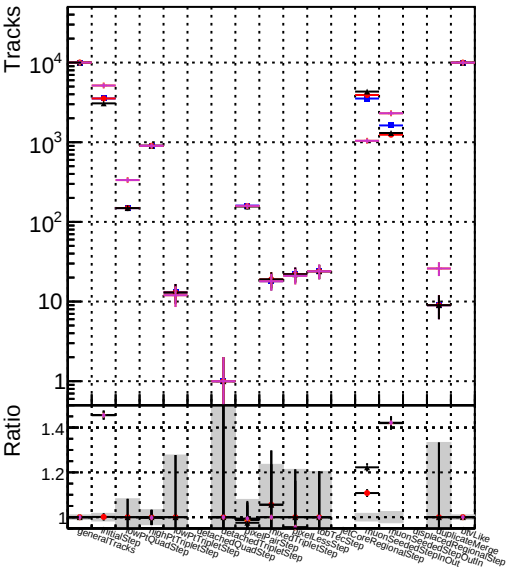
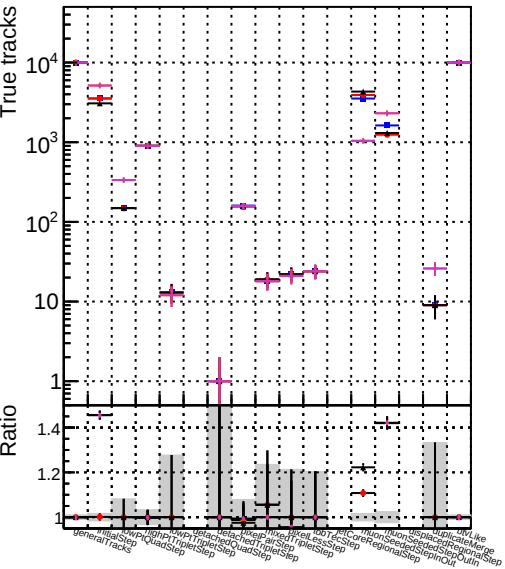


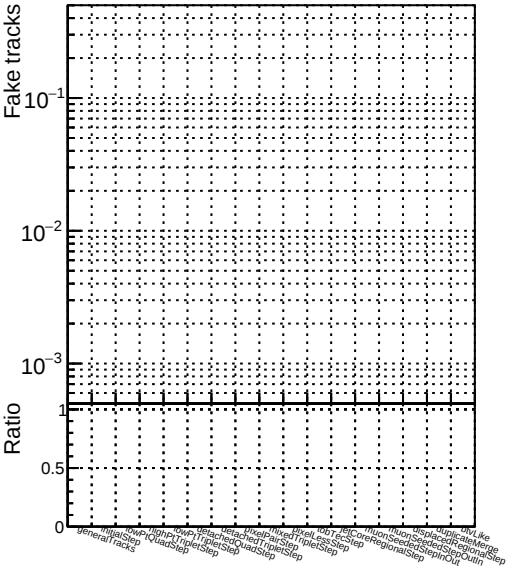
Number of tracks vs collection



Number of true tracks vs collection



Number	Legend
1	DQM_last_step2_pt1to20_eta0p0to0p4
2	DQM_mkFit_step2_pt1to20_eta0p0to0p4
3	DQM_CPEpixel3_step2_pt1to20_eta0p0to0p4



The figure shows the ratio of duplicate tracks for various methods. The y-axis is labeled 'Ratio' and ranges from 0.95 to 1.05. The x-axis lists the methods. A horizontal line at Ratio = 1.0 indicates equal duplication. Most methods have ratios very close to 1.0, indicated by grey vertical bars. One method, 'HaplotypeCaller', has a significantly higher ratio, around 4.0, indicated by a pink vertical bar.

Method	Approximate Ratio
GeneralTracks	1.00
HaplotypeCaller	4.00
HaplotypeCaller-HighDepth	1.00
HaplotypeCaller-Indel	1.00
HaplotypeCaller-SNP	1.00
HaplotypeCaller-Struc	1.00
HaplotypeCaller-TripleSeq	1.00
HaplotypeCaller-QuadrupleSeq	1.00
HaplotypeCaller-PairSeq	1.00
HaplotypeCaller-Riplex	1.00
HaplotypeCaller-RegionSeq	1.00
HaplotypeCaller-Outlier	1.00
HaplotypeCaller-Merge	1.00
HaplotypeCaller-Filter	1.00
HaplotypeCaller-Trim	1.00
HaplotypeCaller-Align	1.00
HaplotypeCaller-Index	1.00
HaplotypeCaller-Store	1.00
HaplotypeCaller-Load	1.00
HaplotypeCaller-Run	1.00
HaplotypeCaller-Exit	1.00

Number of pileup tracks vs collection

