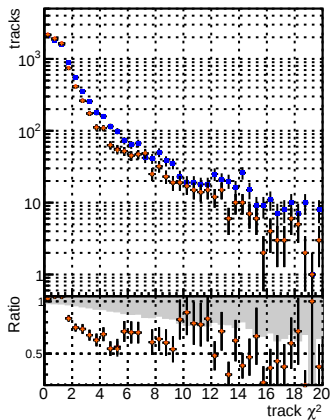
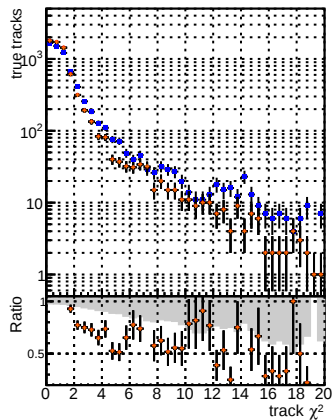


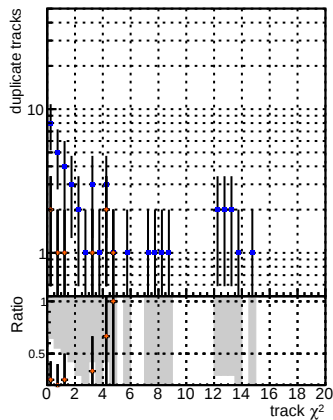
N of reco track vs normalized χ^2



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		BSM V0001	P000000000001	GLO0800	mktFitNewOriginal	RECO
		DOM V0001	P000000000001	GLO0800	mktFitNewOriginal	RECO
		DOM V0001	P000000000001	Global	mktFitNew05	RECO

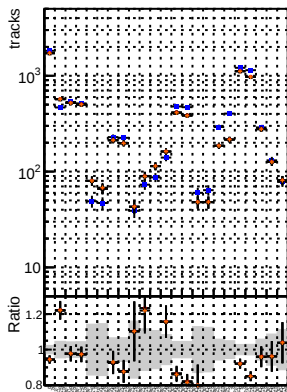


Figure 1 is a scatter plot showing the ratio of duplicate tracks to total tracks for various genomic features. The y-axis is labeled 'Ratio' and ranges from 0 to 1.5. The x-axis is labeled 'duplicate tracks' and ranges from 0 to 1.5. Data points are colored by feature type: blue for repeats, orange for other features, and black for all features. Error bars represent standard deviation. A horizontal line at Ratio = 1.0 indicates the expected ratio for random duplication.

Feature Type	Feature	Ratio (approx.)	Standard Deviation (approx.)
Repeats (Blue)	Alu	0.35	0.15
	LINE1	0.35	0.15
	LINE2	1.05	0.15
	LINE3	1.05	0.15
Other Features (Orange)	IR	0.1	0.1
	IR2	0.1	0.1
	IR3	0.1	0.1
	IR4	0.1	0.1
All Features (Black)	IR	0.1	0.1
	IR2	0.1	0.1
	IR3	0.1	0.1
	IR4	0.1	0.1