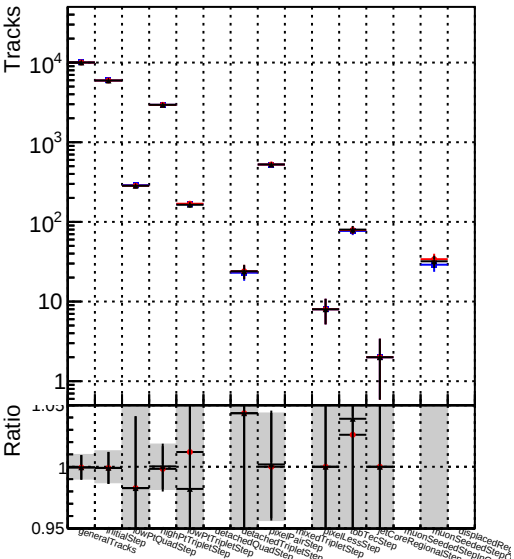
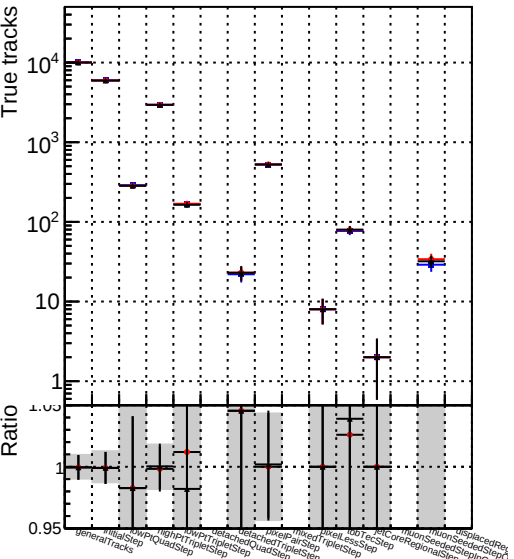


Number of tracks vs collection



Number of true tracks vs collection



Number —●— DQM_mkFit_step2_pt1to1000_eta1p4to1p6
—▲— DQM_pixelCPETemplate_step2_pt1to1000_eta1p4to1p6

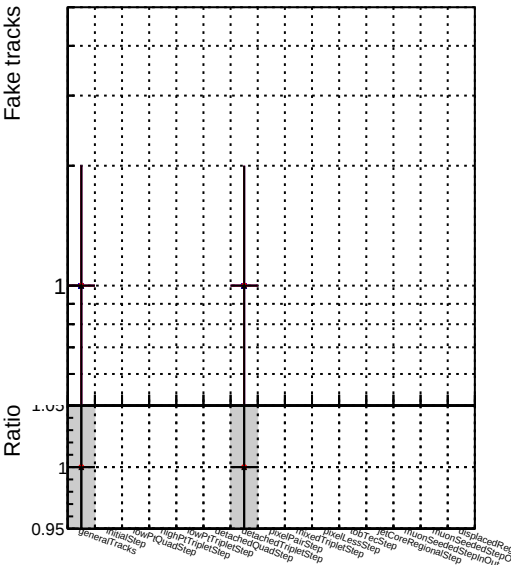


Figure 1 is a log-log plot showing the ratio of duplicate tracks to total tracks for various genomic features. The y-axis is labeled 'Ratio' and ranges from 1 to 10 on a logarithmic scale. The x-axis lists genomic features. The 'General Tracks' bar is grey and has a ratio of 1.5. Other features have ratios between 4 and 10, indicated by blue and red horizontal lines with error bars.

Genomic Feature	Ratio (approx.)
General Tracks	1.5
InitialStep	~4.5
FinalStep	~4.5
InitialQ	~4.5
FinalQ	~4.5
InitialP	~4.5
FinalP	~4.5
InitialT	~4.5
FinalT	~4.5
InitialC	~4.5
FinalC	~4.5
InitialG	~4.5
FinalG	~4.5
InitialA	~4.5
FinalA	~4.5
InitialU	~4.5
FinalU	~4.5
InitialN	~4.5
FinalN	~4.5
InitialS	~4.5
FinalS	~4.5
InitialM	~4.5
FinalM	~4.5
InitialY	~4.5
FinalY	~4.5
InitialK	~4.5
FinalK	~4.5
InitialJ	~4.5
FinalJ	~4.5
InitialI	~4.5
FinalI	~4.5
InitialH	~4.5
FinalH	~4.5
InitialF	~4.5
FinalF	~4.5
InitialE	~4.5
FinalE	~4.5
InitialD	~4.5
FinalD	~4.5
InitialB	~4.5
FinalB	~4.5
InitialV	~4.5
FinalV	~4.5
InitialW	~4.5
FinalW	~4.5
InitialX	~4.5
FinalX	~4.5
InitialZ	~4.5
FinalZ	~4.5
InitialQ	~4.5
FinalQ	~4.5
InitialP	~4.5
FinalP	~4.5
InitialT	~4.5
FinalT	~4.5
InitialC	~4.5
FinalC	~4.5
InitialG	~4.5
FinalG	~4.5
InitialA	~4.5
FinalA	~4.5
InitialU	~4.5
FinalU	~4.5
InitialN	~4.5
FinalN	~4.5
InitialS	~4.5
FinalS	~4.5
InitialM	~4.5
FinalM	~4.5
InitialY	~4.5
FinalY	~4.5
InitialK	~4.5
FinalK	~4.5
InitialJ	~4.5
FinalJ	~4.5
InitialI	~4.5
FinalI	~4.5
InitialH	~4.5
FinalH	~4.5
InitialF	~4.5
FinalF	~4.5
InitialE	~4.5
FinalE	~4.5
InitialD	~4.5
FinalD	~4.5
InitialB	~4.5
FinalB	~4.5
InitialV	~4.5
FinalV	~4.5
InitialW	~4.5
FinalW	~4.5
InitialX	~4.5
FinalX	~4.5
InitialZ	~4.5
FinalZ	~4.5

Number of pileup tracks vs collection

