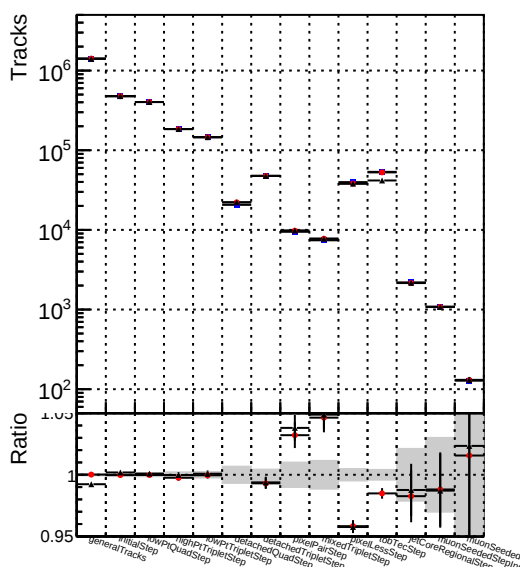
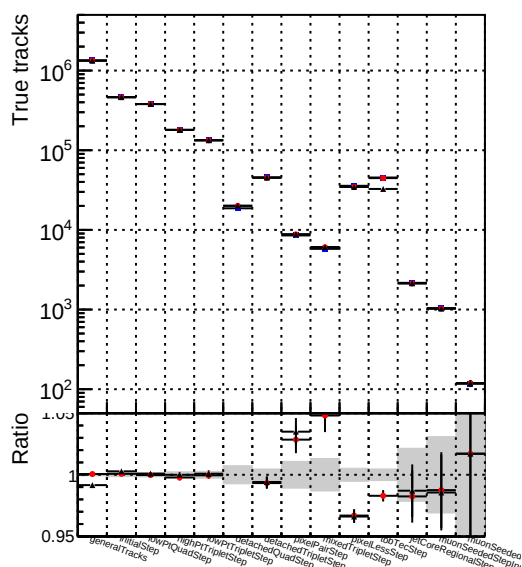


Number of tracks vs collection



Number of true tracks vs collection



Number	Legend
	DQM_V0001_R0000000001_Global_mkFitOLD_RECO
	DQM_V0001_R0000000001_Global_mkFit100_RECO
	DQM_V0001_R0000000001_Global_mkFit100tobtec_RECO

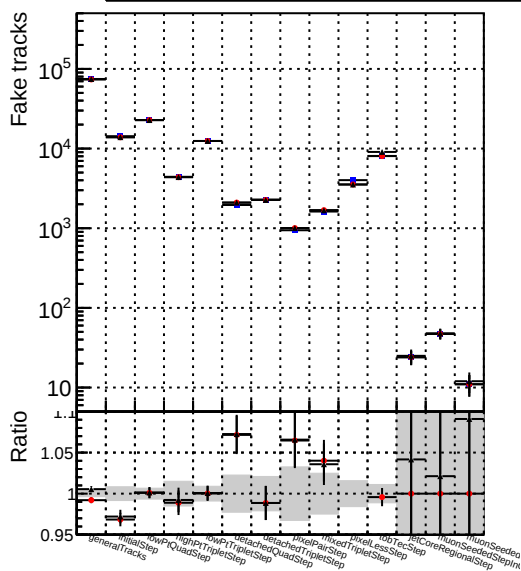


Figure 1 is a combined bar and scatter plot showing the ratio of duplicate tracks for various genomic features. The y-axis is labeled 'Ratio' and ranges from 0.8 to 10,000 on a logarithmic scale. The x-axis lists genomic features: generalTracks, mitochondrialStep, highPTTQuasiStep, highPTTTripStep, detachedQuasiStep, detachedTripStep, totalPairStep, totalTripStep, totalLessStep, totalRefStep, totalSeedsStep, and totalSeedsStep. Grey bars represent the ratio of duplicate tracks to total tracks for each feature. Blue dots with error bars represent the ratio of duplicate tracks to total tracks for each feature. A horizontal line at Ratio = 1.0 indicates the expected ratio if all features were equally represented.

Genomic Feature	Ratio (approx.)
generalTracks	0.85
mitochondrialStep	1.2
highPTTQuasiStep	1.0
highPTTTripStep	1.0
detachedQuasiStep	0.95
detachedTripStep	0.95
totalPairStep	1.0
totalTripStep	1.0
totalLessStep	1.0
totalRefStep	1.0
totalSeedsStep	1.0
totalSeedsStep	1.0

Number of pileup tracks vs collection

