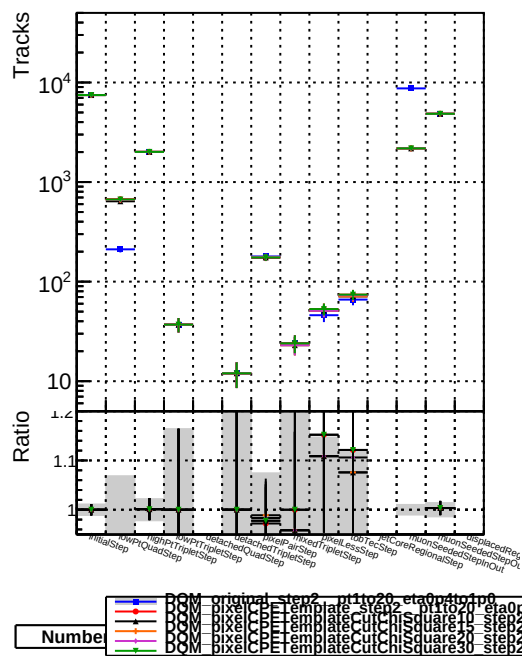
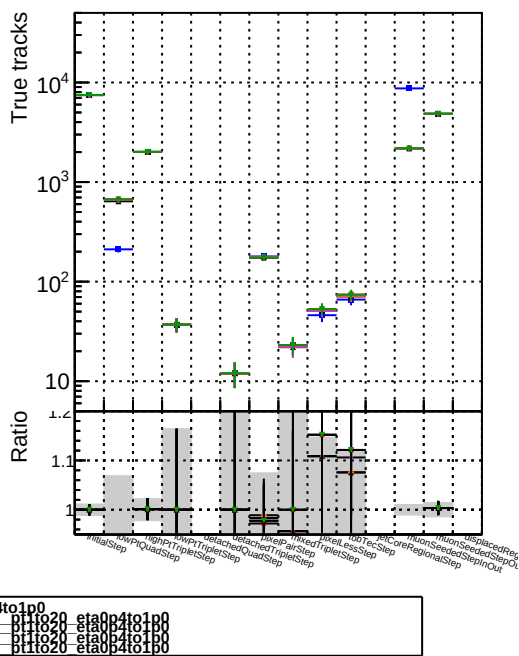


Number of tracks vs collection



Number of true tracks vs collection



Number

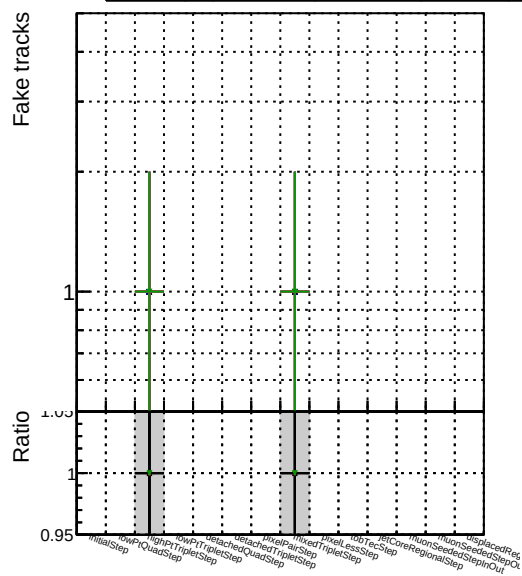


Figure 1 is a log-linear plot showing the ratio of duplicate tracks for various genomic features. The y-axis is labeled 'Ratio' and ranges from 0 to 10^{-1} on a logarithmic scale. The x-axis lists genomic features. A horizontal line is drawn at Ratio = 1. Most features have ratios near 1, with some outliers like 'Triplets' and 'TripletsOut' showing higher ratios.

Genomic Feature	Ratio (approx.)
MissStep	1.0
LowPrTripletStep	1.0
HighPrTripletStep	1.0
LowPrQuadStep	1.0
HighPrQuadStep	1.0
DetachedTripletStep	1.0
DetachedQuadStep	1.0
PooledPairStep	1.0
MixedTripletStep	1.0
FixedTripletStep	1.0
FixedQuadStep	1.0
CoreRegionalStep	1.0
Non-SeededStepIn	1.0
Non-SeededStepOut	1.0
Triplets	~0.15
TripletsOut	~0.12

Number of pileup tracks vs collection

