

	Report							
	22-330_filtered	22-300_filtered	22-324_filtered	22-329A_filtered	22-301_filtered	22-329B_filtered	22-299_filtered	SRR17286018_filtered
# contigs (>= 0 bp)	272	288	239	271	257	235	282	184
# contigs (>= 1000 bp)	154	140	138	139	132	140	130	120
# contigs (>= 5000 bp)	119	114	118	109	101	108	99	103
# contigs (>= 10000 bp)	100	100	101	90	92	89	80	89
# contigs (>= 25000 bp)	66	66	71	65	65	60	64	73
# contigs (>= 50000 bp)	39	40	43	40	45	39	38	42
Total length (>= 0 bp)	5247624	5253353	5368409	5251561	5249696	5246289	5253988	5225422
Total length (>= 1000 bp)	5215568	5215179	5338007	5215834	5216530	5218400	5214138	5207650
Total length (>= 5000 bp)	5128663	5154159	5283787	5148108	5144102	5146123	5134866	5162714
Total length (>= 10000 bp)	4992295	5056136	5163884	5013740	5076097	5006556	4996236	5058778
Total length (>= 25000 bp)	4396297	4488663	4654534	4593563	4654607	4479541	4703365	4776591
Total length (>= 50000 bp)	3381152	3522585	3607277	3660925	3956577	3786781	3741889	3684627
# contigs	165	155	152	152	145	154	147	129
Largest contig	160075	185361	220247	179569	159931	213966	224249	184507
Total length	5223671	5225007	5348096	5224936	5225427	5227854	5226061	5213779
Reference length	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549
GC (%)	63.78	63.78	63.63	63.78	63.78	63.78	63.78	63.77
Reference GC (%)	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78
N50	72480	69621	63287	75538	76587	76466	81953	74291
NG50	72480	69621	63287	75538	76587	76466	81953	74291
N90	18879	19030	21649	22600	24528	21031	24528	26762
NG90	18512	19030	24056	22600	24038	21031	24528	26200
auN	71978.9	77252.7	75852.4	80606.3	81765.7	86718.9	90580.0	79574.0
auNG	71884.3	77170.9	77557.0	80519.8	81685.7	86674.2	90502.3	79318.9
L50	27	26	27	24	24	22	21	24
LG50	27	26	27	24	24	22	21	24
L90	80	76	78	70	67	70	65	70
LG90	81	76	74	70	68	70	65	71
# misassemblies	6	6	23	10	9	8	4	28
# misassembled contigs	5	5	17	8	9	7	3	19
Misassembled contigs length	162792	310243	883342	248993	636397	130611	412173	1060228
# local misassemblies	1	1	2	0	1	2	0	3
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	2
# unaligned mis. contigs	0	0	2	0	0	0	1	0
# unaligned contigs	0 + 1 part	0 + 1 part	2 + 8 part	1 + 0 part	0 + 1 part	0 + 0 part	1 + 0 part	0 + 4 part
Unaligned length	828	637	205087	578	1012	0	689	60470
Genome fraction (%)	99.770	99.810	98.227	99.734	99.783	99.840	99.830	98.411
Duplication ratio	1.000	1.000	1.000	1.001	1.001	1.000	1.000	1.000
# N's per 100 kbp	4.02	5.59	5.57	4.84	4.40	4.50	6.79	15.84
# mismatches per 100 kbp	2.32	2.34	11.58	6.68	3.37	1.36	2.18	16.94
# indels per 100 kbp	0.46	0.42	1.50	0.44	0.94	0.25	0.98	2.86
Largest alignment	160075	182983	159868	179326	159931	213723	159968	184238
Total aligned length	5220789	5222932	5139645	5222408	5221625	5224243	5223290	5148154
NA50	71079	69285	60695	74332	75562	76466	76587	66091
NGA50	71079	69285	61305	74332	75562	76466	76587	66091
NA90	18512	18874	12496	21357	22988	21031	24528	22988
NGA90	18512	18874	16754	21357	22988	21031	24528	22072
auNA	71046.3	74086.8	66637.2	79766.7	76818.3	86524.6	82849.8	72257.1
auNGA	70952.9	74008.3	68134.7	79681.1	76743.1	86480.1	82778.7	72025.4
LA50	27	27	30	24	25	22	23	27
LGA50	27	27	29	24	25	22	23	27
LA90	82	78	91	72	71	70	67	78
LGA90	82	78	84	72	71	70	67	79

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

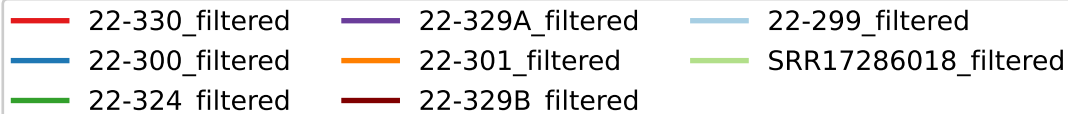
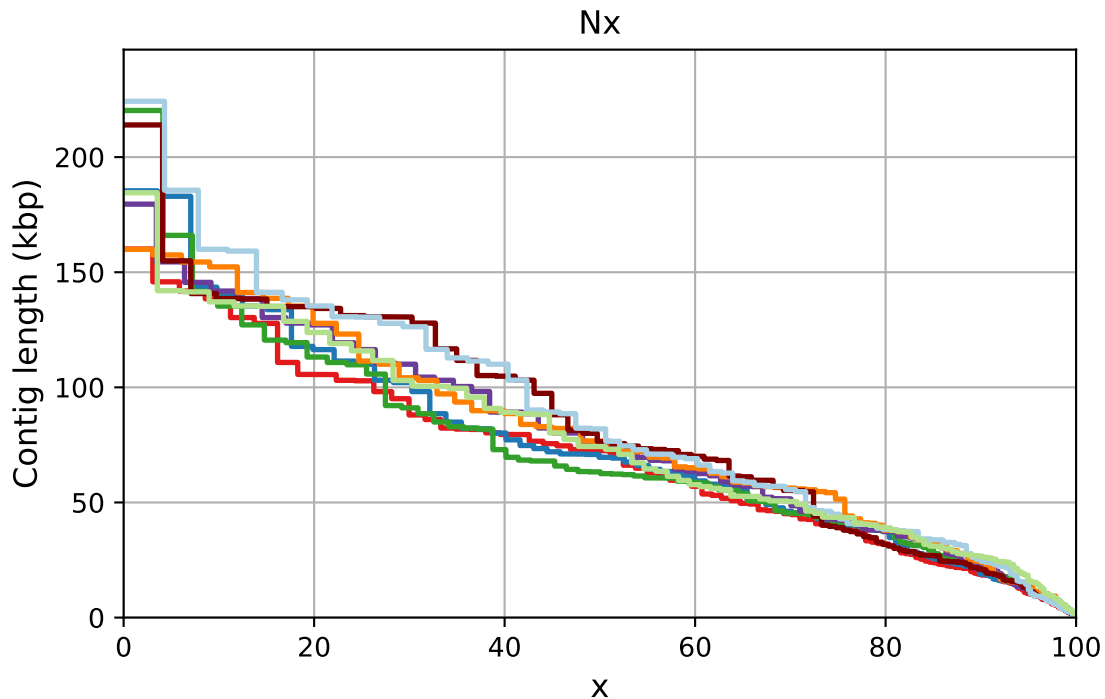
	22-330_filtered	22-300_filtered	22-324_filtered	22-329A_filtered	22-301_filtered	22-329B_filtered	22-299_filtered	SRR17286018_filtered
# misassemblies	6	6	23	10	9	8	4	28
# contig misassemblies	6	6	23	10	9	8	4	28
# c. relocations	0	0	2	0	0	0	0	2
# c. translocations	6	6	21	10	9	8	4	26
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0	0
# misassembled contigs	5	5	17	8	9	7	3	19
Misassembled contigs length	162792	310243	883342	248993	636397	130611	412173	1060228
# local misassemblies	1	1	2	0	1	2	0	3
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	2
# unaligned mis. contigs	0	0	2	0	0	0	1	0
# mismatches	121	122	595	349	176	71	114	872
# indels	24	22	77	23	49	13	51	147
# indels (<= 5 bp)	12	6	26	11	23	1	28	72
# indels (> 5 bp)	12	16	51	12	26	12	23	75
Indels length	896	1190	1586	935	1482	770	1353	2933

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

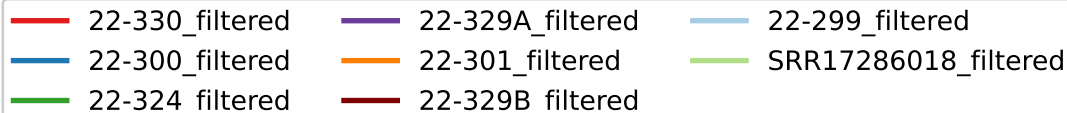
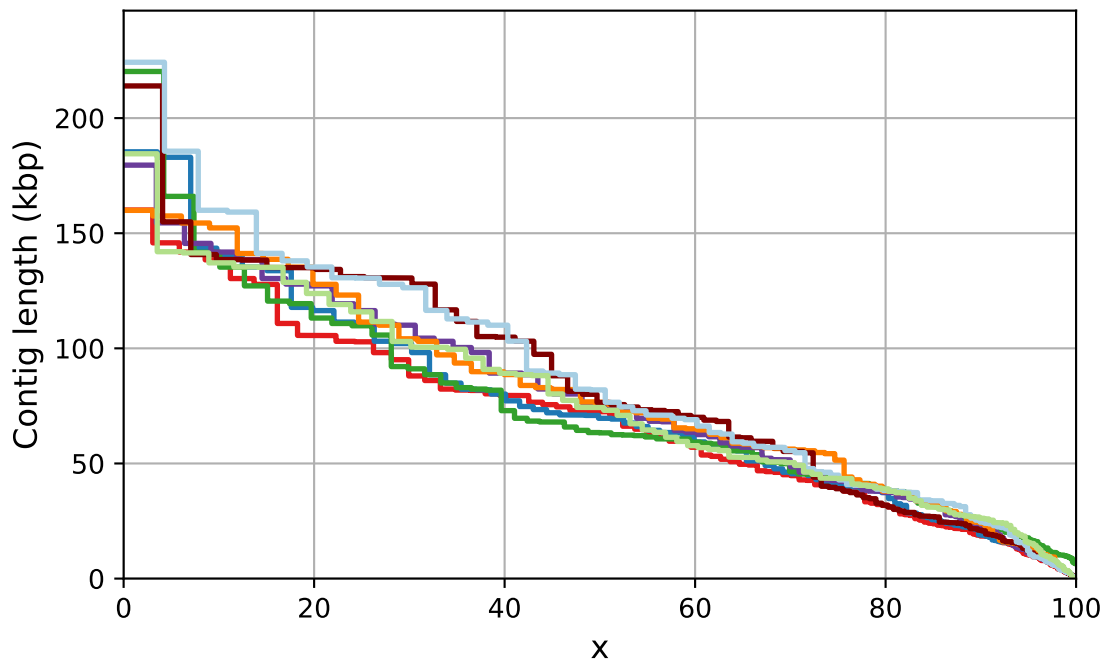
Unaligned report

	22-330_filtered	22-300_filtered	22-324_filtered	22-329A_filtered	22-301_filtered	22-329B_filtered	22-299_filtered	SRR17286018_filtered
# fully unaligned contigs	0	0	2	1	0	0	1	0
Fully unaligned length	0	0	15084	578	0	0	689	0
# partially unaligned contigs	1	1	8	0	1	0	0	4
Partially unaligned length	828	637	190003	0	1012	0	0	60470
# N's	210	292	298	253	230	235	355	826

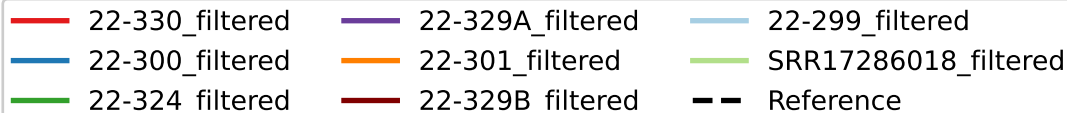
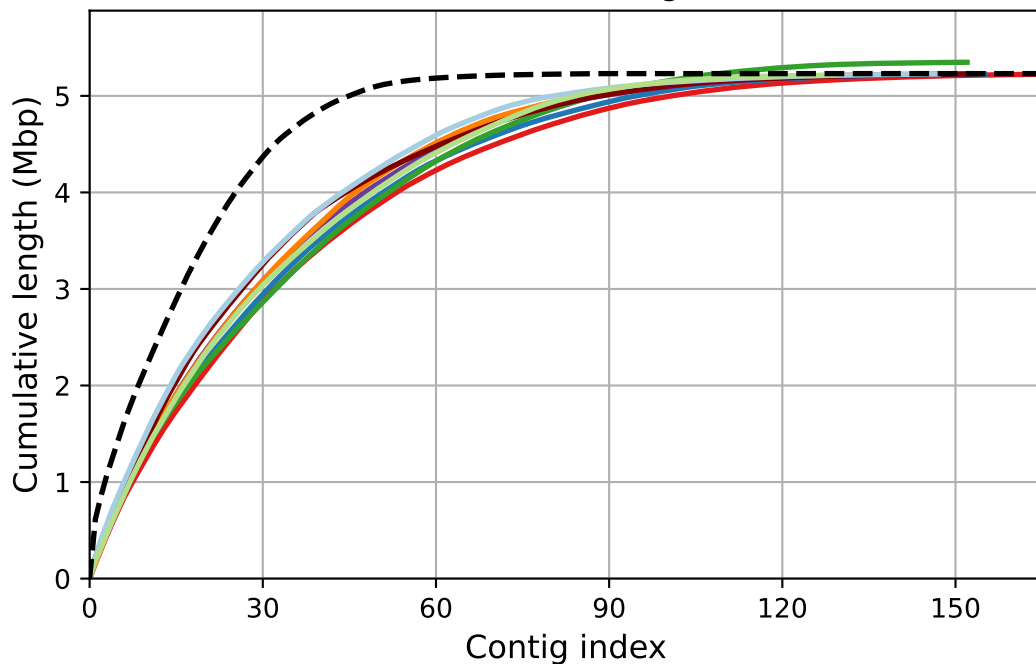
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



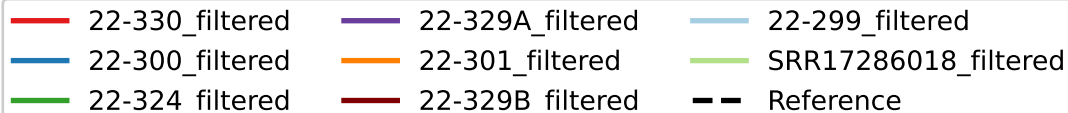
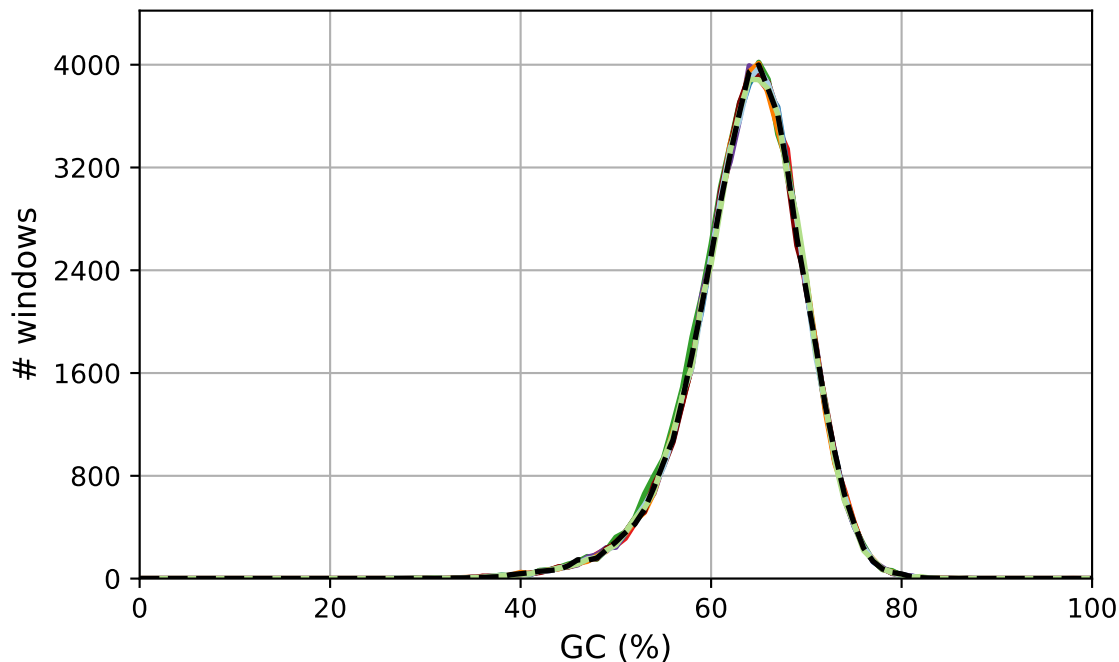
NGx



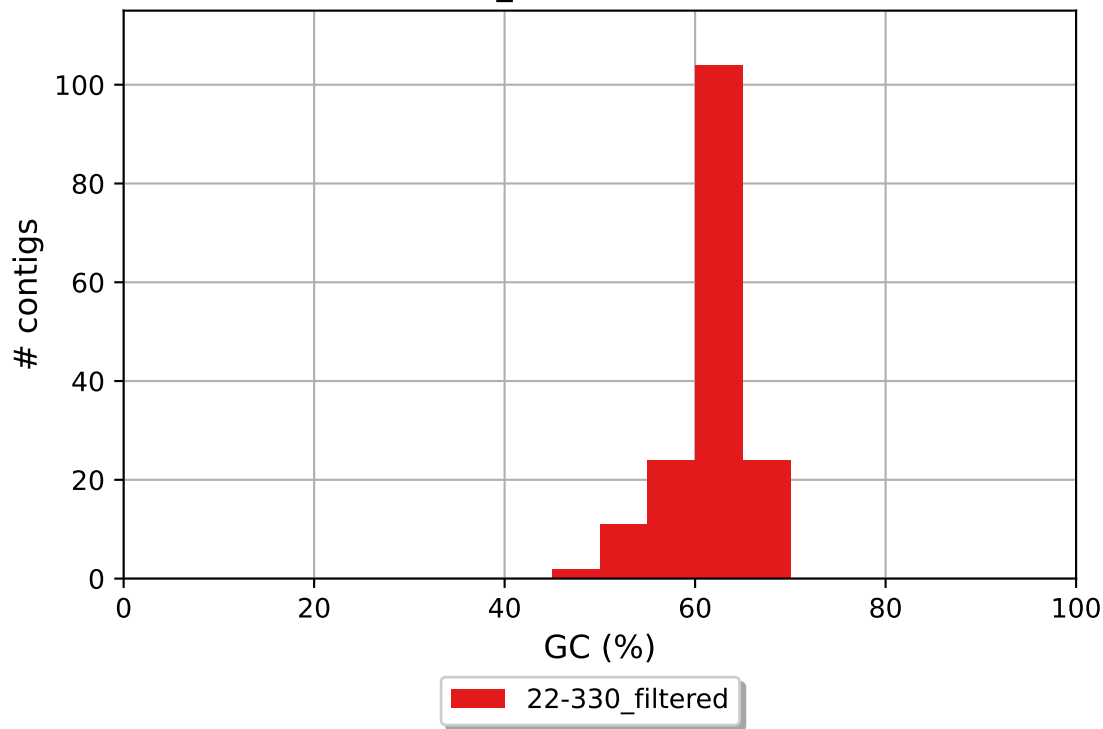
Cumulative length



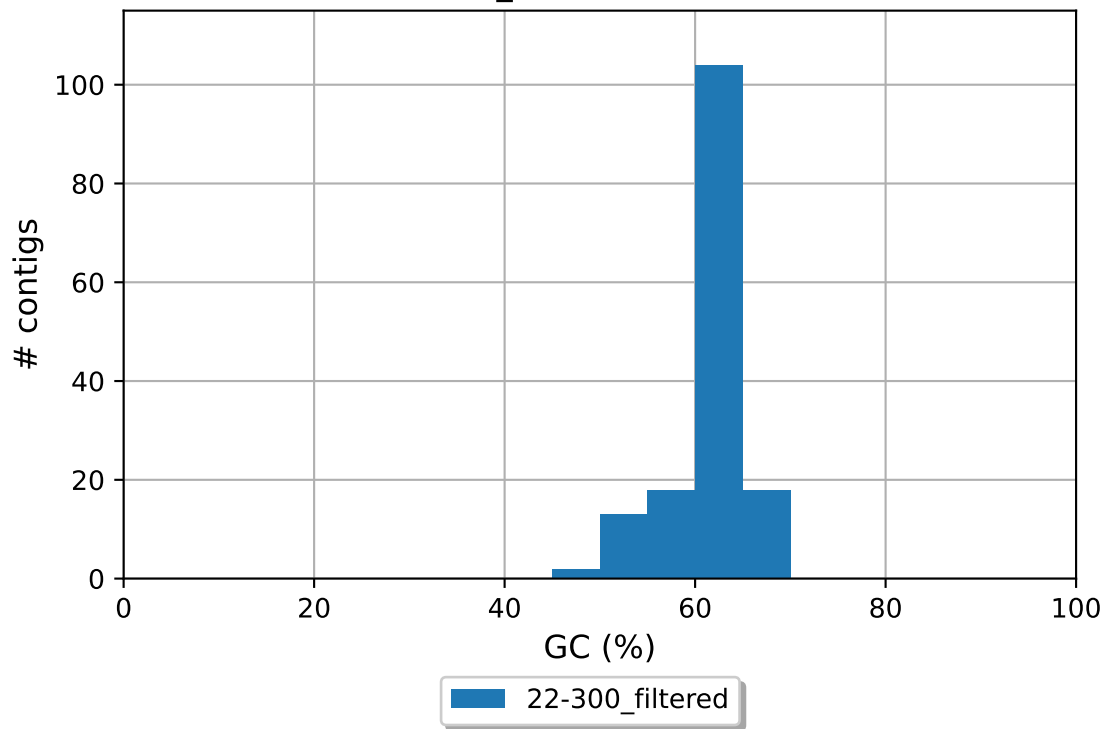
GC content



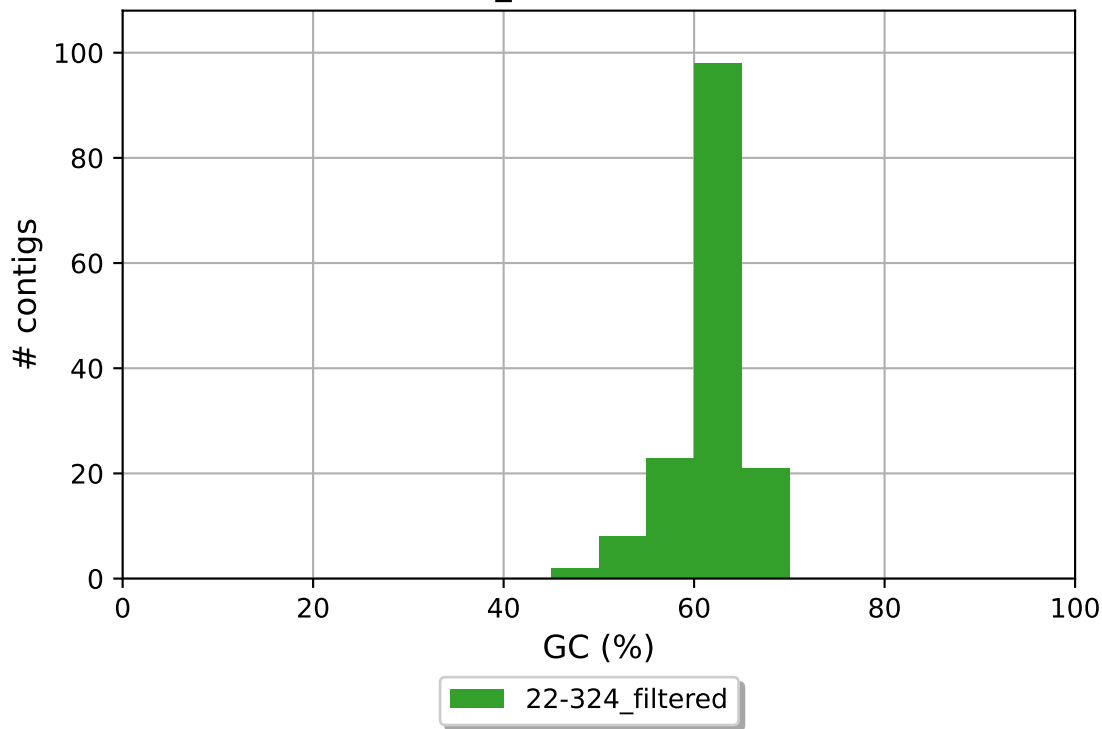
22-330_filtered GC content



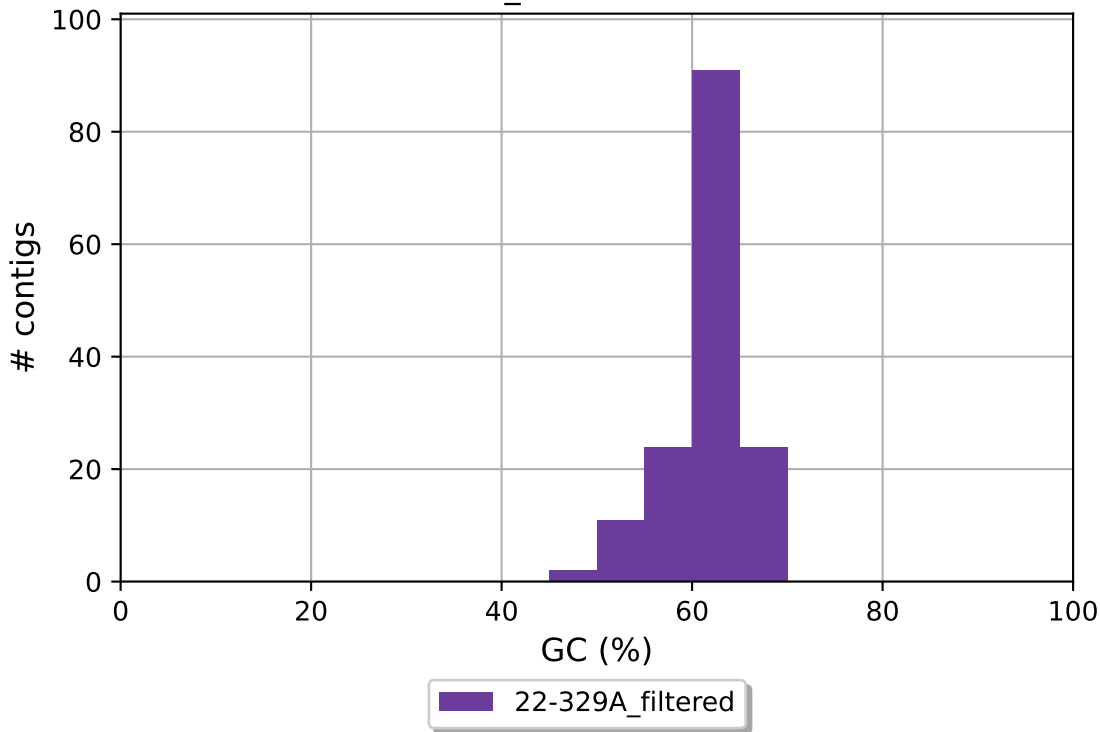
22-300_filtered GC content



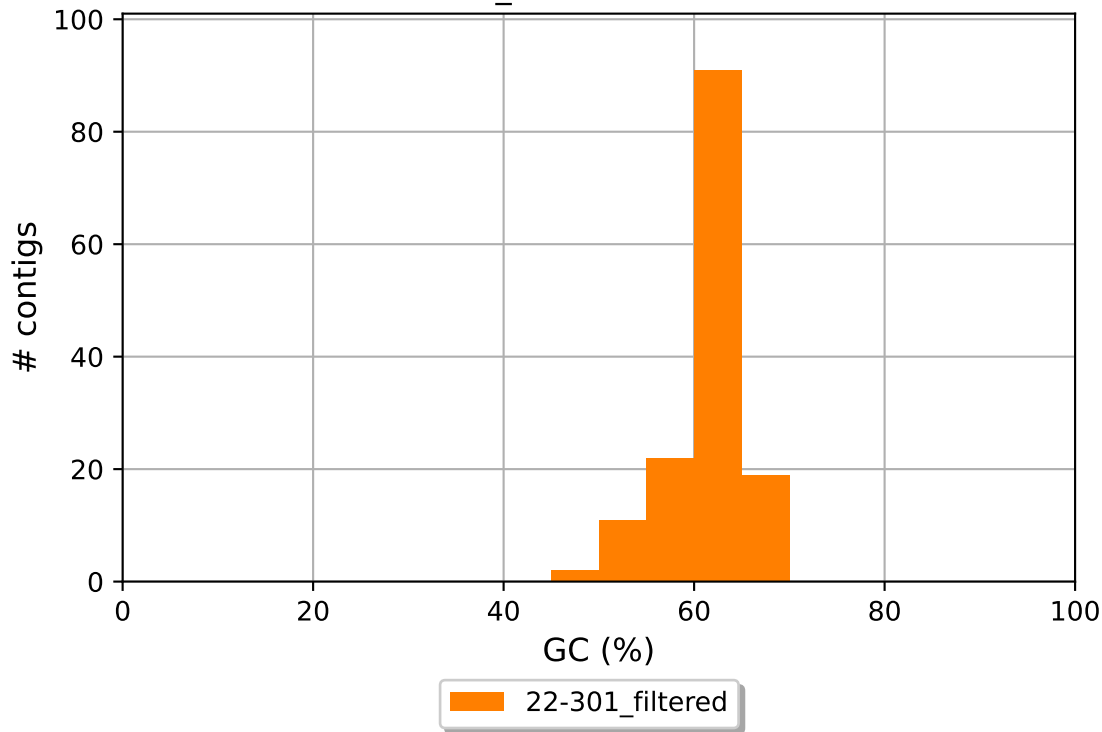
22-324_filtered GC content



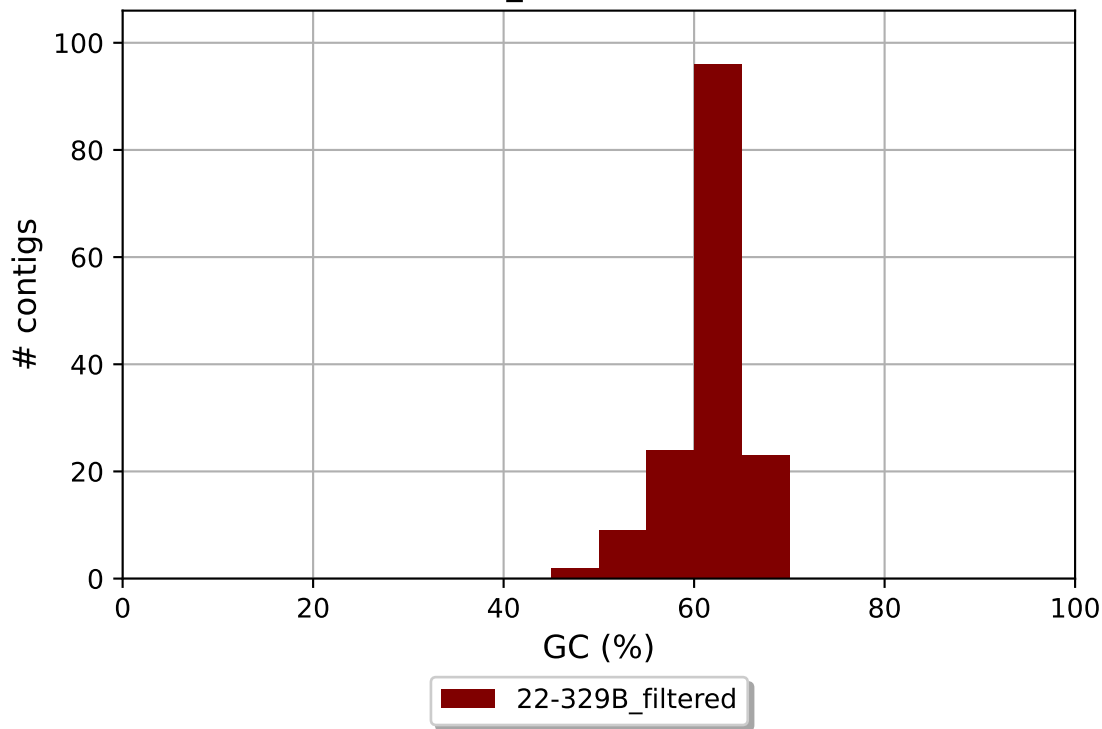
22-329A_filtered GC content



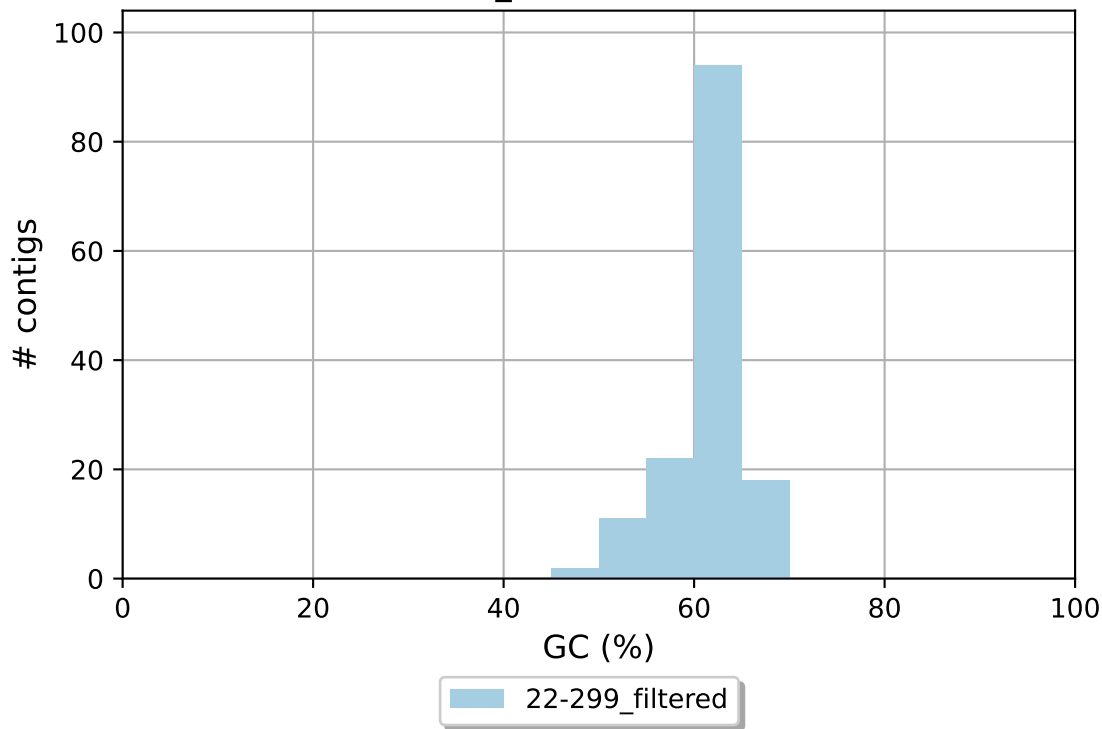
22-301_filtered GC content



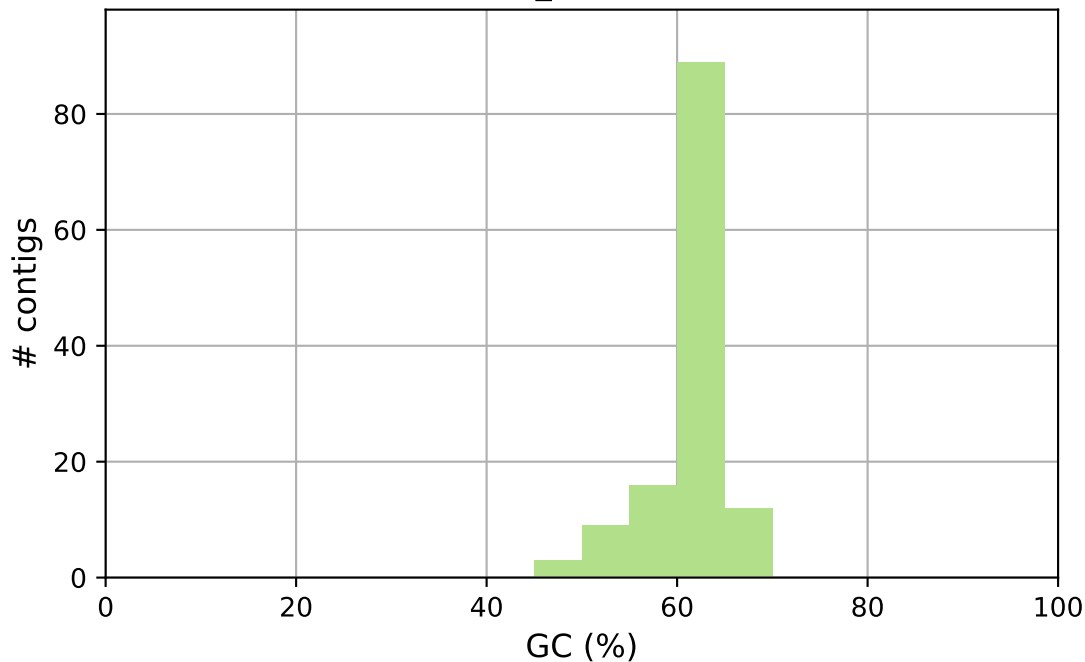
22-329B_filtered GC content



22-299_filtered GC content

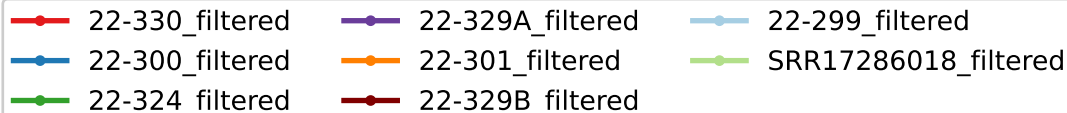
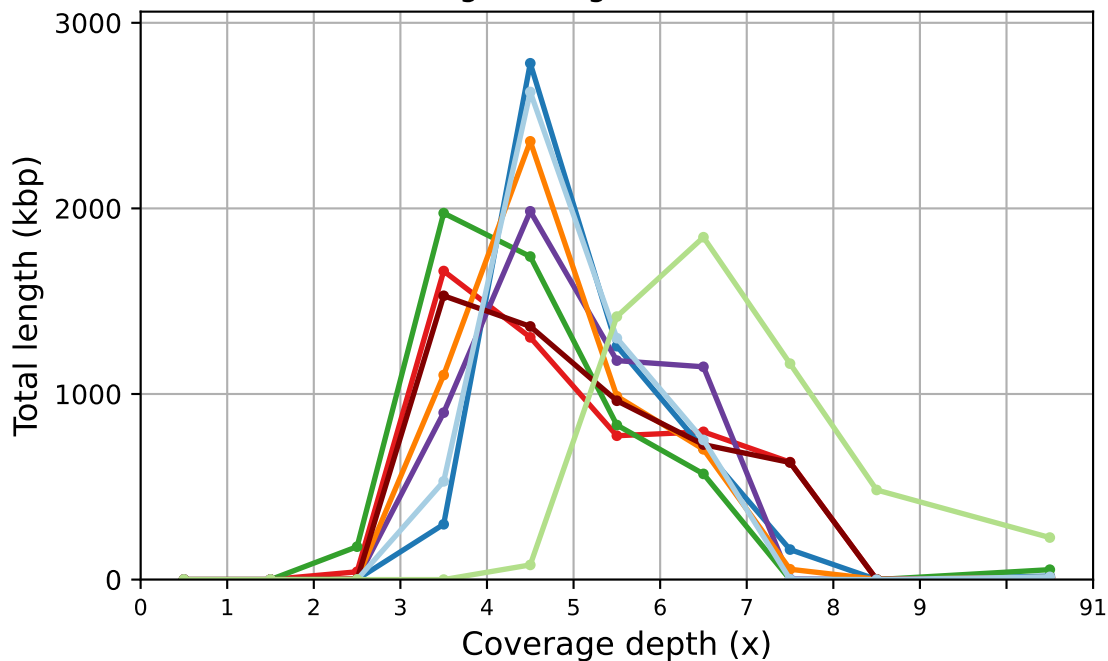


SRR17286018_filtered GC content

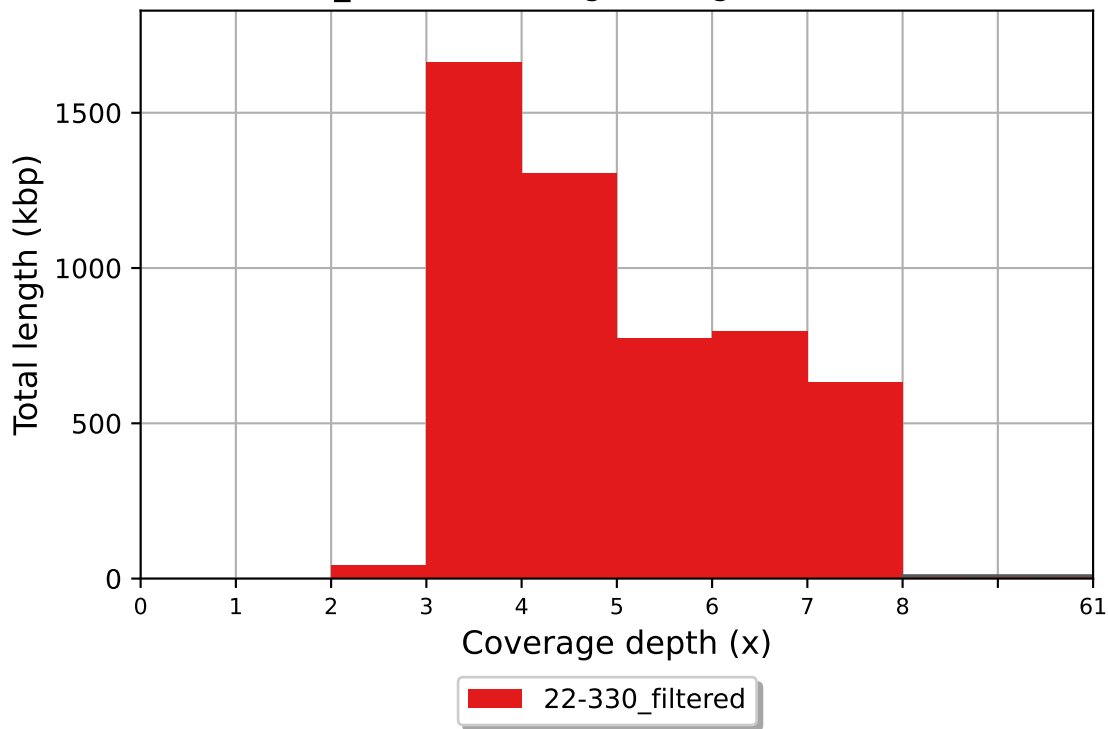


SRR17286018_filtered

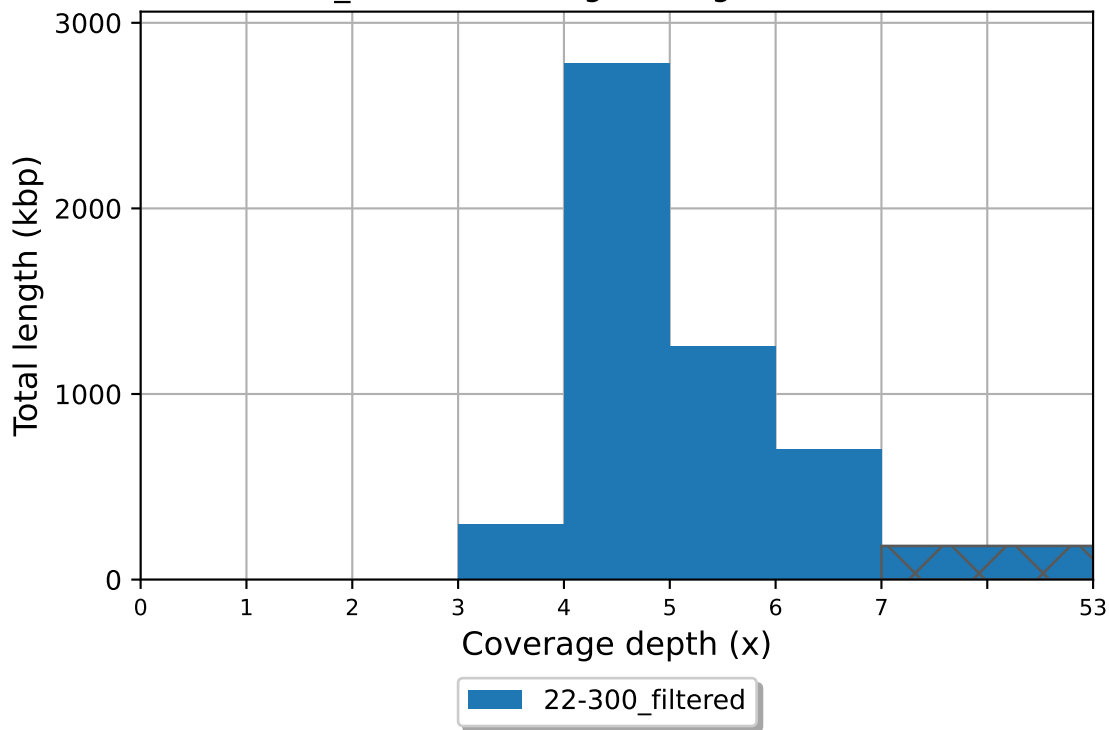
Coverage histogram (bin size: 1x)



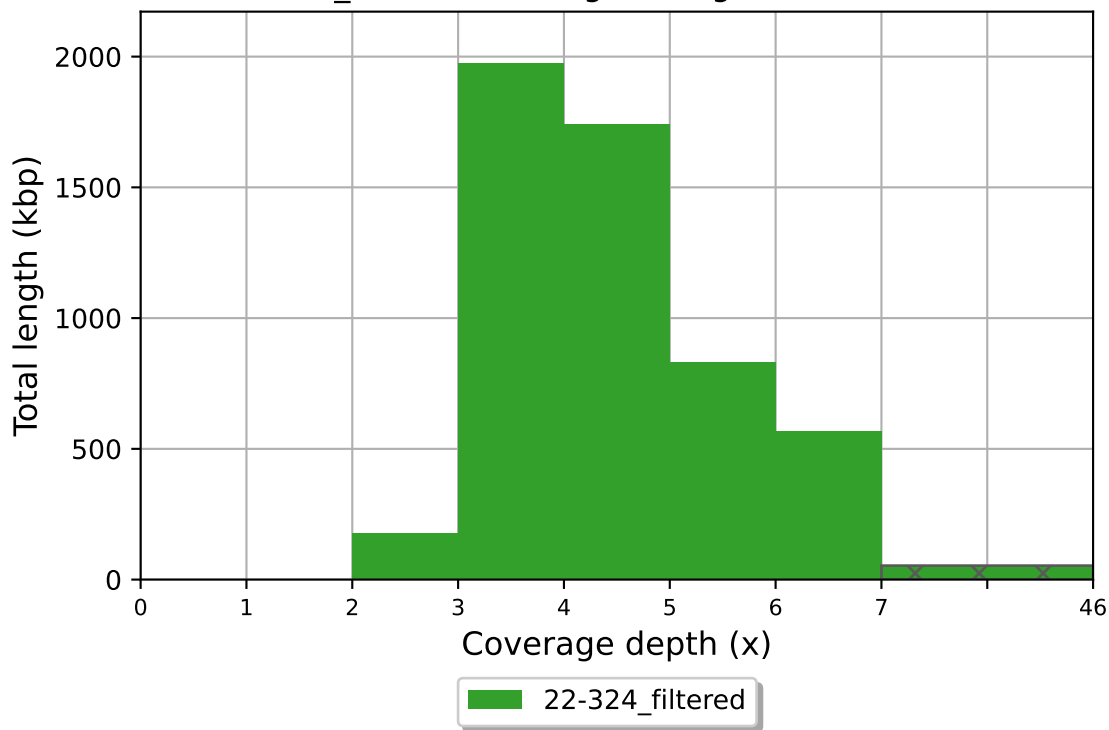
22-330_filtered coverage histogram (bin size: 1x)



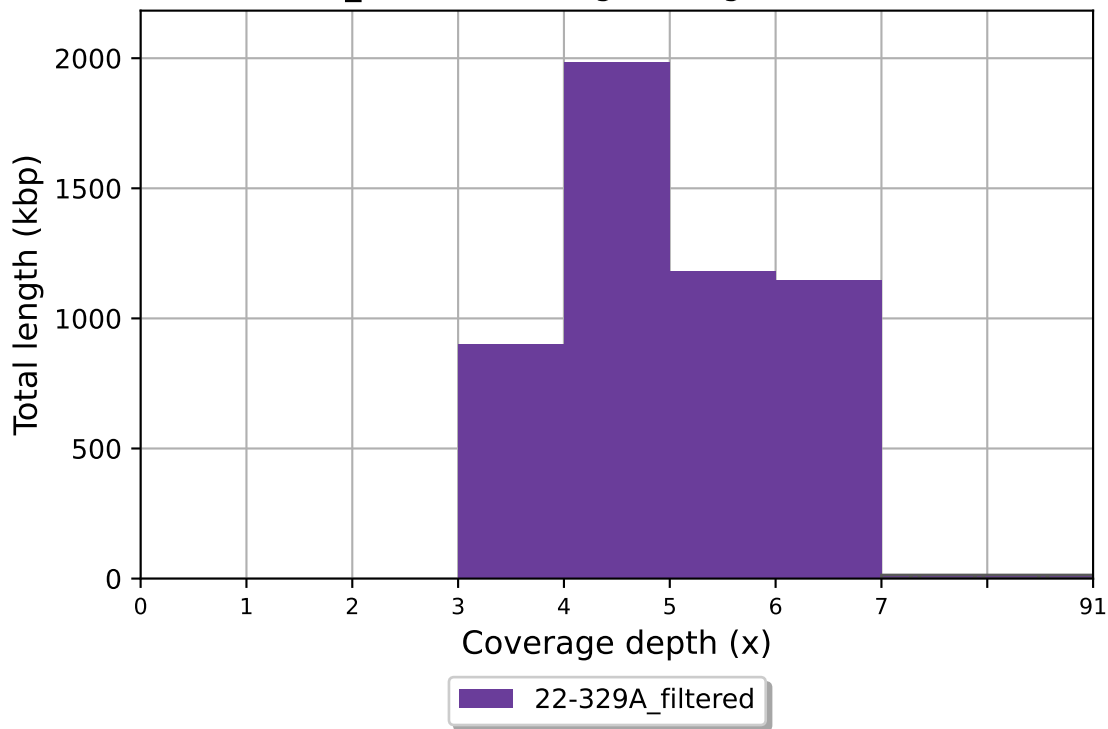
22-300_filtered coverage histogram (bin size: 1x)



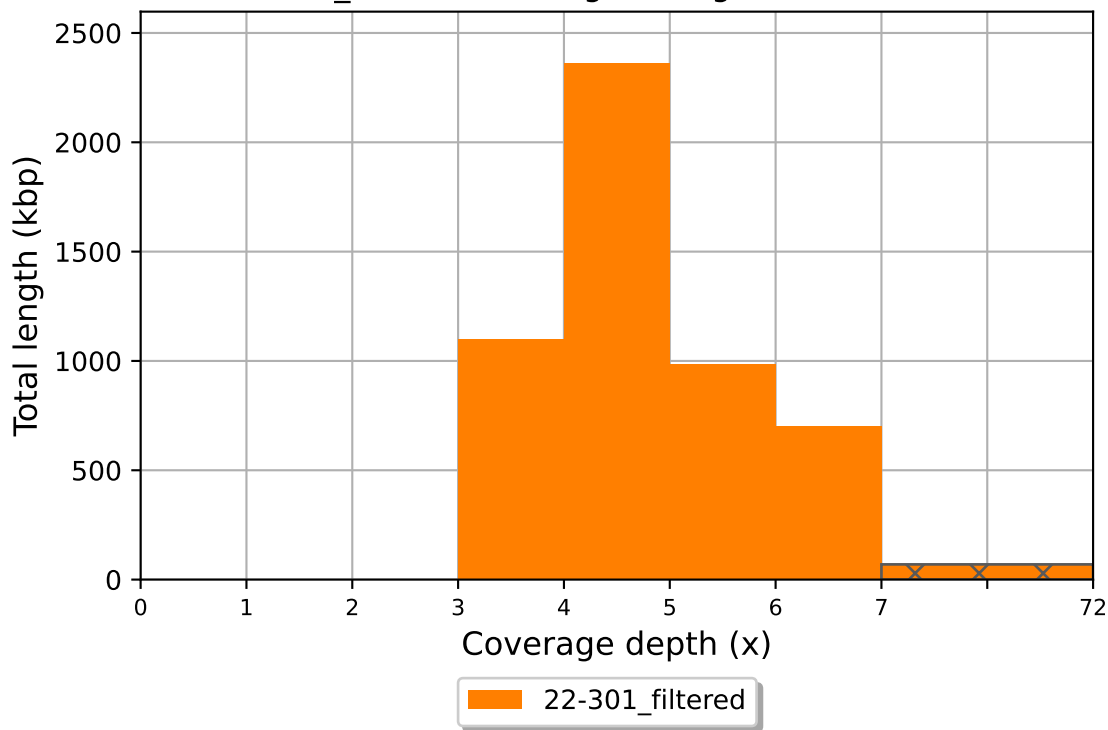
22-324_filtered coverage histogram (bin size: 1x)



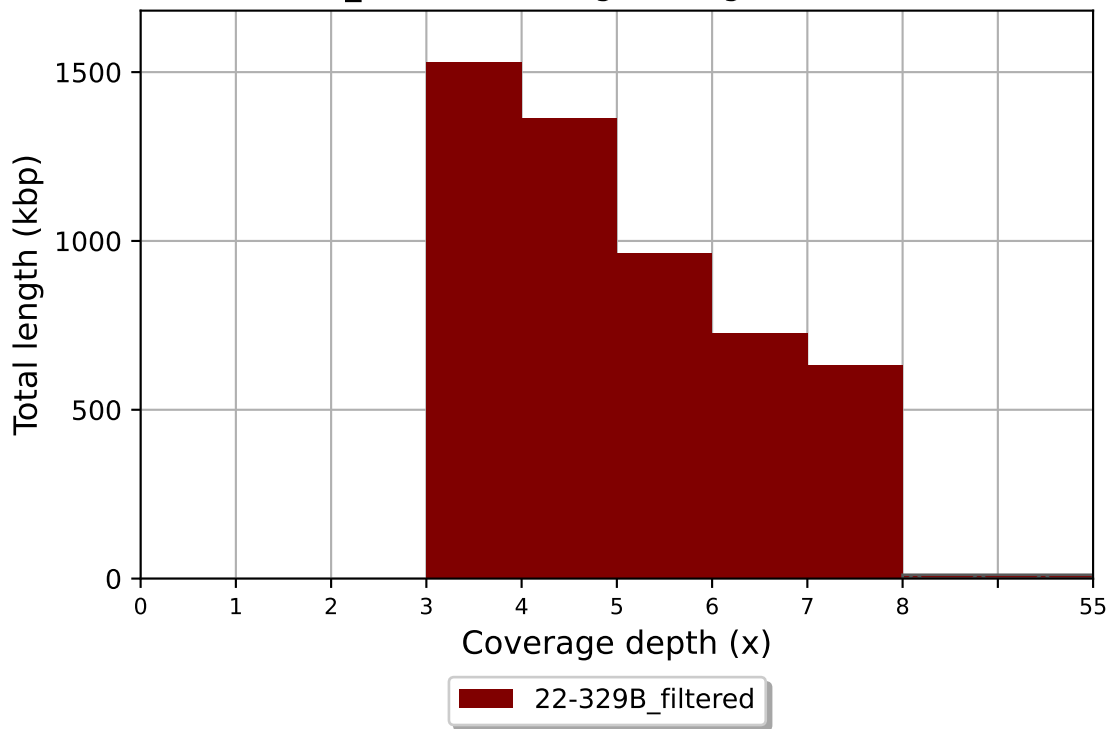
22-329A_filtered coverage histogram (bin size: 1x)



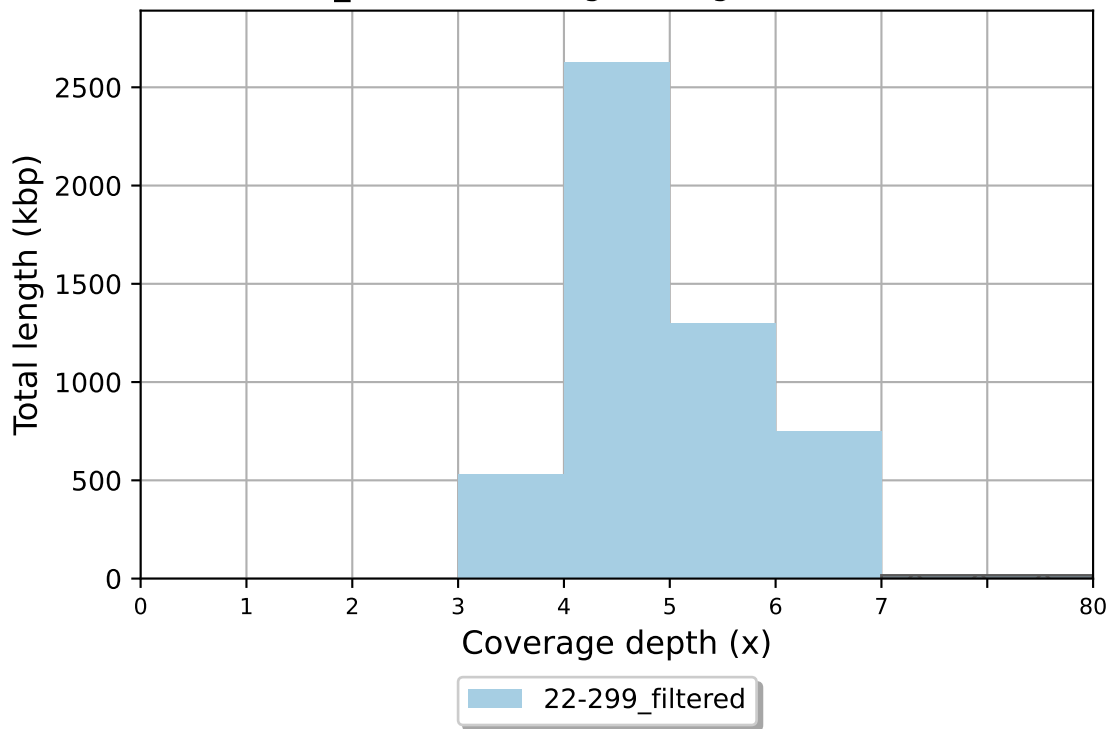
22-301_filtered coverage histogram (bin size: 1x)



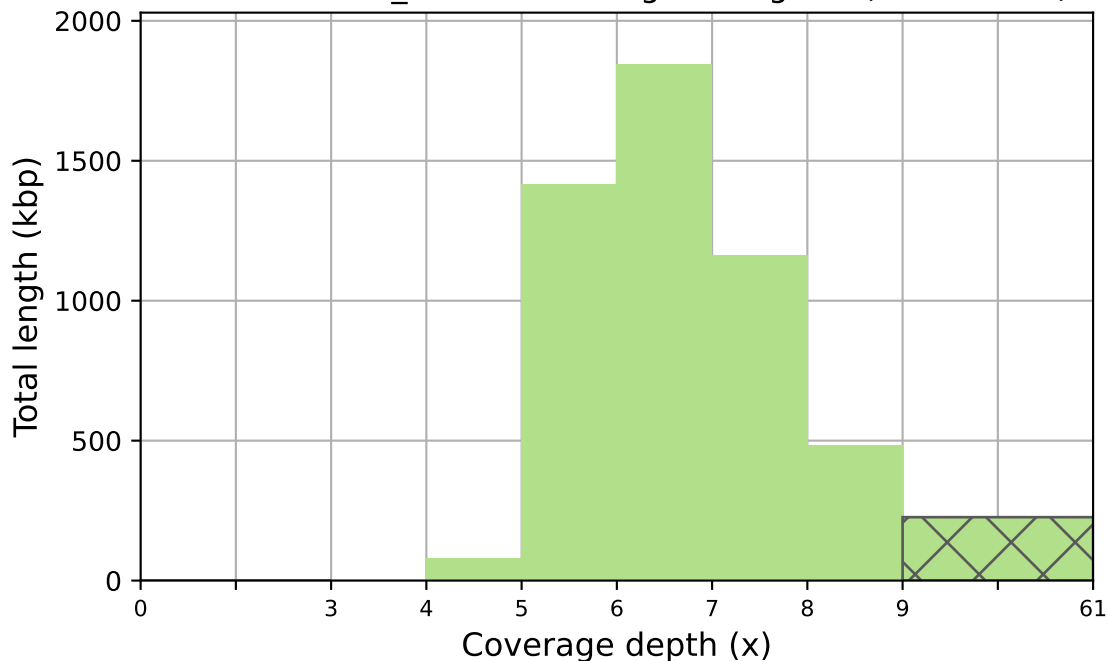
22-329B_filtered coverage histogram (bin size: 1x)



22-299_filtered coverage histogram (bin size: 1x)

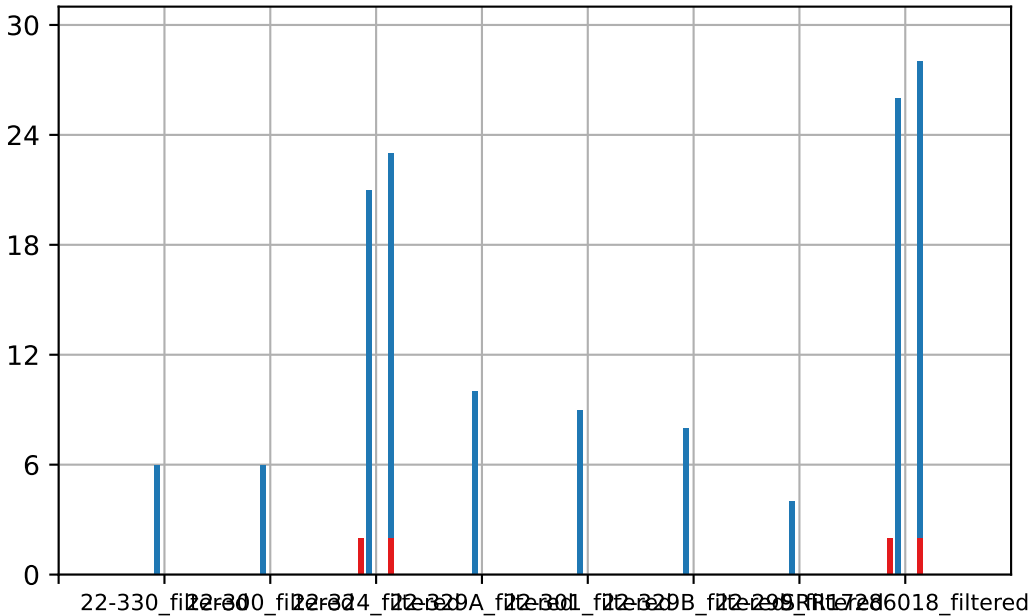


SRR17286018_filtered coverage histogram (bin size: 1x)



SRR17286018_filtered

Misassemblies



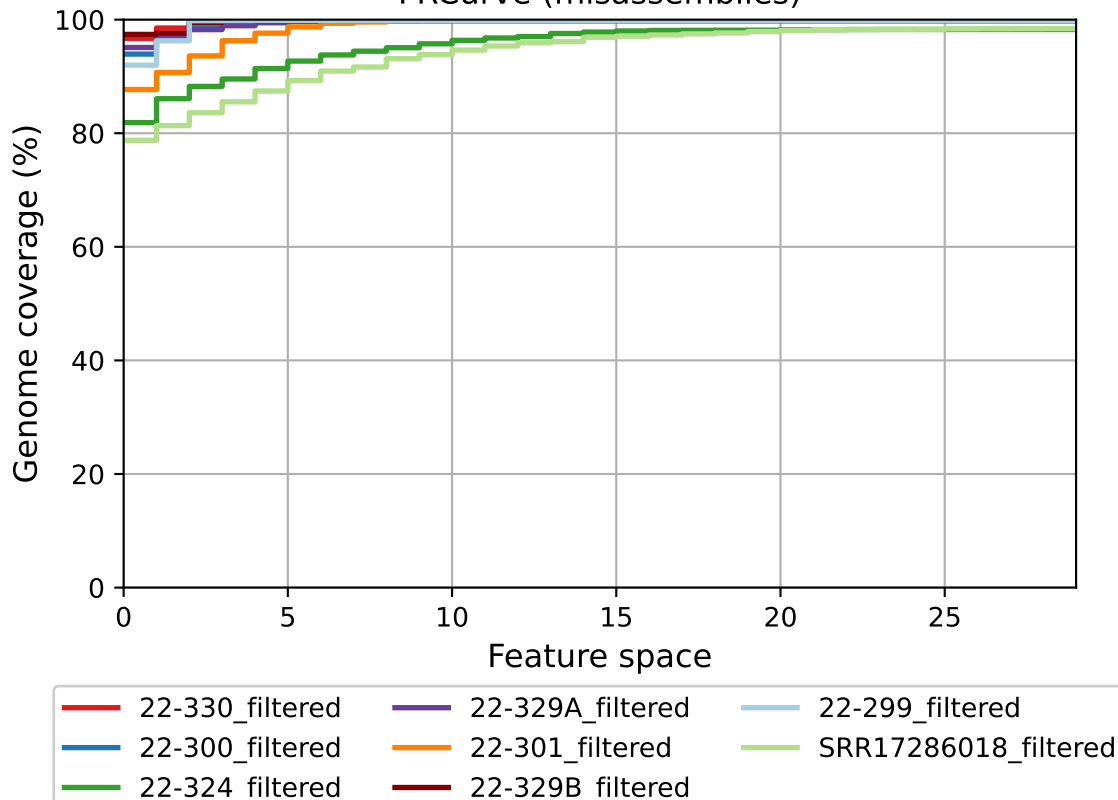
114

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# relocations
```

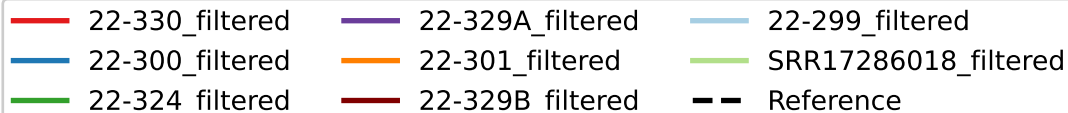
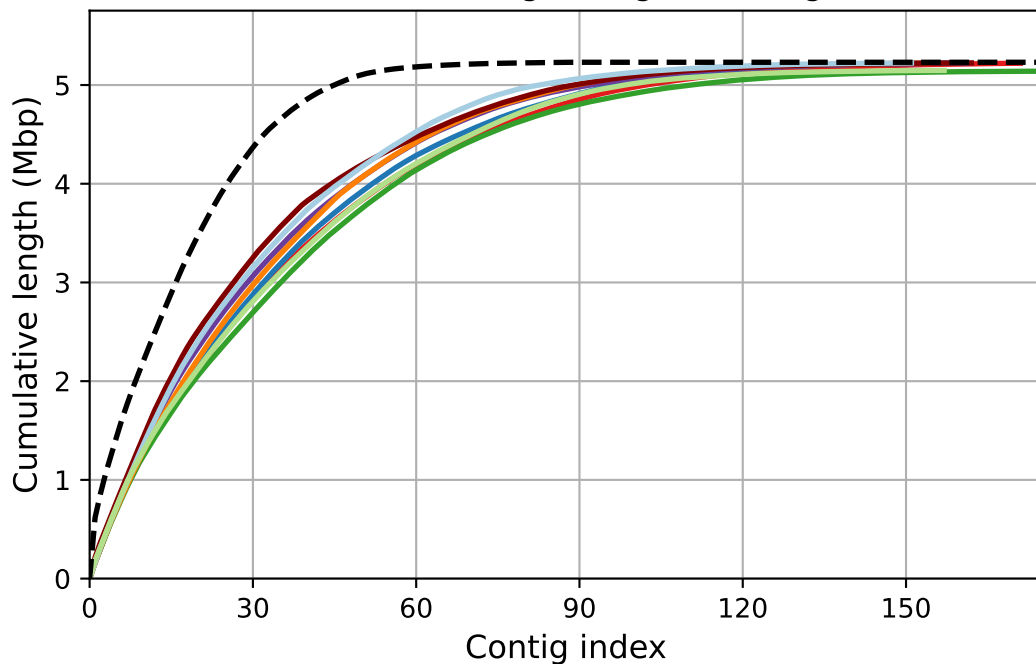
11

translocations

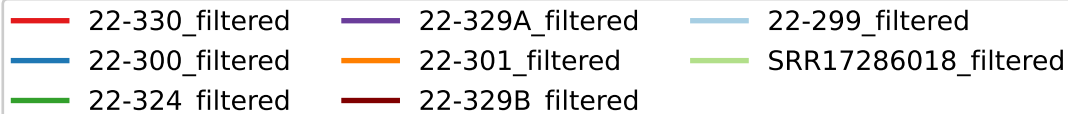
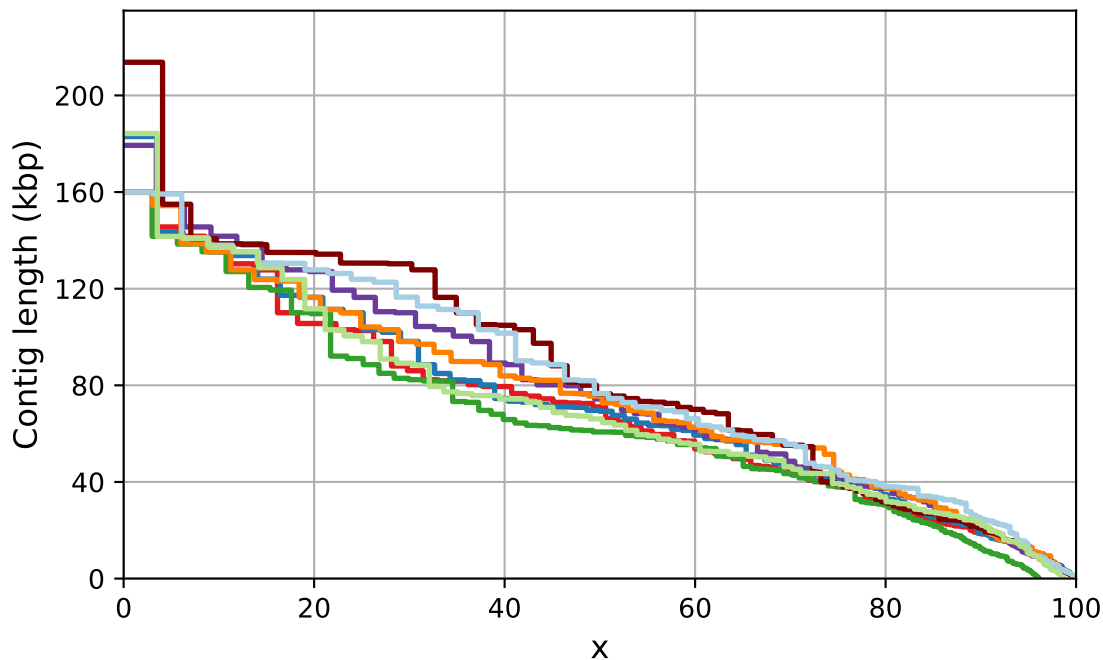
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



NGAx

