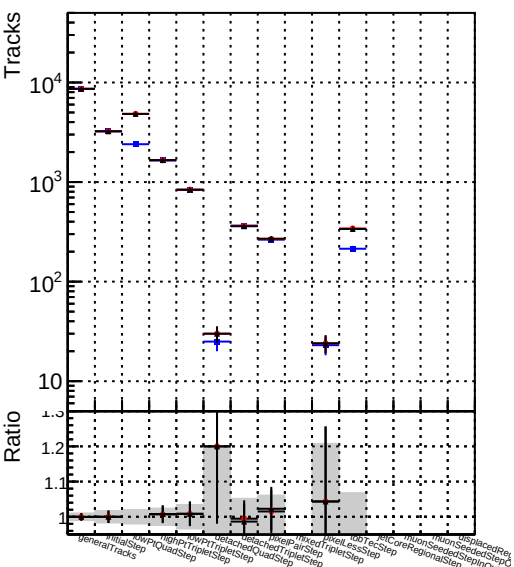
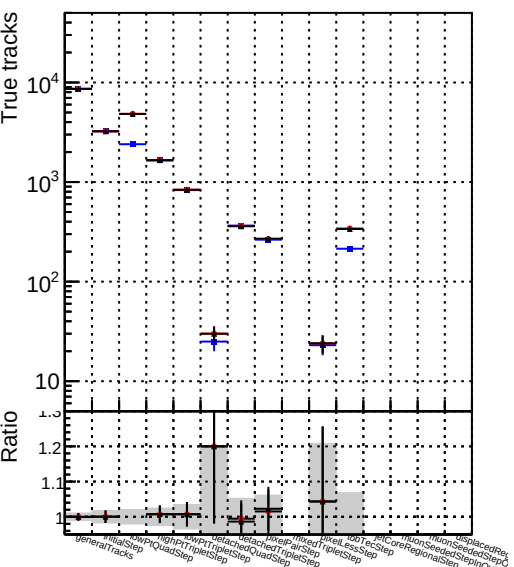


Number of tracks vs collection



Number of true tracks vs collection



Number

- DQM_original_step2_pt0p1to1_eta1p4to1p6
- DQM_mkFit_step2_pt0p1to1_eta1p4to1p6
- ▲— DQM_pixelCPETemplate_step2_pt0p1to1_eta1p4to1p6

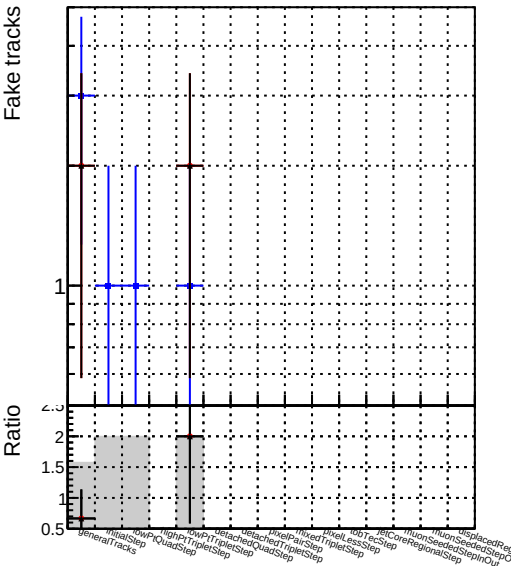


Figure 1 is a dot plot showing the ratio of duplicate tracks for various genomic features. The y-axis is labeled 'Ratio' and ranges from 0.8 to 10 on a logarithmic scale. The x-axis lists 20 genomic features. Each feature has a central dot representing the mean ratio and a vertical error bar representing the range. The 'Duplicate tracks' feature is highlighted with a blue dot and error bar, while all other features have red dots and error bars. A horizontal line is drawn at Ratio = 1.0.

Genomic Feature	Mean Ratio (approx.)	Ratio Range (approx.)
Duplicate tracks	2.5	1.8 - 3.5
GeneralTracks	0.85	0.8 - 1.2
RepeatStep	0.85	0.8 - 1.2
ContigStep	0.85	0.8 - 1.2
RefStep	0.85	0.8 - 1.2
UnplacedStep	0.85	0.8 - 1.2
UnplacedOutStep	0.85	0.8 - 1.2
UnplacedInStep	0.85	0.8 - 1.2
UnplacedOutInStep	0.85	0.8 - 1.2
UnplacedInOutStep	0.85	0.8 - 1.2
UnplacedOutInOutStep	0.85	0.8 - 1.2
UnplacedInOutInStep	0.85	0.8 - 1.2
UnplacedInOutInOutStep	0.85	0.8 - 1.2
UnplacedInOutInOutInStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInOutStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInOutInStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInOutInOutStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInOutInOutInStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInOutInOutInOutStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInOutInOutInOutInStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInOutInOutInOutInOutStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInOutInOutInOutInOutInStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInOutInOutInOutInOutInOutStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInOutInOutInOutInOutInOutInStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInOutInOutInOutInOutInOutInOutStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInOutInOutInOutInOutInOutInOutInStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInStep	0.85	0.8 - 1.2
UnplacedInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutStep	0.85	0.8 - 1.2
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UnplacedInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInOutInStep	0.85	0.8 - 1.2
UnplacedInOutStep	0.85	0.8 - 1.2
UnplacedInOutInStep	0.85	0.8 - 1.2
UnplacedInOutStep	0.85	0.8 - 1.2
UnplacedInOutInStep	0.85	0.8 - 1.2
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UnplacedInOutStep	0.85	0.8 - 1.2
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UnplacedInOutStep	0.85	0.8 - 1.2
UnplacedInOutInStep	0.85	0.8 - 1.2
UnplacedInOutStep	0.85	0.8 - 1.2
UnplacedInOutInStep	0.85	0.8 - 1.2
UnplacedInOutStep	0.85	0.8 - 1.2

Number of pileup tracks vs collection

