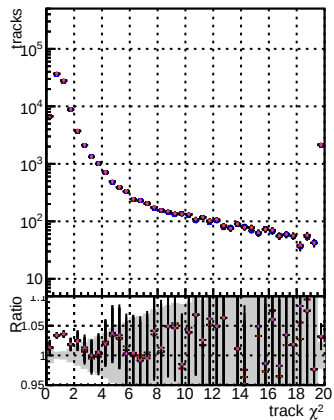
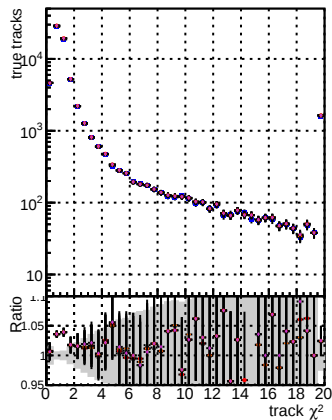


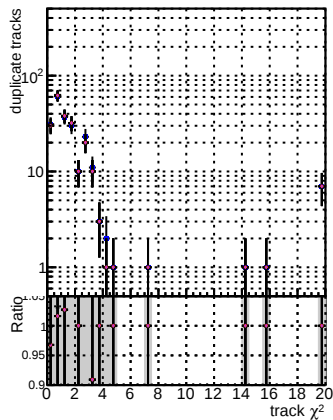
N of reco track vs normalized χ^2



N of associated (recoToSim) tracks vs normalized χ^2



N of associated (recoToSim) looper tracks vs normalized χ^2



N of reco track vs. s

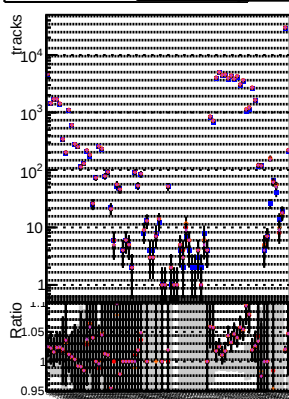


Figure 1 is a scatter plot showing the ratio of duplicate tracks to total tracks for various genomic features. The y-axis is labeled 'Ratio' and ranges from 0.9 to 1.0. The x-axis is labeled 'duplicate tracks' and ranges from 0 to 10^2. The plot shows data points for different genomic features, with error bars indicating variability. The ratio is generally close to 1.0, except for a few outliers at higher duplicate track counts.