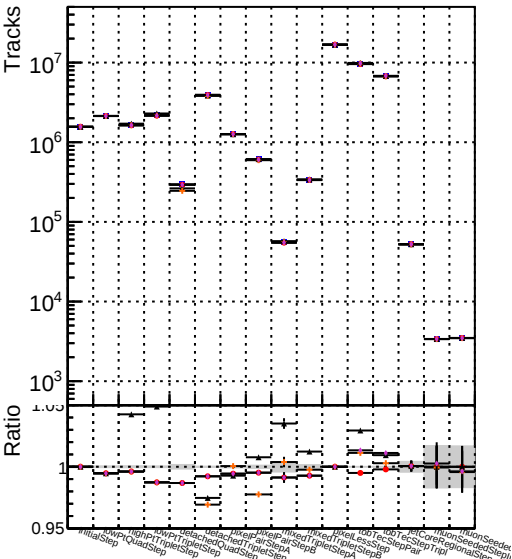
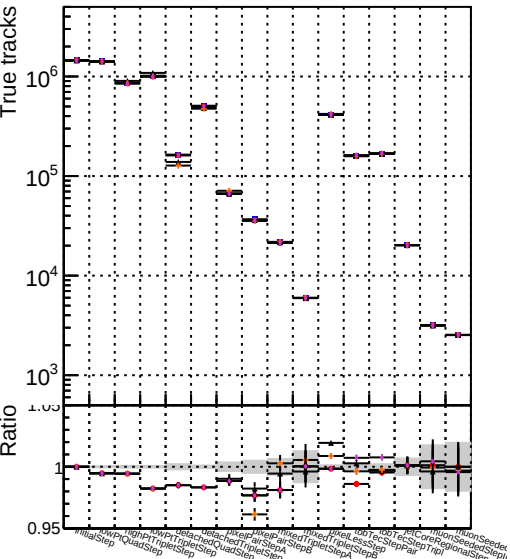


Number of tracks vs collection



Number of true tracks vs collection



Number	Symbol	DOM	TT	MKFITLowPto	MODIF
	▲	DOM	TT	MKFITLowPto	MODIF
	●	DOM	TT	MKFITLowPtt	MODIF
	●	DOM	TT	MKFITandPless	MODIF

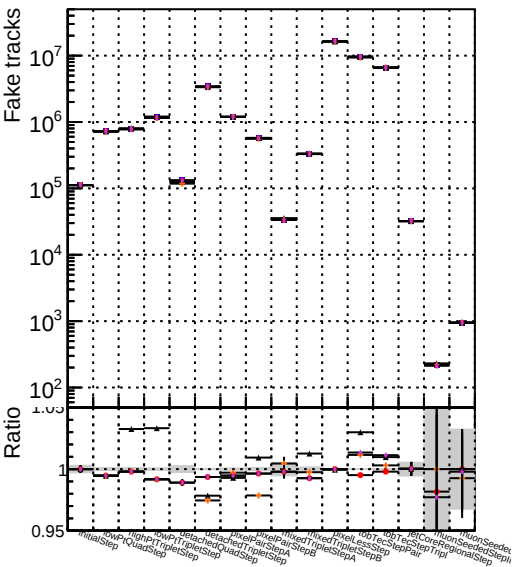


Figure 1 consists of two vertically stacked panels sharing a common x-axis with 20 genomic features. The top panel, titled 'Duplicate tracks', is a log-scale plot with y-axis values from 10^0 to 10^6 . It shows data points with error bars for each feature. The bottom panel, titled 'Ratio', is a log-scale plot with y-axis values from 0.95 to 10. It shows the ratio of duplicate tracks for each feature, with a horizontal line at 1.00. Shaded grey regions in the bottom panel indicate confidence intervals. The features on the x-axis are: InitialStep, HighStep, LowStep, RecStep, RegionStep, InitialStep, HighStep, LowStep, RecStep, RegionStep, InitialStep, HighStep, LowStep, RecStep, RegionStep, InitialStep, HighStep, LowStep, RecStep, RegionStep, InitialStep, HighStep, LowStep, RecStep, RegionStep.

Number of pileup tracks vs collection

