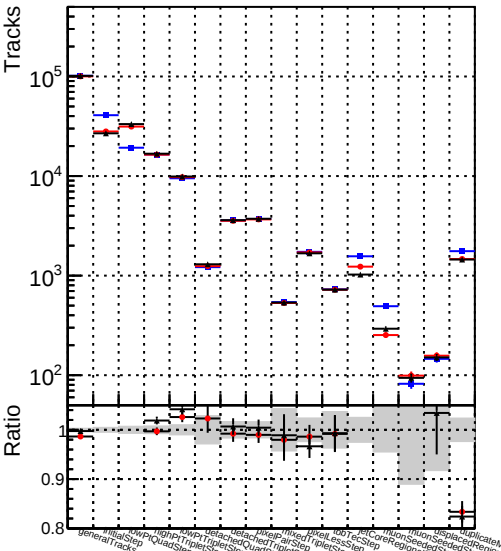
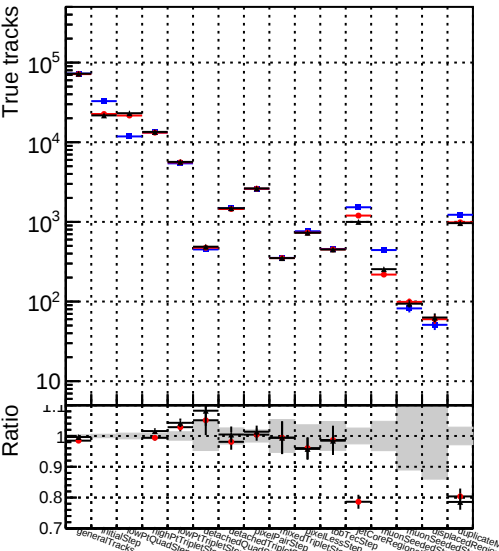


Number of tracks vs collection



Number of true tracks vs collection



Number

- DQM_original
- DQM_testMkFitExport_initialStep
- DQM_testMkFitExportFit_initialStep

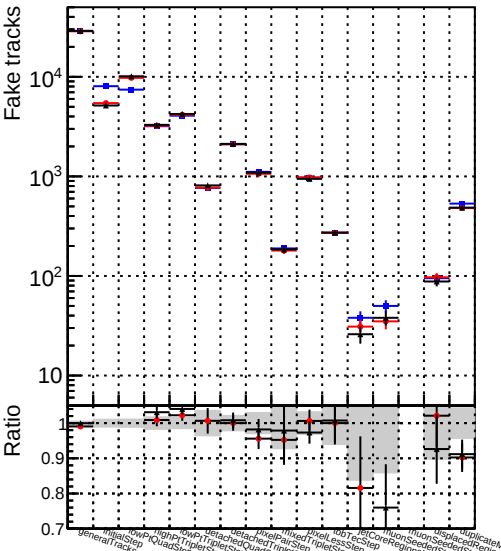


Figure 1: A log-linear plot showing the ratio of duplicate tracks to total tracks for various genomic features. The y-axis is 'Ratio' on a log scale from 0.8 to 10². The x-axis lists genomic features. The 'General track' has a ratio of approximately 0.85. The 'Quadruplet' track has a ratio of approximately 1.0. The 'Highly conserved' track has a ratio of approximately 1.5. The 'Predicted' track has a ratio of approximately 100. The 'Duplicate tracks' track has a ratio of approximately 100. The 'General track' is highlighted with a grey shaded area.

Number of pileup tracks vs collection

