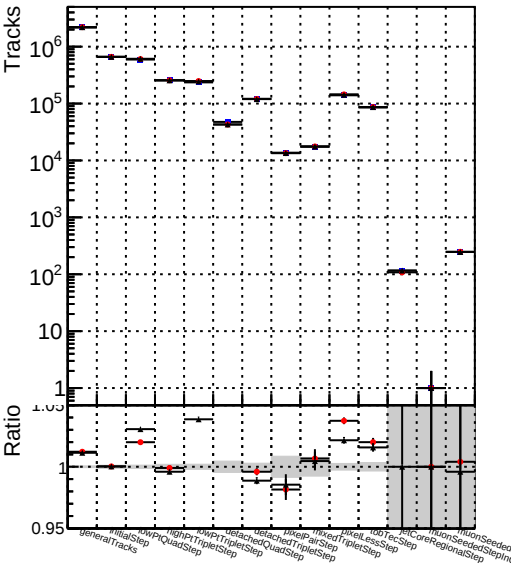
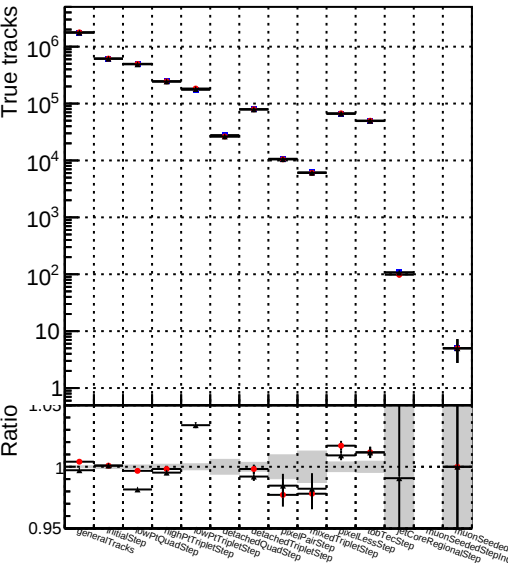


Number of tracks vs collection



Number of true tracks vs collection



Number	●	DQM_TT_CKFLowPtQ_ORIG
	▲	DQM_TT_CKFLowPtQ_MODIF

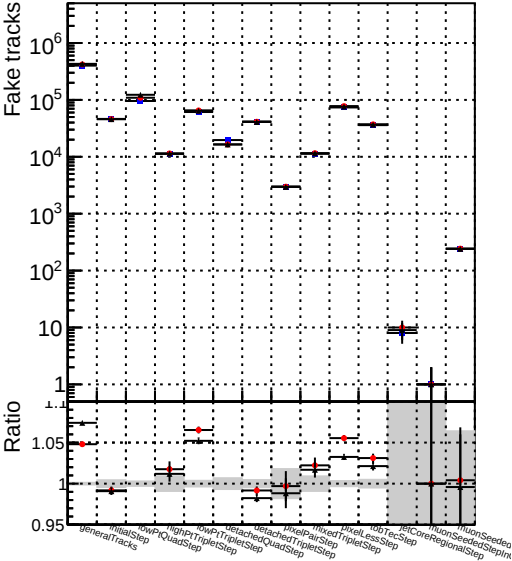


Figure 1 consists of two panels. The top panel is a log-scale plot of 'Duplicate tracks' (y-axis, 1 to 10⁵) versus 'Ratio' (x-axis, 1 to 10⁵). The bottom panel is a log-scale plot of 'Ratio' (y-axis, 1 to 10⁵) versus 'Ratio' (x-axis, 1 to 10⁵). Both panels show data points with error bars for various genomic features. The features are: generalTracks, chr1Step, chr2Step, chr3Step, chr4Step, chr5Step, chr6Step, chr7Step, chr8Step, chr9Step, chr10Step, chr11Step, chr12Step, chr13Step, chr14Step, chr15Step, chr16Step, chr17Step, chr18Step, chr19Step, chr20Step, chr21Step, chr22Step, chr23Step, chr24Step, chr25Step, chr26Step, chr27Step, chr28Step, chr29Step, chr30Step, chrXStep, chrYStep, chrZStep, chrWStep, chrVStep, chrUStep, chrTStep, chrSStep, chrRStep, chrQStep, chrPStep, chrOStep, chrNStep, chrMStep, chrLStep, chrKStep, chrJStep, chrIStep, chrHStep, chrGStep, chrFStep, chrEStep, chrDStep, chrCStep, chrBStep, chrAStep, chrZStep, chrYStep, chrXStep, chrWStep, chrVStep, chrUStep, chrTStep, chrSStep, chrRStep, chrQStep, chrPStep, chrOStep, chrNStep, chrMStep, chrLStep, chrKStep, chrJStep, chrIStep, chrHStep, chrGStep, chrFStep, chrEStep, chrDStep, chrCStep, chrBStep, chrAStep.

Number of pileup tracks vs collection

