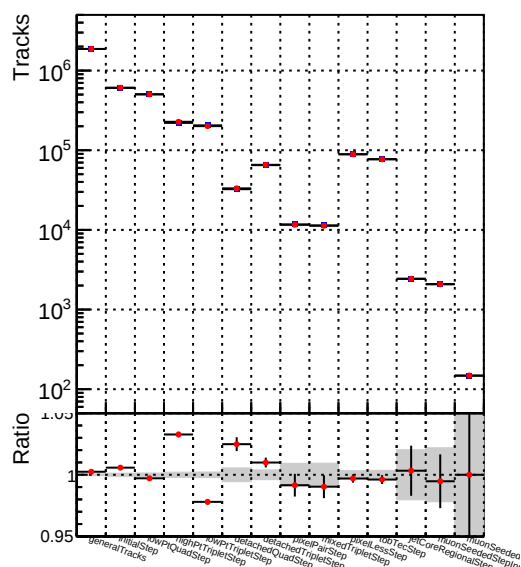
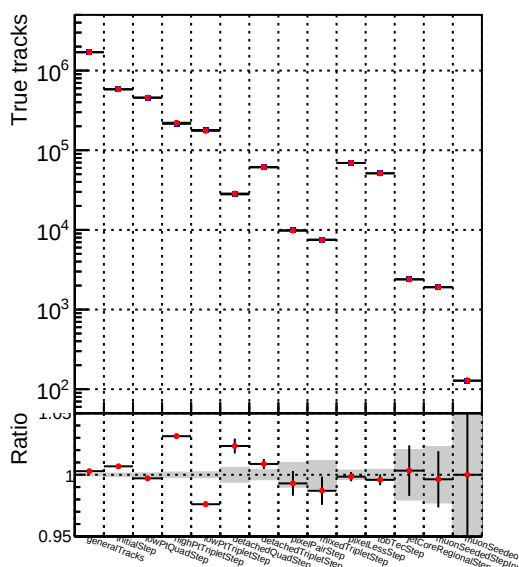


Number of tracks vs collection



Number of true tracks vs collection



Number	Label
1	DQM_TT_PR43146_swap

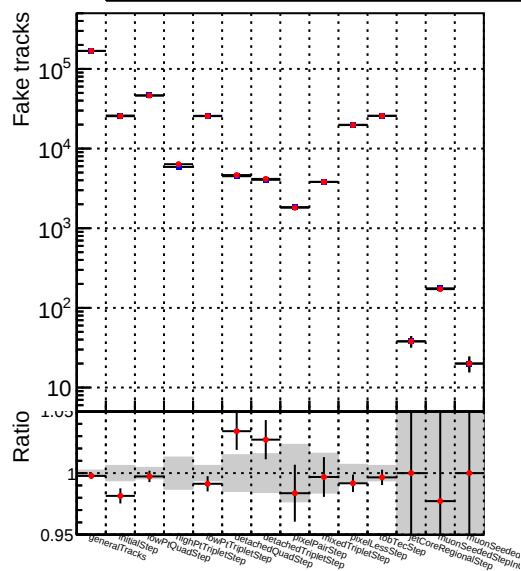


Figure 1 is a log-linear plot showing the ratio of duplicate tracks for various genomic features. The y-axis is labeled 'Ratio' and ranges from 0.95 to 10^5 on a logarithmic scale. The x-axis lists genomic features: generalTracks, initialTracks, lowPr, highPr, QuadStep, lowPrTripletStep, detachedTripletStep, detachedQuadStep, lowPrPairStep, pairedTripletStep, TripletLessStep, lowPrTriStep, and lowPrRegionStep. The plot shows data points with error bars and shaded regions representing different genomic features.

Number of pileup tracks vs collection

