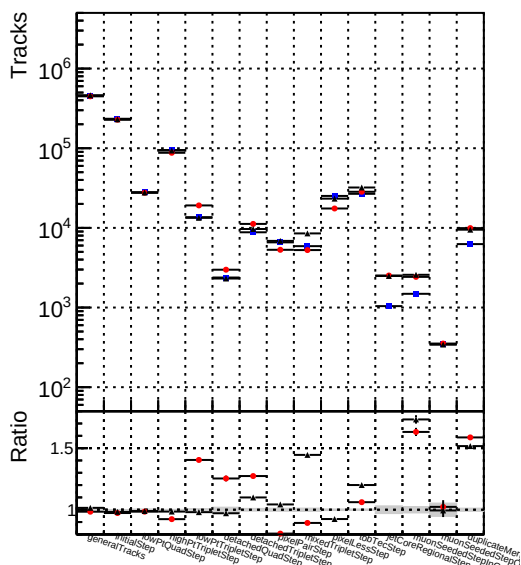
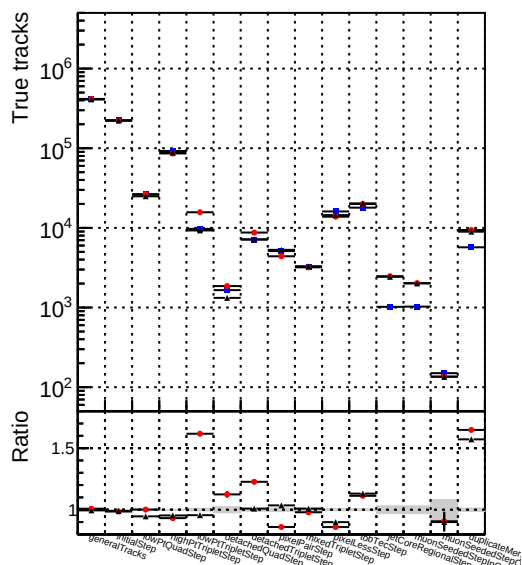


Number of tracks vs collection



Number of true tracks vs collection



Number		DQM_V0001_R0000000001_Global_mkFit1_RECO
		DQM_V0001_R0000000001_Global_mkFit2_RECO

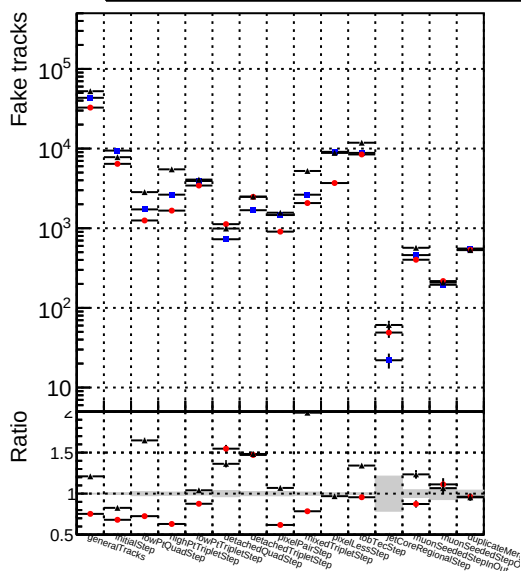


Figure 1: A log-linear plot showing the ratio of duplicate tracks to total tracks for various genomic features. The y-axis is 'Ratio' on a log scale from 0 to 10⁴. The x-axis lists genomic features. A horizontal line at Ratio = 1 indicates the expected ratio for random distribution. Most features have ratios significantly above 1, indicating enrichment. 'Duplicate tracks' and 'general tracks' are the most enriched, with ratios near 10⁴. 'Repeat tracks' and 'Transcript tracks' are also enriched, with ratios around 10. 'Gene tracks' and 'Protein tracks' are near 1. 'Chromosome tracks' and 'Chromatid tracks' are below 1, with ratios around 0.1.

Number of pileup tracks vs collection

