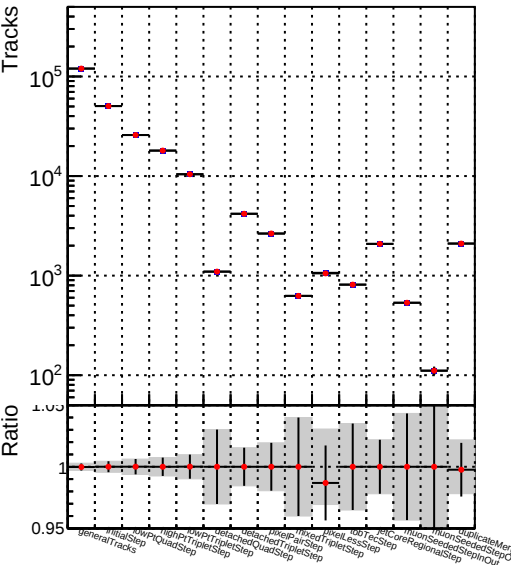
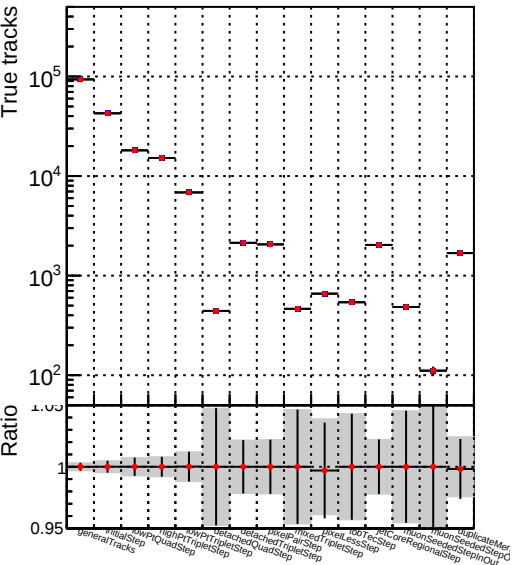


Number of tracks vs collection



Number of true tracks vs collection



 DQM_V0001_R0000000001_Global_mkFit1000o_RECO

Number —●— DQM_V0001_R000000001_Global_mkFit1000_RECO

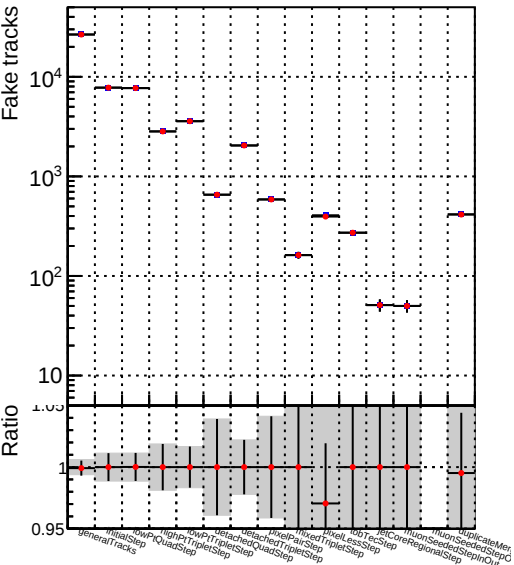


Figure 1: A log-linear plot showing the ratio of duplicate tracks to total tracks for various genomic features. The y-axis is 'Ratio' on a log scale from 0.95 to 100. The x-axis lists genomic features. Most features have a ratio of 1.0, indicated by a red dot on a horizontal line. 'Duplicate tracks' has a ratio of approximately 150, indicated by a red dot above a horizontal line. 'WardTrio' has a ratio of approximately 8, indicated by a red dot above a horizontal line. 'WardTrio' also has a vertical error bar extending from approximately 4 to 15. 'WardTrio' is shaded gray. 'WardTrio' is the only feature with a ratio significantly above 1.0.

Number of pileup tracks vs collection

