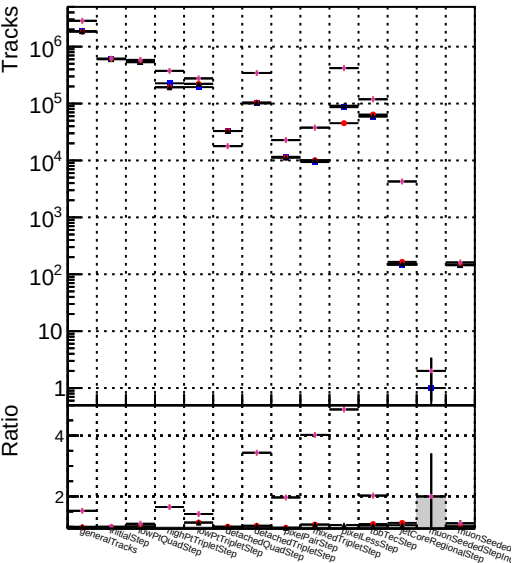
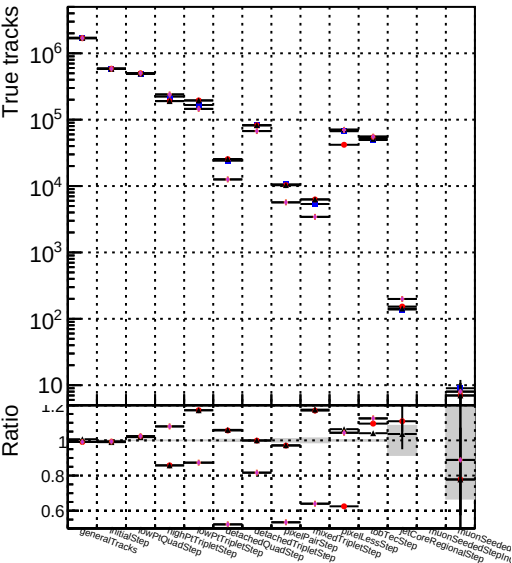


Number of tracks vs collection



Number of true tracks vs collection



Number	Symbol	DOMstep3	TT	chrPixelLess
	—▲—	DOMstep3	TT	chrPixelLess
	—+—	DOMstep3	TT	default-relf4
	—+—	DOMstep3	TT	default-relf5

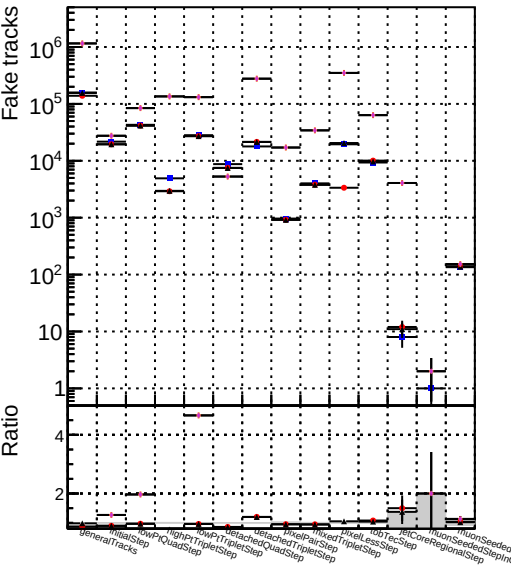


Figure 1 is a log-log plot showing the ratio of duplicate tracks for various genomic features. The y-axis is labeled 'Ratio' and ranges from 0.5 to 10⁵. The x-axis lists the following features: GeneralTracks, InitialStep, WDRStep, RQuasiStep, HighPITripleStep, LowPITripleStep, DetachedQuasiStep, DetachedTripleStep, HighPairStep, MidPairStep, PilelessStep, WDRStep, WDRCoreStep, WDRRegionalStep, WDRSeedsStep, and WDRSeedsStep. The plot shows that the ratio of duplicate tracks is generally high for most features, with a significant drop for WDRSeedsStep. A horizontal line at Ratio = 1.0 is shown for reference.

Number of pileup tracks vs collection

