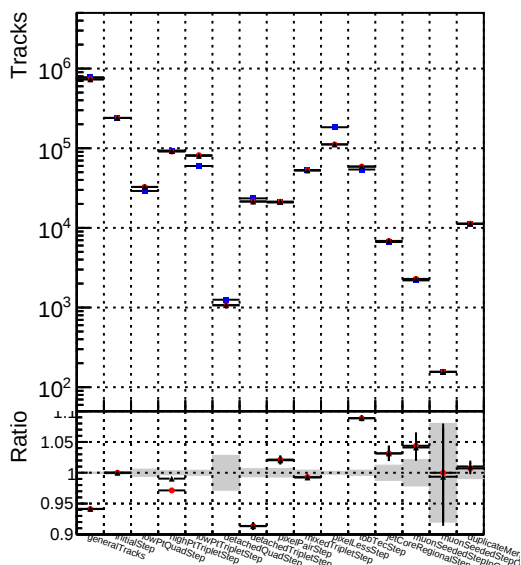
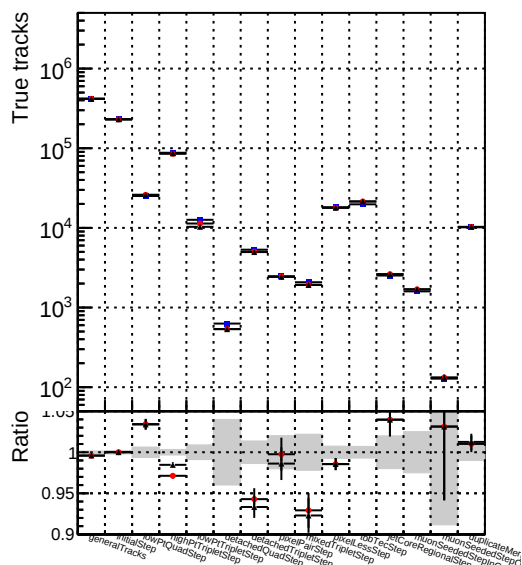


Number of tracks vs collection



Number of true tracks vs collection



Number	Model
1	DQM_mkFit_TT_base_8iter_noSel
2	DQM_mkFit_TT_retrainOldFiles_v2_8iter2_noSel

Number	Model
1	DQM_mkFit_TT_base_8iter_noSel
2	DQM_mkFit_TT_retrainOldFiles_v2_8iter2_noSel

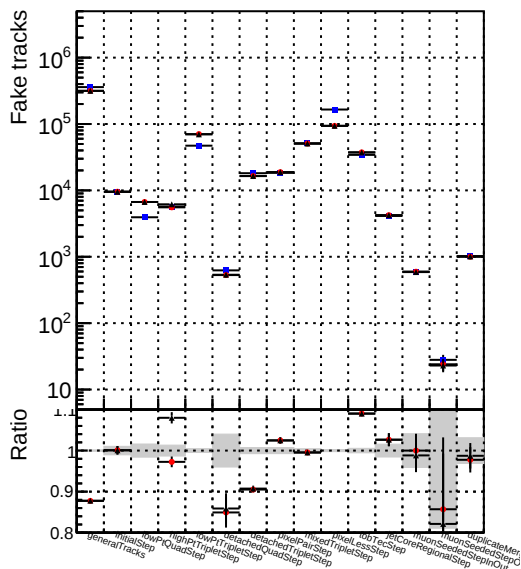


Figure 1 consists of two panels. The top panel is a log-scale scatter plot showing the number of duplicate tracks for 18 genomic features. The y-axis is labeled 'Duplicate tracks' and ranges from 10^0 to 10^4 . The bottom panel is a linear-scale bar chart showing the ratio of duplicate tracks to total tracks for the same features. The y-axis is labeled 'Ratio' and ranges from 1.0 to 1.5. Red dots and bars represent the 'core' set, while blue dots and bars represent the 'non-core' set. Error bars are shown for all data points.

Genomic Feature	Core Ratio (approx.)	Non-Core Ratio (approx.)	Core Duplicate Tracks (approx.)	Non-Core Duplicate Tracks (approx.)
generalTracks	1.0	1.0	10000	10000
duplStep	1.0	1.0	2.5	4.5
coreTripletStep	1.0	1.0	15	12
nonCoreTripletStep	1.0	1.0	8	12
coreQuadrupletStep	1.0	1.0	7	12
nonCoreQuadrupletStep	1.0	1.0	6	12
corePentupletStep	1.0	1.0	2.5	2.5
nonCorePentupletStep	1.0	1.0	2.5	2.5
coreHexupletStep	1.0	1.0	2.5	2.5
nonCoreHexupletStep	1.0	1.0	2.5	2.5
coreHeptupletStep	1.0	1.0	2.5	2.5
nonCoreHeptupletStep	1.0	1.0	2.5	2.5
coreOctupletStep	1.0	1.0	2.5	2.5
nonCoreOctupletStep	1.0	1.0	2.5	2.5
coreNonSelfOverlap	1.0	1.0	2.5	2.5
nonCoreNonSelfOverlap	1.0	1.0	2.5	2.5
coreSelfOverlap	1.0	1.0	2.5	2.5
nonCoreSelfOverlap	1.0	1.0	2.5	2.5
coreRepeatStep	1.0	1.0	2.5	2.5
nonCoreRepeatStep	1.0	1.0	2.5	2.5
coreRepeatStep	1.0	1.0	2.5	2.5
nonCoreRepeatStep	1.0	1.0	2.5	2.5

Number of pileup tracks vs collection

