TREND ANALYSIS REPORT

Updated 25-July-2020 14:34

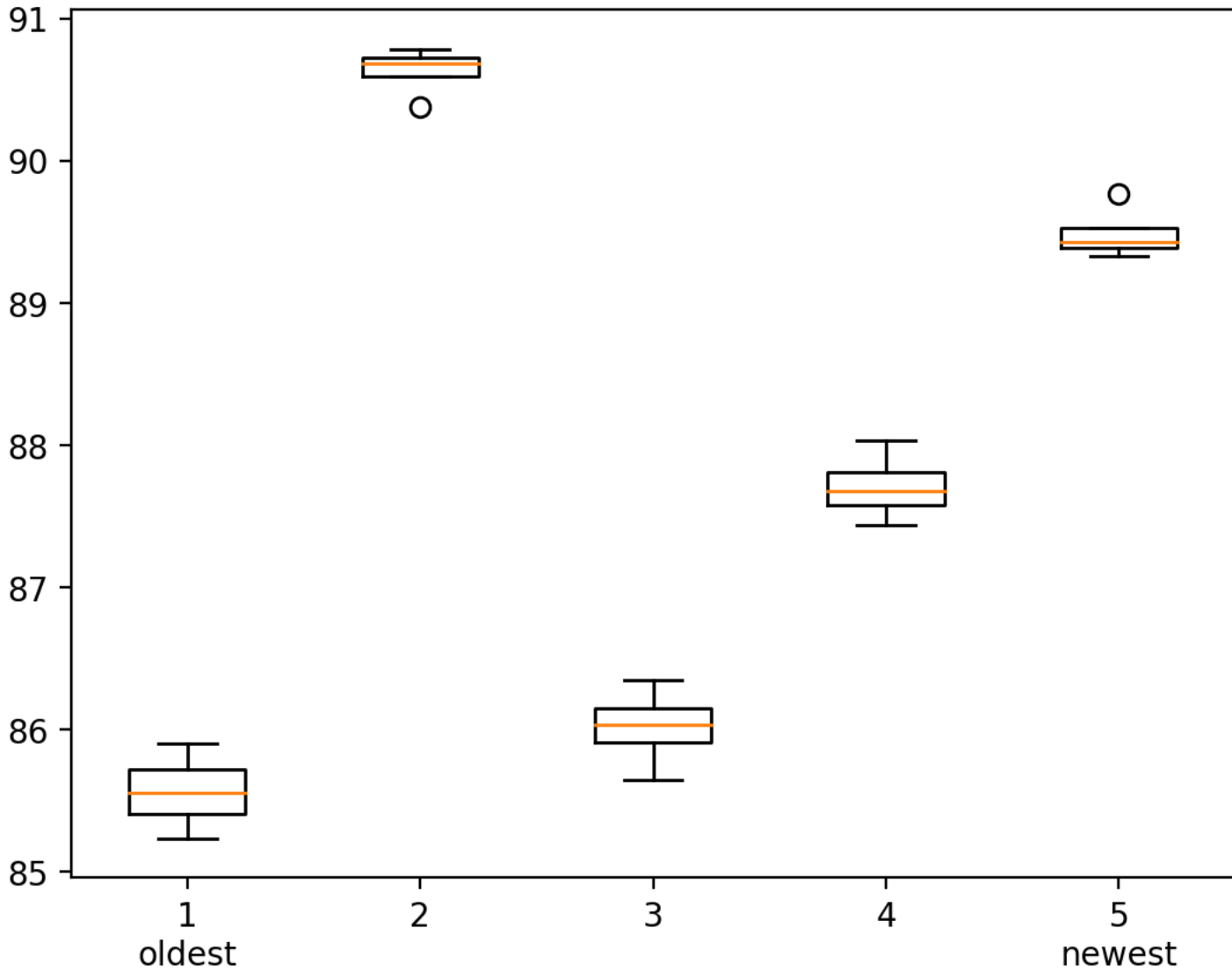
Run names

.

Run Number	Run Name
1 oldest	002_200515_NB551068_0327_AH5W7YBGXF_NGS306D_WES51
2	002_200626_NB552085_0068_AHM5NGBGXF_NGS345A_WES_WES58
3	002_200629_NB551068_0331_AHM5G2BGXF_NGS345B_WES58
4	002_200701_NB552085_0069_AHHHHCBGXF_NGS345C_WES58
5 newest	002_200722_NB551068_0333_AHHHG7BGXF_NGS348_WES

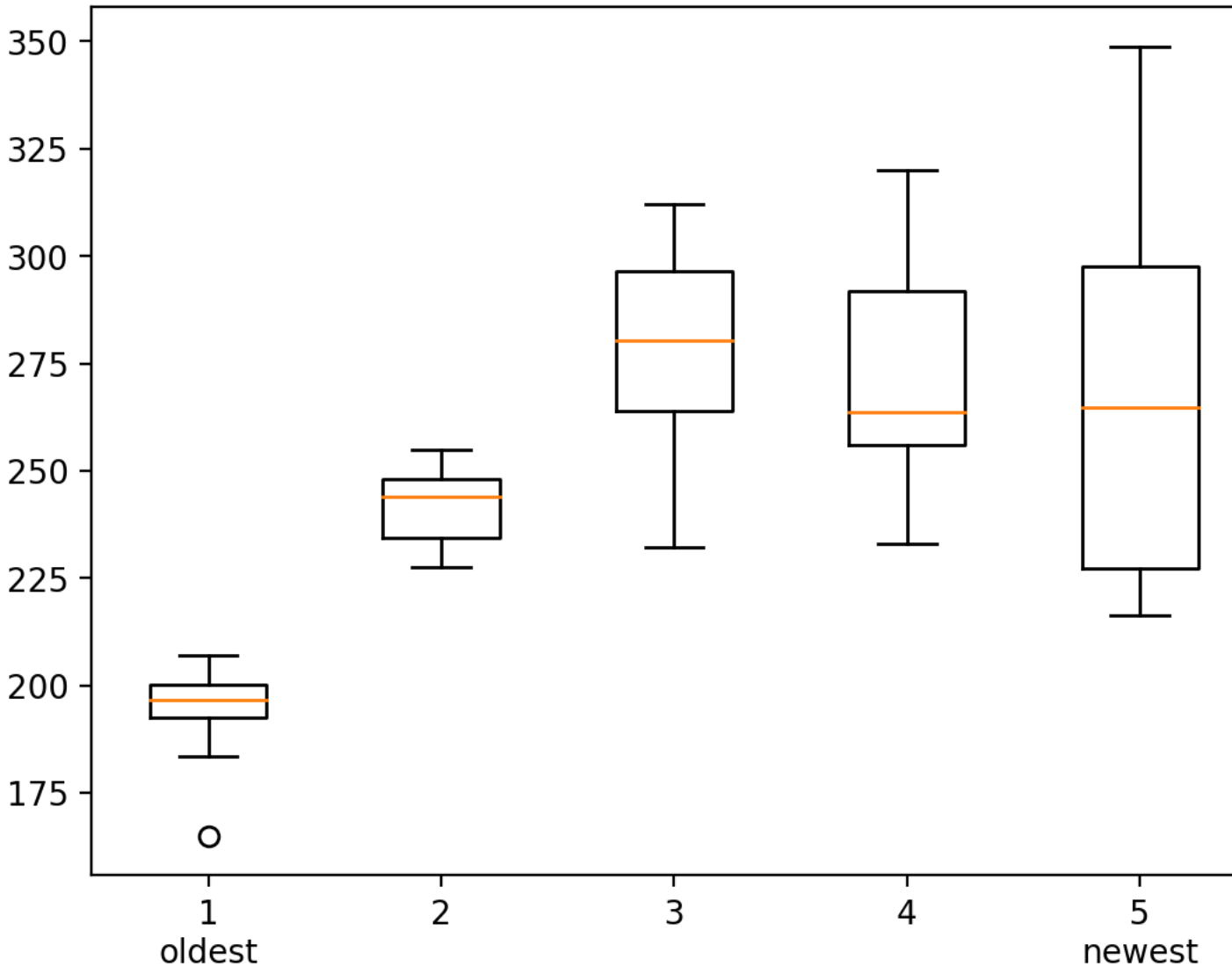
BCL2Fastq Q30 percentage

Boxplots showing the percentage of bases >= Q30. Values within each boxplot are for each lane. This shows hoe well the base calling has performed on the sequencer.



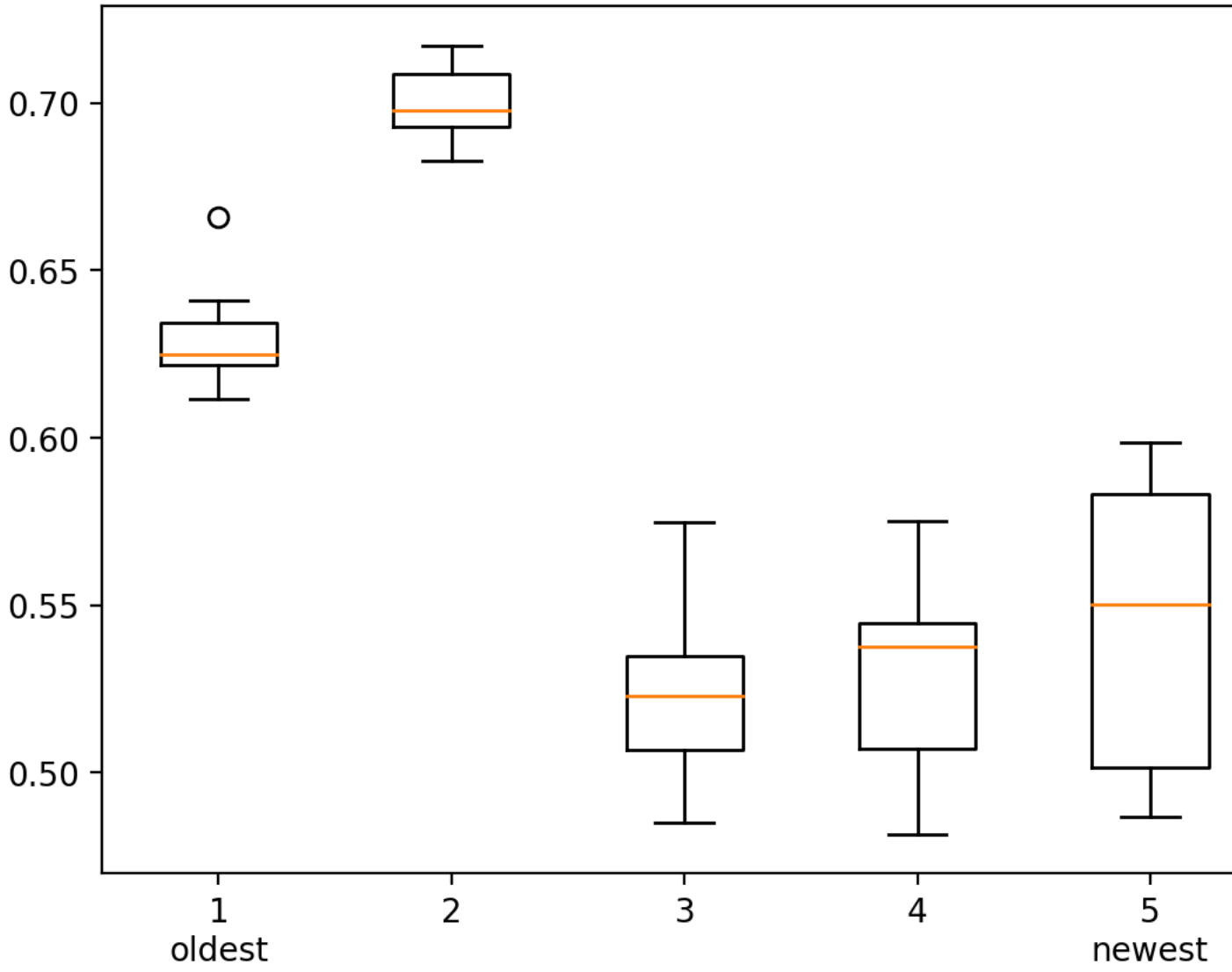
Picard Insert Sizes

Boxplots showing the range and spread of insert sizes. This will highlight DNA fragmentation.



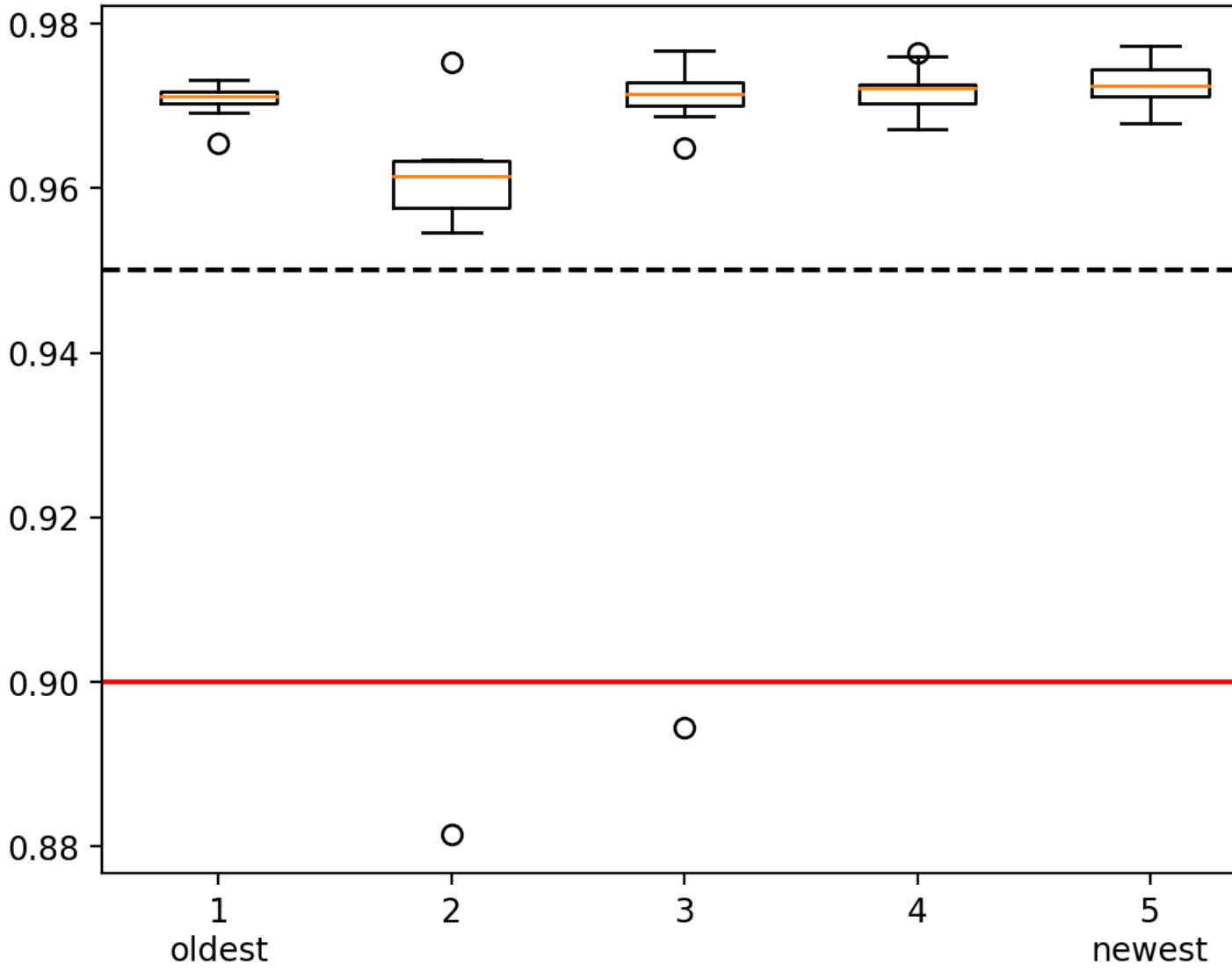
on_target_vs_selected

The % of on and near bait bases that are on as opposed to near (as defined by the BED file containing the capture regions..



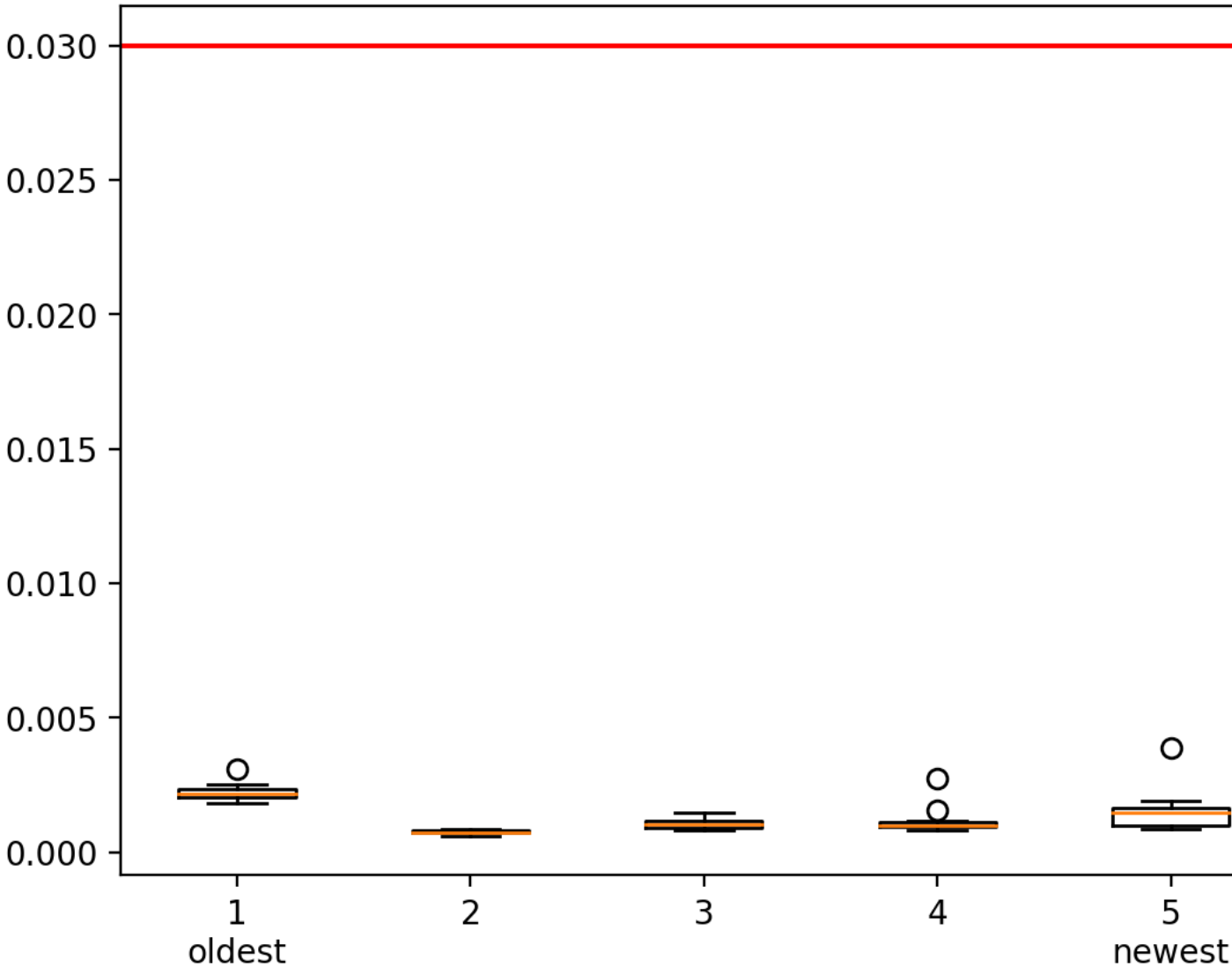
target_bases_at_20X

Boxplot showing the % of bases in the target regions which are covered at >= 20X. Samples below 90% are failed. Samples above 95% pass. Samples between 90-95% may be analysed with caution.



Contamination

The contamination estimate as calculated by VerifyBAMID (FREEMIX). A sample is considered contaminated when FREEMIX > 0.03.


0.030
0.025
0.020
0.015
0.010
0.005
0.000
1
oldest
2
3
4
5
newest