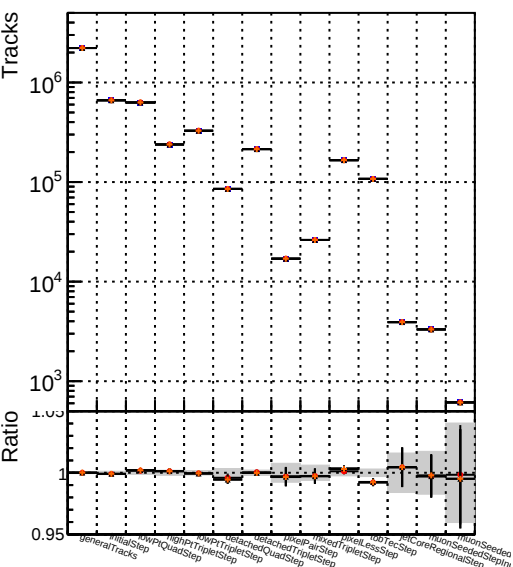
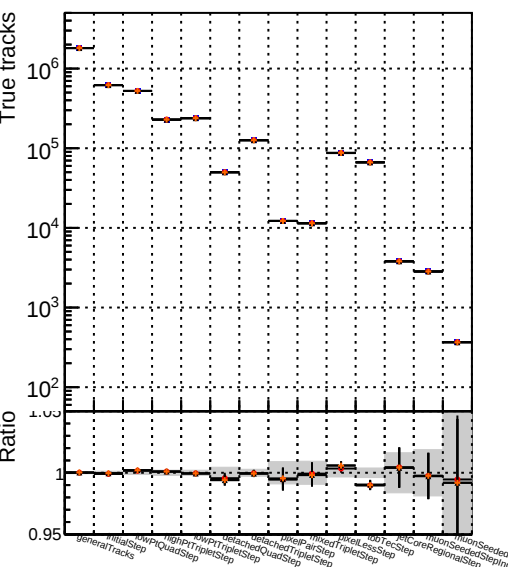


Number of tracks vs collection



Number of true tracks vs collection



Number DQM_mkFit_TTNEW
 DQM_mkFit_TTNEW50
 DQM_mkFit_TTNEW100

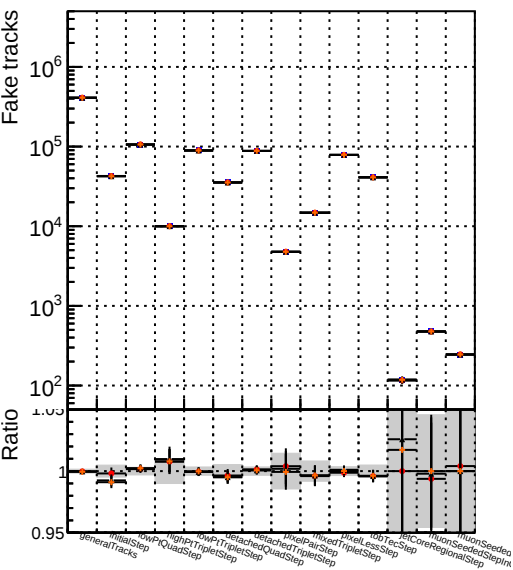


Figure 1 is a log-log plot showing the number of duplicate tracks (Y-axis, ranging from 10⁰ to 10⁵) versus the ratio of duplicate tracks to total tracks (X-axis, ranging from 0.95 to 10). The plot displays data points with error bars for various genomic features, categorized into two groups: 'general tracks' (left) and 'tracks with specific annotations' (right). The 'general tracks' group shows a high number of duplicate tracks (around 10⁴ to 10⁵) and a ratio of duplicate tracks to total tracks around 1. The 'tracks with specific annotations' group shows a lower number of duplicate tracks (around 10² to 10³) and a ratio of duplicate tracks to total tracks around 1. The plot indicates that the number of duplicate tracks is generally high, and the ratio of duplicate tracks to total tracks is generally high, suggesting a high degree of duplication.

Number of pileup tracks vs collection

