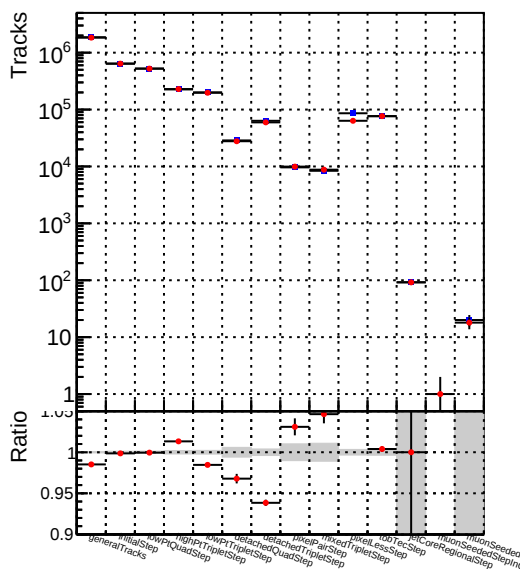
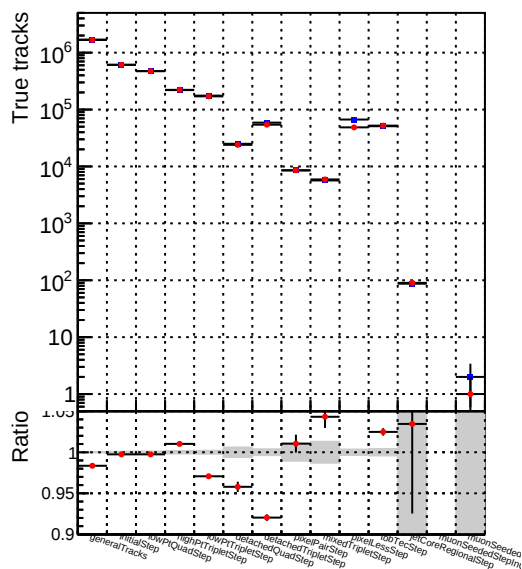


Number of tracks vs collection



Number of true tracks vs collection



Number —●— DOM mkEit TTold

Number	DOM	mkEit	TTold
1	1.00	1.00	1.00
2	1.00	1.00	1.00
3	1.00	1.00	1.00
4	1.00	1.00	1.00
5	1.00	1.00	1.00
6	1.00	1.00	1.00
7	1.00	1.00	1.00
8	1.00	1.00	1.00
9	1.00	1.00	1.00
10	1.00	1.00	1.00
11	1.00	1.00	1.00
12	1.00	1.00	1.00
13	1.00	1.00	1.00
14	1.00	1.00	1.00
15	1.00	1.00	1.00
16	1.00	1.00	1.00
17	1.00	1.00	1.00
18	1.00	1.00	1.00
19	1.00	1.00	1.00
20	1.00	1.00	1.00
21	1.00	1.00	1.00
22	1.00	1.00	1.00
23	1.00	1.00	1.00
24	1.00	1.00	1.00
25	1.00	1.00	1.00
26	1.00	1.00	1.00
27	1.00	1.00	1.00
28	1.00	1.00	1.00
29	1.00	1.00	1.00
30	1.00	1.00	1.00
31	1.00	1.00	1.00
32	1.00	1.00	1.00
33	1.00	1.00	1.00
34	1.00	1.00	1.00
35	1.00	1.00	1.00
36	1.00	1.00	1.00
37	1.00	1.00	1.00
38	1.00	1.00	1.00
39	1.00	1.00	1.00
40	1.00	1.00	1.00
41	1.00	1.00	1.00
42	1.00	1.00	1.00
43	1.00	1.00	1.00
44	1.00	1.00	1.00
45	1.00	1.00	1.00
46	1.00	1.00	1.00
47	1.00	1.00	1.00
48	1.00	1.00	1.00
49	1.00	1.00	1.00
50	1.00	1.00	1.00
51	1.00	1.00	1.00
52	1.00	1.00	1.00
53	1.00	1.00	1.00
54	1.00	1.00	1.00
55	1.00	1.00	1.00
56	1.00	1.00	1.00
57	1.00	1.00	1.00
58	1.00	1.00	1.00
59	1.00	1.00	1.00
60	1.00	1.00	1.00
61	1.00	1.00	1.00
62	1.00	1.00	1.00
63	1.00	1.00	1.00
64	1.00	1.00	1.00
65	1.00	1.00	1.00
66	1.00	1.00	1.00
67	1.00	1.00	1.00
68	1.00	1.00	1.00
69	1.00	1.00	1.00
70	1.00	1.00	1.00
71	1.00	1.00	1.00
72	1.00	1.00	1.00
73	1.00	1.00	1.00
74	1.00	1.00	1.00
75	1.00	1.00	1.00
76	1.00	1.00	1.00
77	1.00	1.00	1.00
78	1.00	1.00	1.00
79	1.00	1.00	1.00
80	1.00	1.00	1.00
81	1.00	1.00	1.00
82	1.00	1.00	1.00
83	1.00	1.00	1.00
84	1.00	1.00	1.00
85	1.00	1.00	1.00
86	1.00	1.00	1.00
87	1.00	1.00	1.00
88	1.00	1.00	1.00
89	1.00	1.00	1.00
90	1.00	1.00	1.00

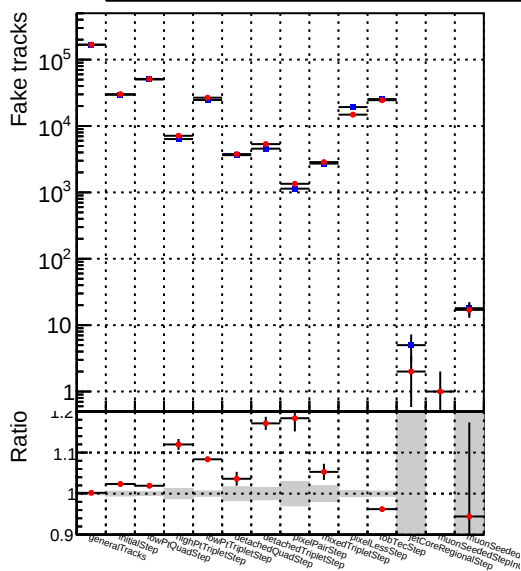


Figure 1: A log-log plot showing the ratio of duplicate tracks to total tracks for various genomic features. The y-axis is 'Duplicate tracks' on a log scale from 10^2 to 10^5 . The x-axis is 'Ratio' on a log scale from 0.8 to 1.2. The plot shows data points with error bars for various genomic features, including GeneralTracks, UniqStep, HighPTriplesStep, DetachedQuadStep, TriplesStep, PairStep, MixedStep, TriplesLessStep, PTriplesStep, and RegionSeedsStep. The data points are clustered around a ratio of 1.0, indicating that the number of duplicate tracks is approximately equal to the number of total tracks for most features.

Number of pileup tracks vs collection

