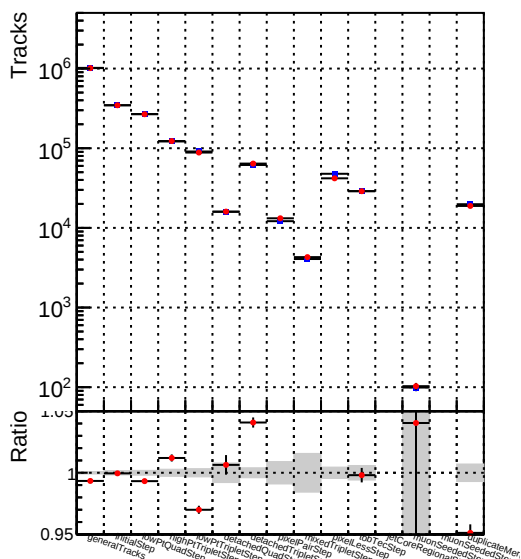
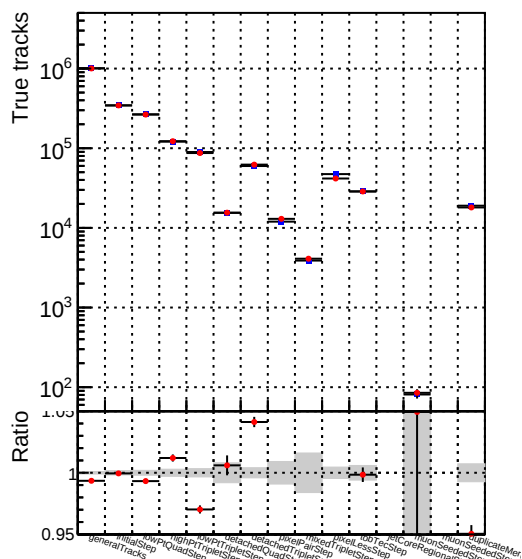


Number of tracks vs collection



Number of true tracks vs collection



Number DOM_mkFit_XiminiusNORPU_OLDF6iters

Number	Series
1	DQM_mkFit_XiminusNOPU_OLD6iters

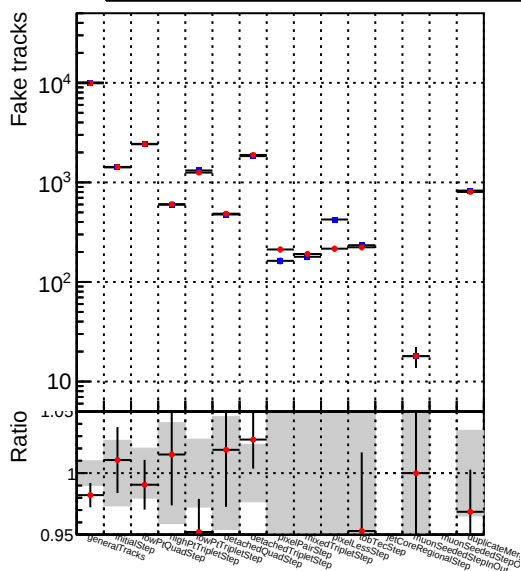


Figure 1 is a log-log plot showing the ratio of duplicate tracks to total tracks for various genomic features. The y-axis is labeled 'Duplicate tracks' and ranges from 10⁰ to 10⁴. The x-axis is labeled 'Ratio' and ranges from 10⁻² to 10⁰. The plot shows that duplicate tracks are most prevalent in 'general tracks' and 'repeats', with ratios around 10⁴ and 10³ respectively. Other features like 'transcripts' and 'genes' have ratios around 10². The 'ratio' of duplicate tracks to total tracks is generally low, around 10⁻¹ to 10⁰.

Number of pileup tracks vs collection

