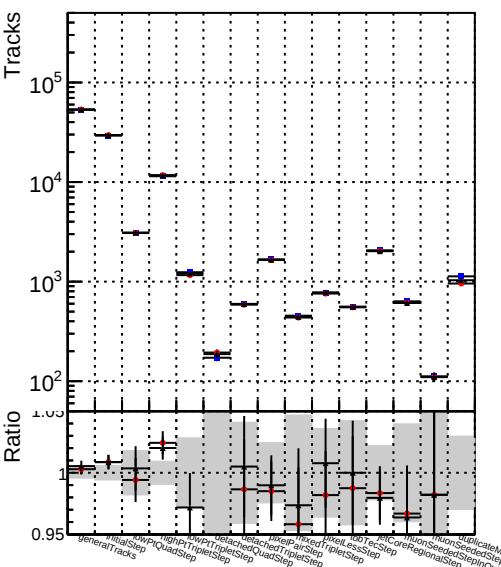
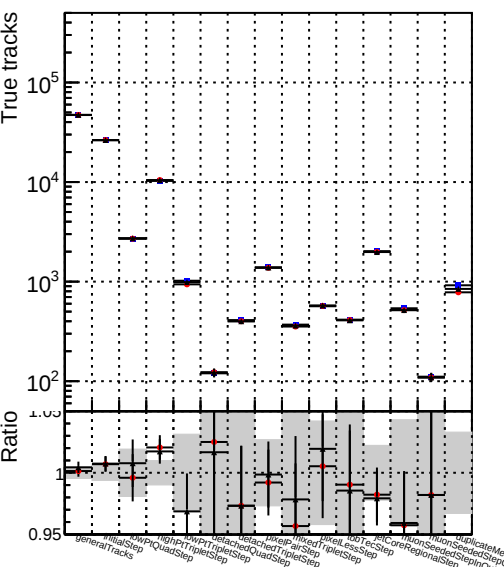


Number of tracks vs collection



Number of true tracks vs collection



Number	File Name
1	/data2/legianni/standalone-May24/CMSSW_13_2_X_2023-06-05-1100/src/DQM_TT_mkFit-DQM_mod_updatedmod-127
2	DQM_TT_mkFit-DQM_update-mod127

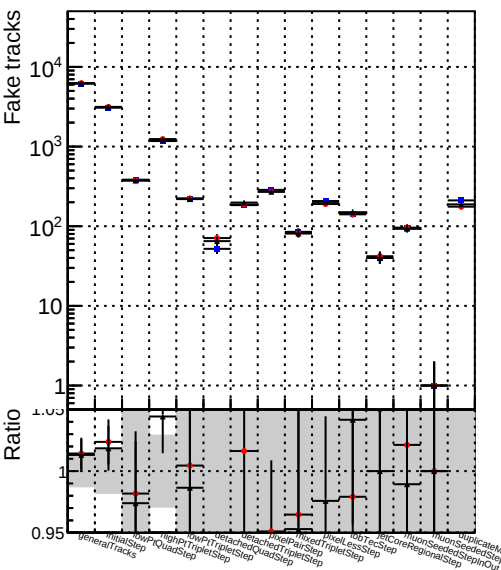


Figure 1 is a dot plot showing the ratio of duplicate tracks to general tracks for various genomic features. The y-axis is labeled 'Ratio' and ranges from 0.8 to 10² on a log scale. The x-axis lists genomic features: general tracks, initialStep, finalStep, highPT, lowPT, detached, joined, paired, unpaired, left, right, eccStep, nonSeeded, seeded, and repeatMask. Each feature has a blue dot representing the ratio, a red horizontal line indicating the 1:1 ratio, and a grey shaded area representing the confidence interval. The 'general tracks' feature has a ratio significantly above 1, while most other features are close to or below 1.

Genomic Feature	Ratio (approx.)
general tracks	~50
initialStep	~1.1
finalStep	~1.0
highPT	~1.0
lowPT	~1.0
detached	~1.0
joined	~1.0
paired	~1.0
unpaired	~1.0
left	~1.0
right	~1.0
eccStep	~1.0
nonSeeded	~1.0
seeded	~1.0
repeatMask	~1.0

Number of pileup tracks vs collection

