the mutation rate is clearly above the Mean Error Rate, but others that are below or at the limit. In this library there was a synthesis bias where the mutations are most represented in the first region, this translates, usually, into bad coverage.

