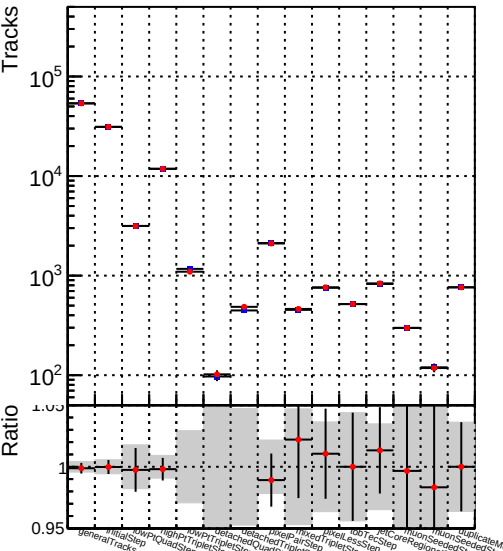
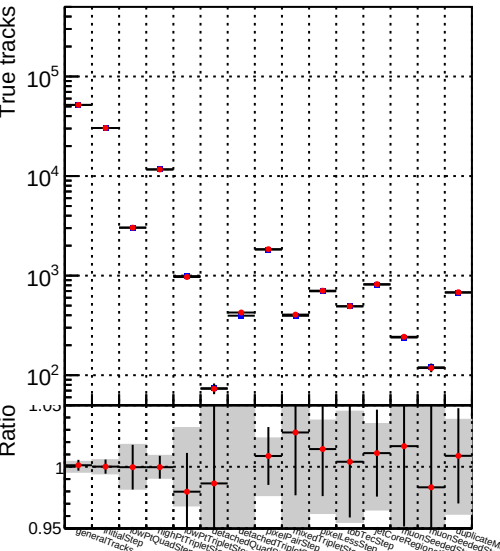


Number of tracks vs collection



Number of true tracks vs collection



Number	File Name
1	DQM_CKF_TT_retrainOldFiles125_v2_prelimWPM_epoch2

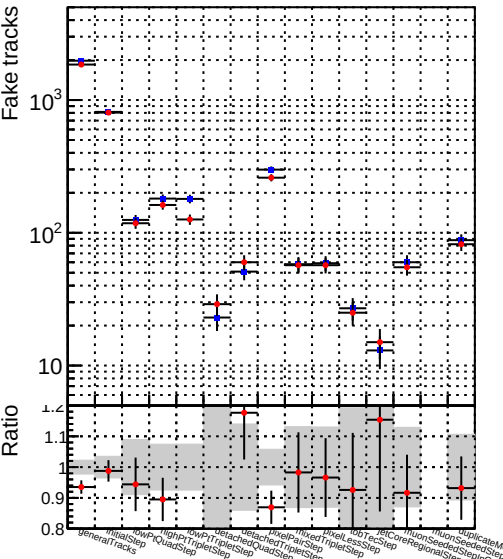


Figure 1: A dot plot showing the ratio of duplicate tracks for various genomic features. The y-axis is 'Ratio' on a log scale from 0.8 to 10². The x-axis lists genomic features. Each feature has a grey shaded region representing a range and a black dot with error bars representing a mean and standard deviation. The 'Duplicate tracks' feature has a ratio significantly above 10². 'Highly repetitive tracks' and 'Lowly repetitive tracks' have ratios around 10. 'Repetitive tracks' and 'Non-repetitive tracks' have ratios around 2. 'General tracks' has a ratio around 1.0. 'Non-repetitive tracks' has a ratio around 0.85.

Number of pileup tracks vs collection

