

Report

	22-301_filtered	SRR17286018_filtered	22-324_filtered	22-329A_filtered	22-299_filtered	22-300_filtered	22-329B_filtered	22-330_filtered
# contigs (>= 0 bp)	252	183	240	267	277	282	238	272
# contigs (>= 1000 bp)	129	120	138	138	129	140	140	154
# contigs (>= 5000 bp)	100	103	119	108	99	114	108	119
# contigs (>= 10000 bp)	90	89	102	89	80	100	89	100
# contigs (>= 25000 bp)	64	73	71	64	64	66	60	66
# contigs (>= 50000 bp)	45	42	43	39	38	40	39	39
Total length (>= 0 bp)	5249769	5225323	5368097	5251165	5253365	5252816	5246561	5247624
Total length (>= 1000 bp)	5216855	5207728	5336942	5216657	5213559	5216390	5218282	5215571
Total length (>= 5000 bp)	5152873	5162792	5286107	5148931	5136587	5155370	5146005	5128697
Total length (>= 10000 bp)	5079762	5058856	5166204	5014563	4996238	5057347	5006438	4992329
Total length (>= 25000 bp)	4671326	4776669	4640843	4594386	4703367	4489874	4479447	4396331
Total length (>= 50000 bp)	4002719	3684627	3593619	3661748	3741889	3522585	3786687	3381186
# contigs	142	129	153	150	147	154	154	165
Largest contig	159931	184507	207457	179569	224249	185361	213966	160109
Total length	5225752	5213857	5347785	5225181	5226380	5225709	5227736	5223674
Reference length	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549
GC (%)	63.78	63.77	63.63	63.78	63.78	63.78	63.78	63.78
Reference GC (%)	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78
N50	82172	74291	62516	76466	81953	69621	76466	72480
NG50	82172	74291	63287	76466	81953	69621	76466	72480
N90	24528	26762	21357	22600	24528	19030	21031	18879
NG90	24528	26200	24056	22600	24528	19030	21031	18512
auN	83046.4	79574.2	74861.5	83269.4	90578.8	77261.2	86718.0	71980.9
auNG	82970.2	79320.2	76539.4	83184.0	90506.6	77189.7	86671.4	71886.3
L50	23	24	28	23	21	26	22	27
LG50	23	24	27	23	21	26	22	27
L90	66	70	79	69	65	76	70	80
LG90	66	71	74	69	65	76	70	81
# misassemblies	8	28	24	11	5	6	8	6
# misassembled contigs	8	19	18	9	3	5	7	5
Misassembled contigs length	577938	1060228	886557	426349	418568	310243	130611	162792
# local misassemblies	1	3	3	0	0	1	2	1
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	2	0	0	0	0	0	0
# unaligned mis. contigs	0	0	2	0	1	0	0	0
# unaligned contigs	0 + 1 part	0 + 4 part	2 + 8 part	0 + 1 part	1 + 0 part	0 + 1 part	0 + 0 part	0 + 1 part
Unaligned length	1012	60470	205087	948	689	637	0	828
Genome fraction (%)	99.806	98.411	98.220	99.732	99.834	99.821	99.840	99.771
Duplication ratio	1.000	1.000	1.000	1.001	1.000	1.000	1.000	1.000
# N's per 100 kbp	4.40	15.84	5.76	4.84	6.79	5.59	4.50	4.02
# mismatches per 100 kbp	2.43	16.94	11.69	6.63	2.39	2.37	1.42	2.32
# indels per 100 kbp	0.80	2.86	1.52	0.44	1.00	0.42	0.27	0.46
Largest alignment	159931	184238	159868	179326	159968	182983	213723	160109
Total aligned length	5222065	5148154	5139332	5222332	5223511	5223460	5224125	5220823
NA50	76724	66091	60695	74332	76587	69285	76466	71079
NGA50	76724	66091	61305	74332	76587	69285	76466	71079
NA90	23778	22988	12496	21357	24528	18874	21031	18512
NGA90	23778	22072	15740	21357	24528	18874	21031	18512
auNA	78123.8	72256.0	66292.5	79760.9	82843.1	74093.0	86523.8	71048.3
auNGA	78052.1	72025.4	67778.4	79679.0	82777.1	74024.4	86477.2	70955.0
LA50	25	27	30	24	23	27	22	27
LGA50	25	27	29	24	23	27	22	27
LA90	69	78	92	72	67	78	70	82
LGA90	69	79	85	72	67	78	70	82

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

	22-301_filtered	SRR17286018_filtered	22-324_filtered	22-329A_filtered	22-299_filtered	22-300_filtered	22-329B_filtered	22-330_filtered
# misassemblies	8	28	24	11	5	6	8	6
# contig misassemblies	8	28	24	11	5	6	8	6
# c. relocations	0	2	2	0	0	0	0	0
# c. translocations	8	26	22	11	5	6	8	6
# 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	8	19	18	9	3	5	7	5
Misassembled contigs length	577938	1060228	886557	426349	418568	310243	130611	162792
# local misassemblies	1	3	3	0	0	1	2	1
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	2	0	0	0	0	0	0
# unaligned mis. contigs	0	0	2	0	1	0	0	0
# mismatches	127	872	601	346	125	124	74	121
# indels	42	147	78	23	52	22	14	24
# indels (<= 5 bp)	17	72	26	11	29	6	1	12
# indels (> 5 bp)	25	75	52	12	23	16	13	12
Indels length	1466	2933	1612	935	1354	1190	867	896

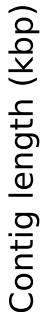
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).









Unaligned report

	22-301_filtered	SRR17286018_filtered	22-324_filtered	22-329A_filtered	22-299_filtered	22-300_filtered	22-329B_filtered	22-330_filtered
# fully unaligned contigs	0	0	2	0	1	0	0	0
Fully unaligned length	0	0	15084	0	689	0	0	0
# partially unaligned contigs	1	4	8	1	0	1	0	1
Partially unaligned length	1012	60470	190003	948	0	637	0	828
# N's	230	826	308	253	355	292	235	210

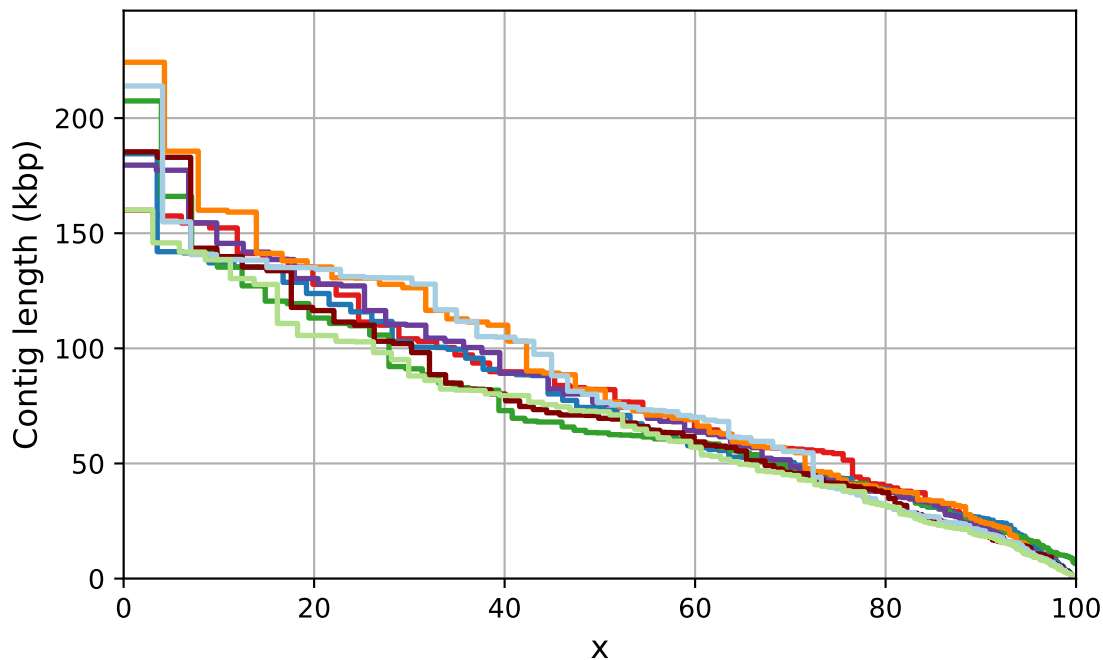
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



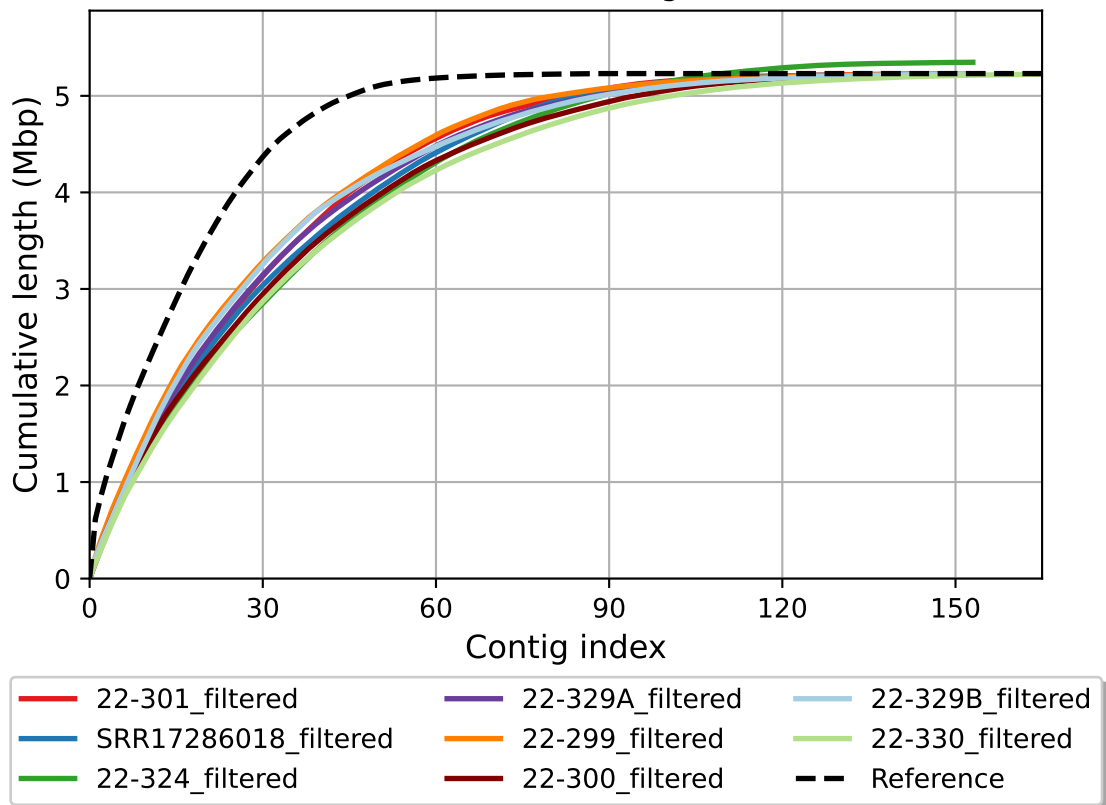
-  22-301_filtered
  22-329A_filtered
  22-329B_filtered
 SRR17286018_filtered
  22-299_filtered
  22-330_filtered
 22-324_filtered
  22-300_filtered

NGx

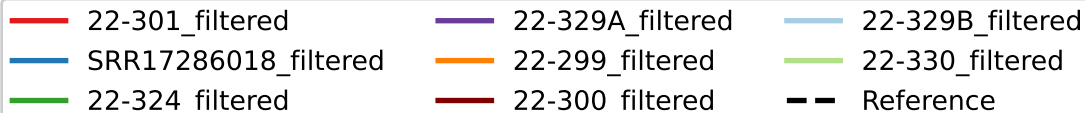
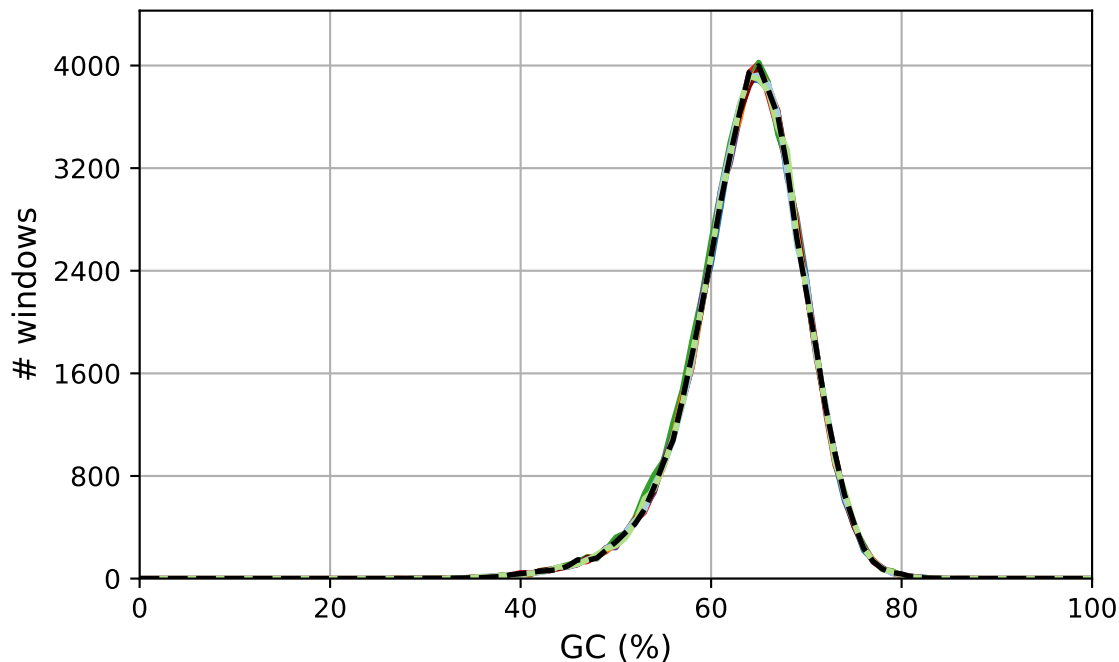


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|----------------------|------------------|------------------|
| 22-301_filtered | 22-329A_filtered | 22-329B_filtered |
| SRR17286018_filtered | 22-299_filtered | 22-330_filtered |
| 22-324_filtered | 22-300_filtered | |

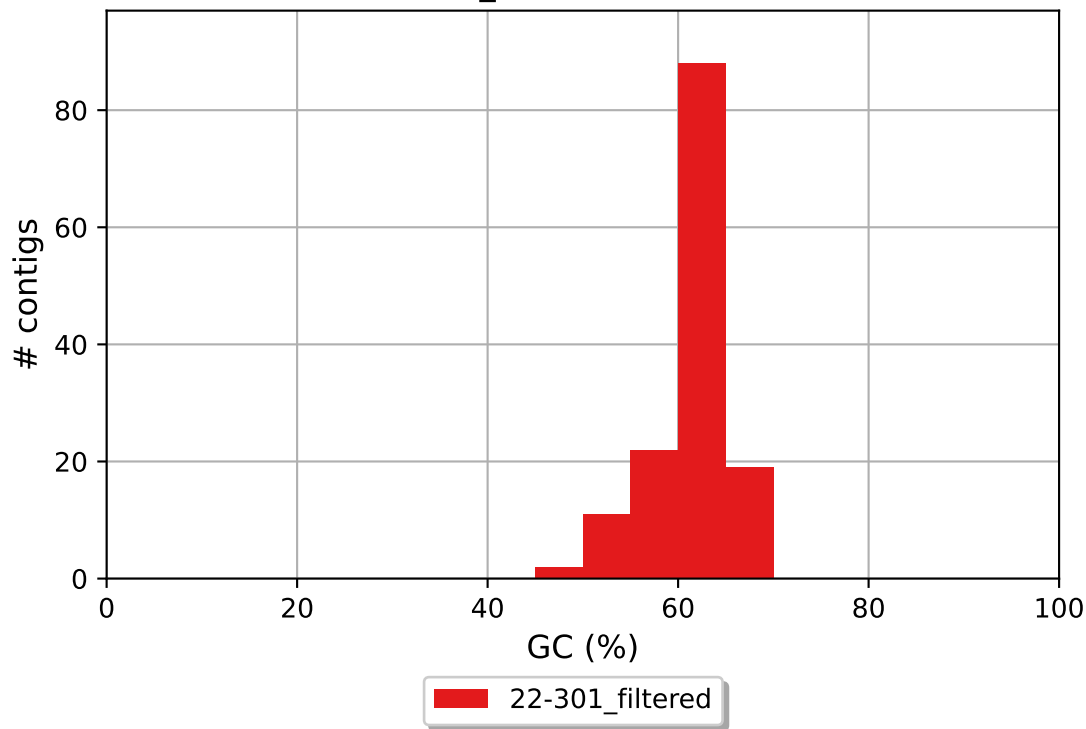
Cumulative length



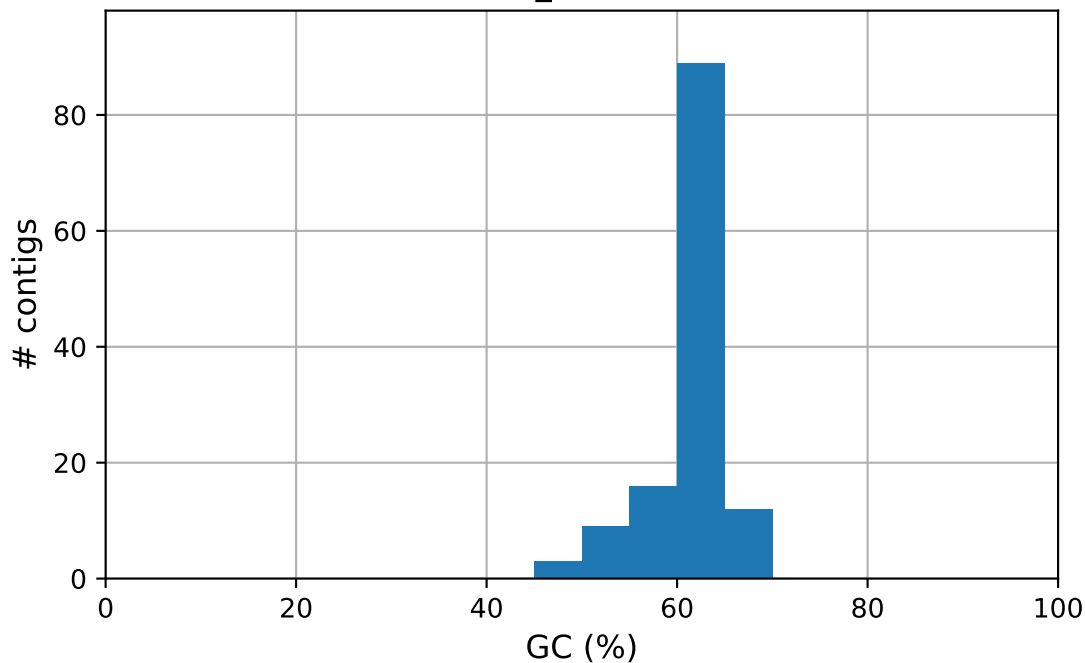
GC content



22-301_filtered GC content

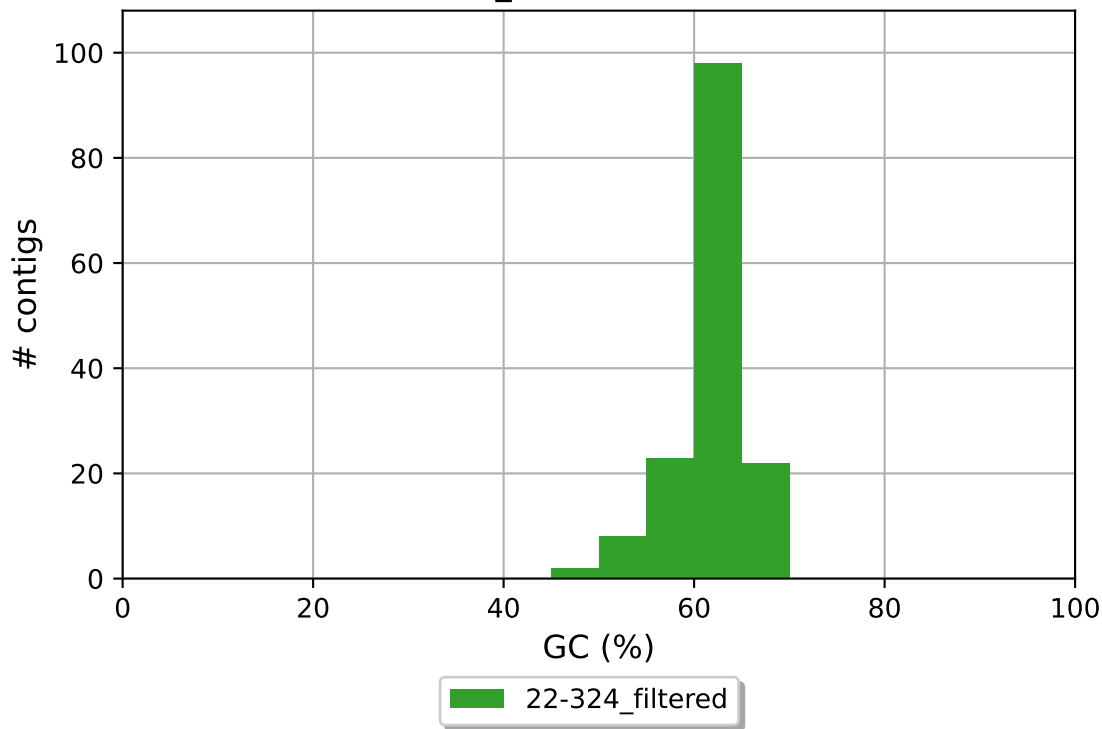


SRR17286018_filtered GC content

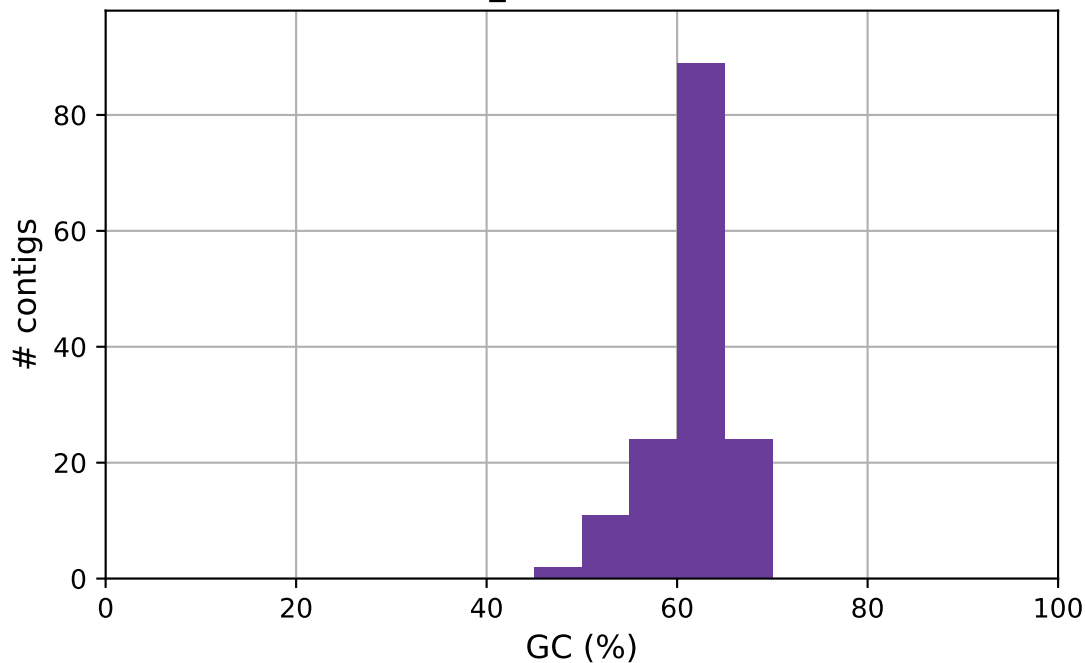


SRR17286018_filtered

22-324_filtered GC content

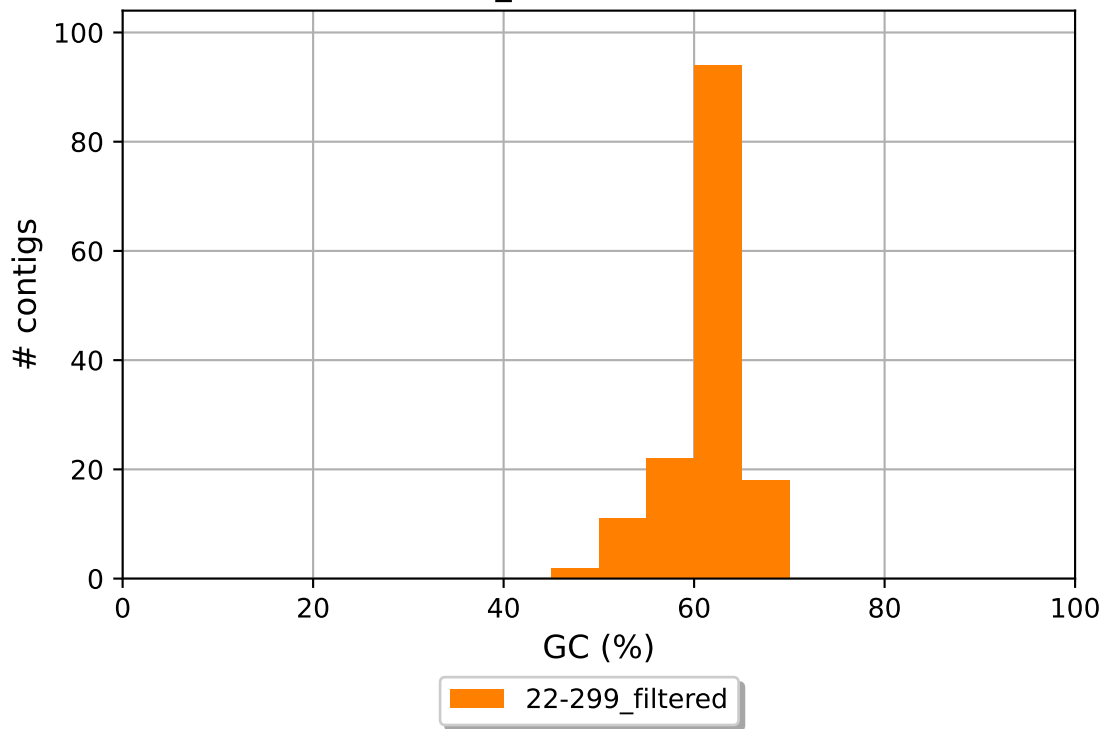


22-329A_filtered GC content

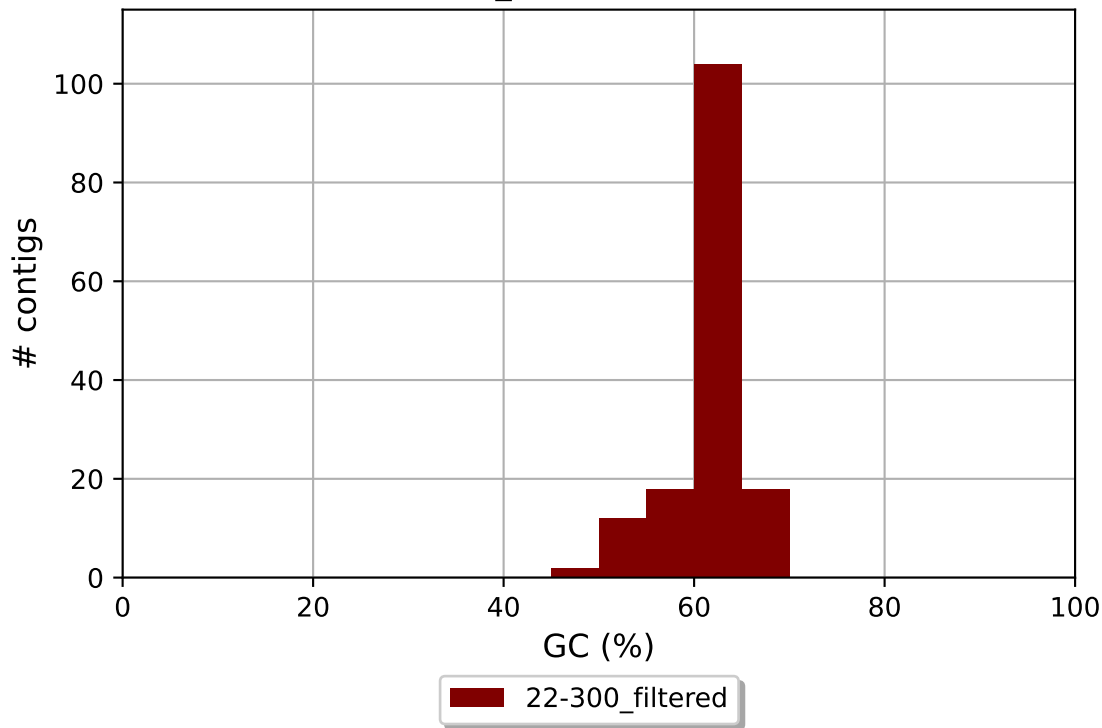


22-329A_filtered

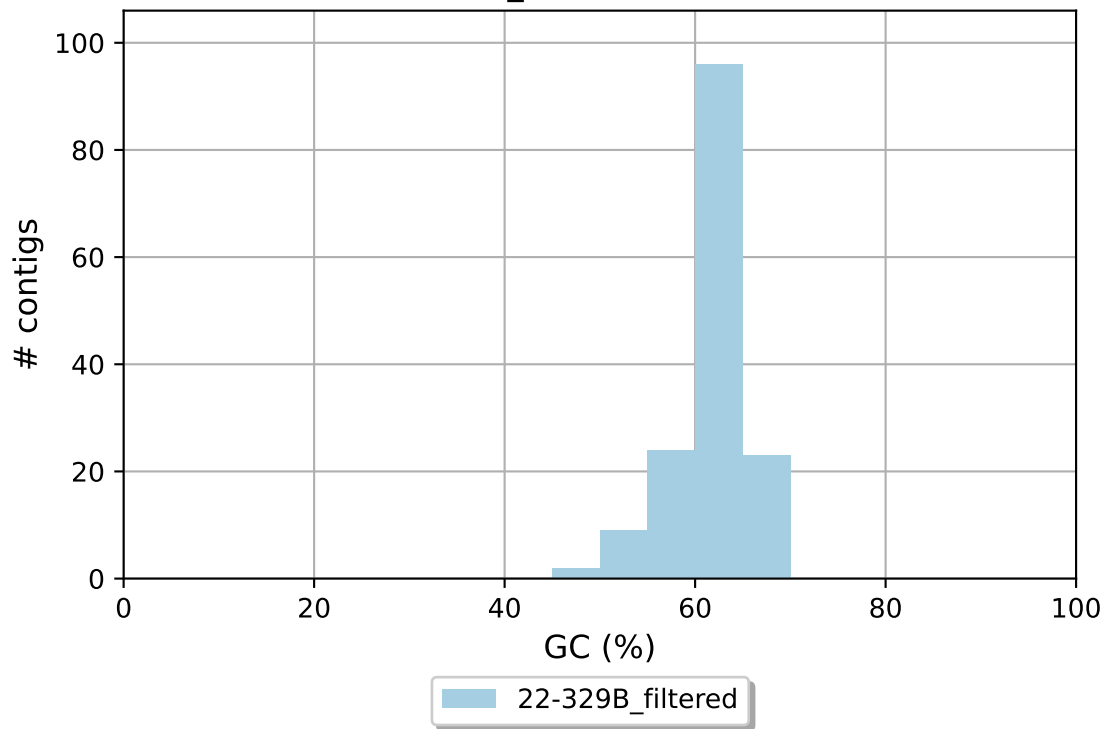
22-299_filtered GC content



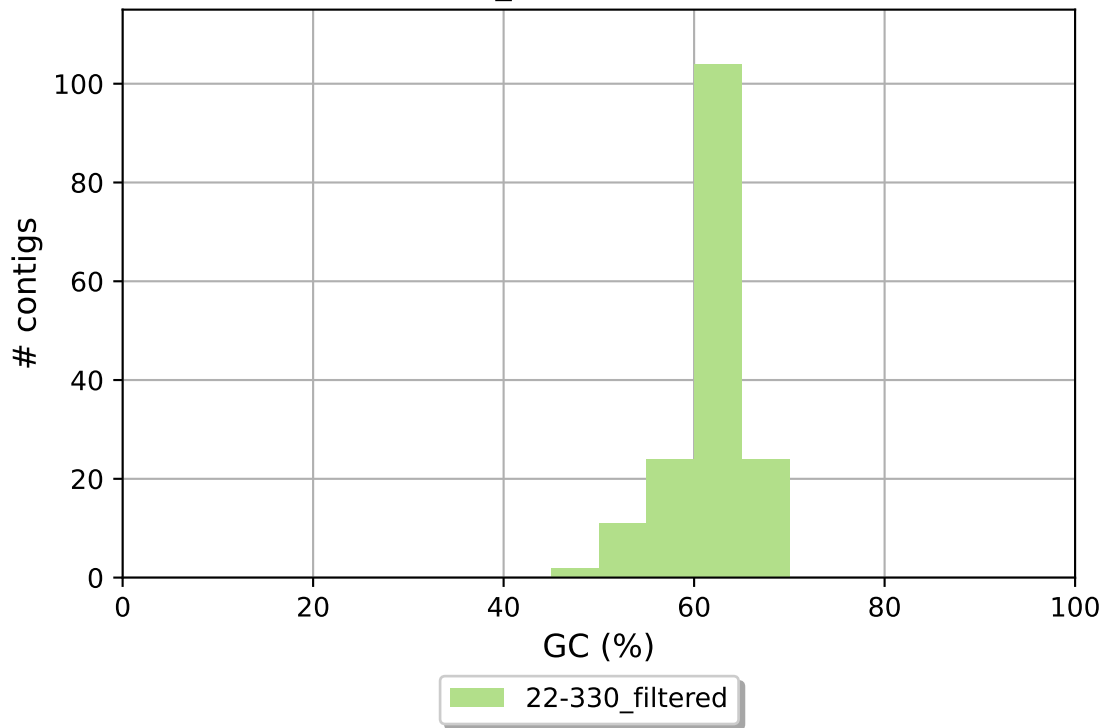
22-300_filtered GC content



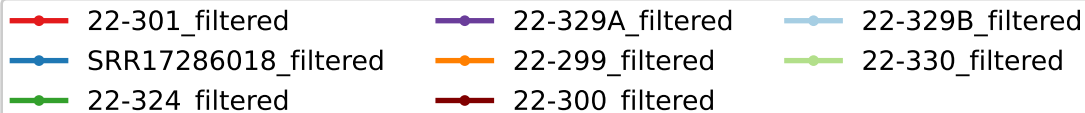
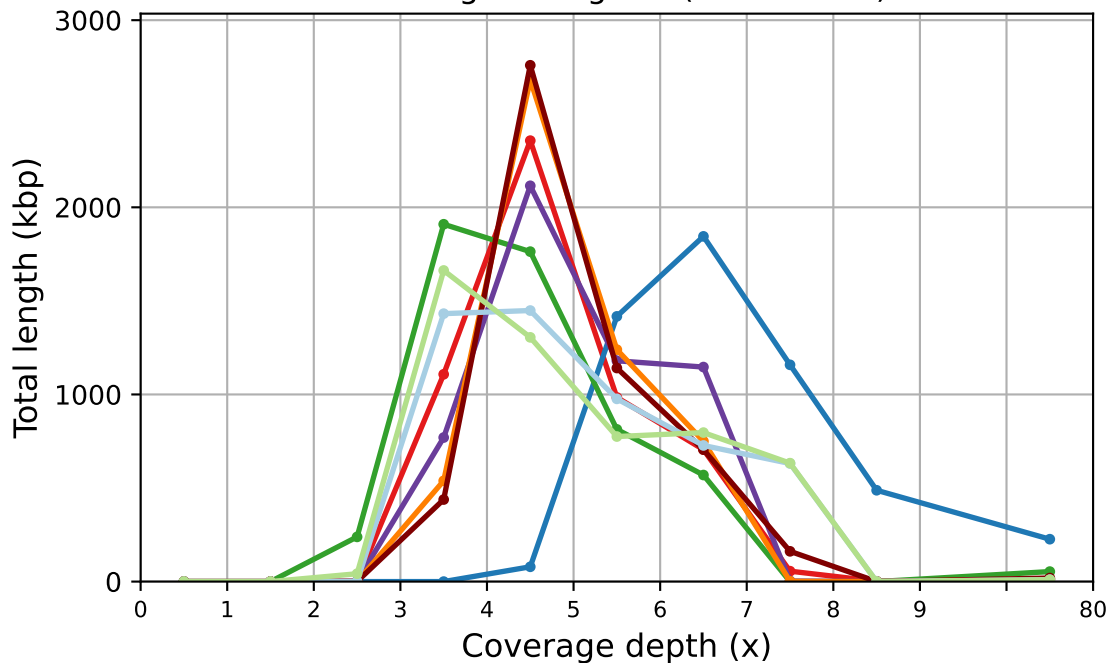
22-329B_filtered GC content



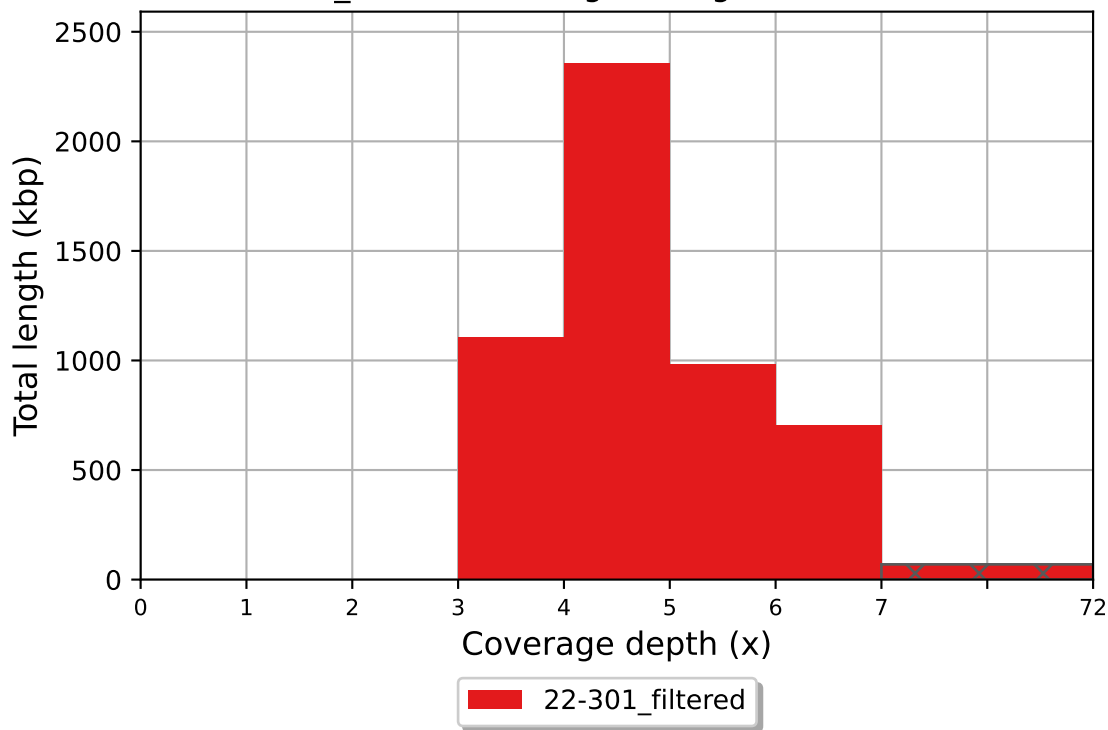
22-330_filtered GC content



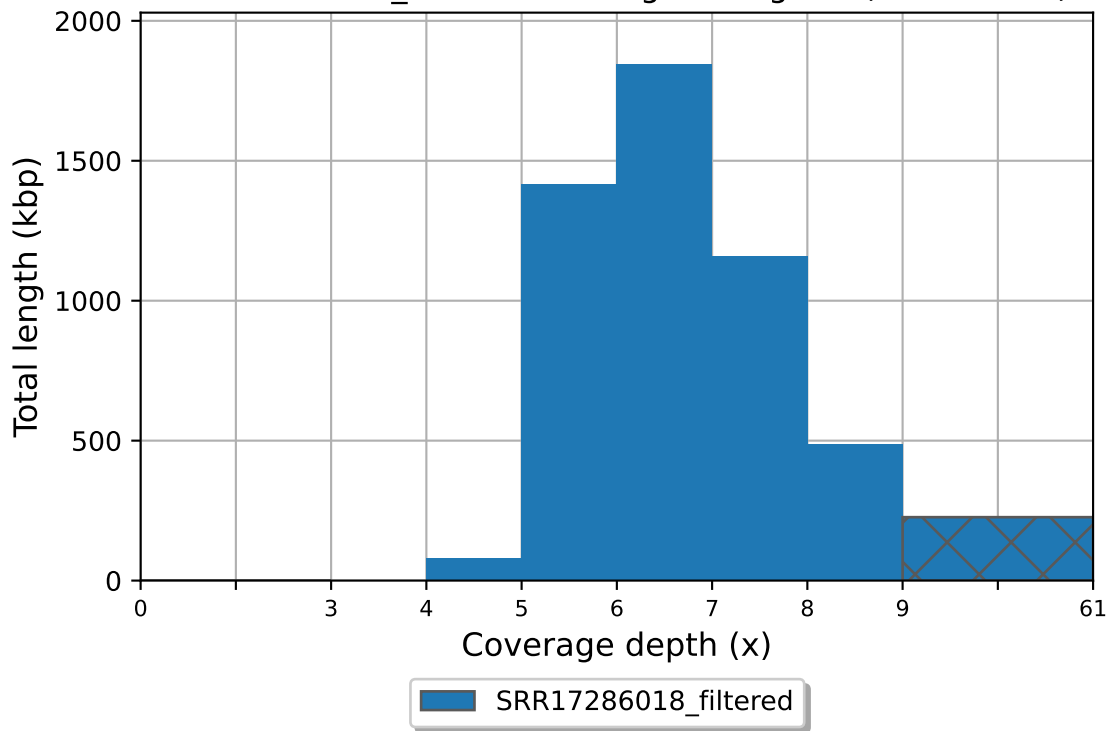
Coverage histogram (bin size: 1x)



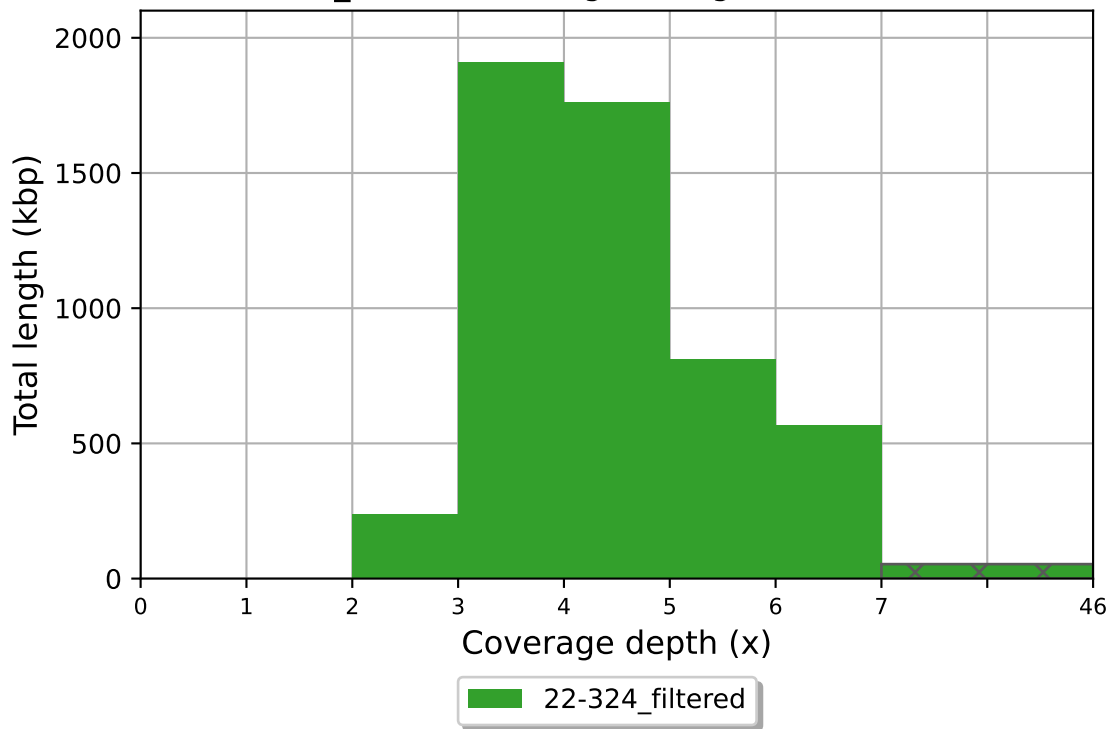
22-301_filtered coverage histogram (bin size: 1x)



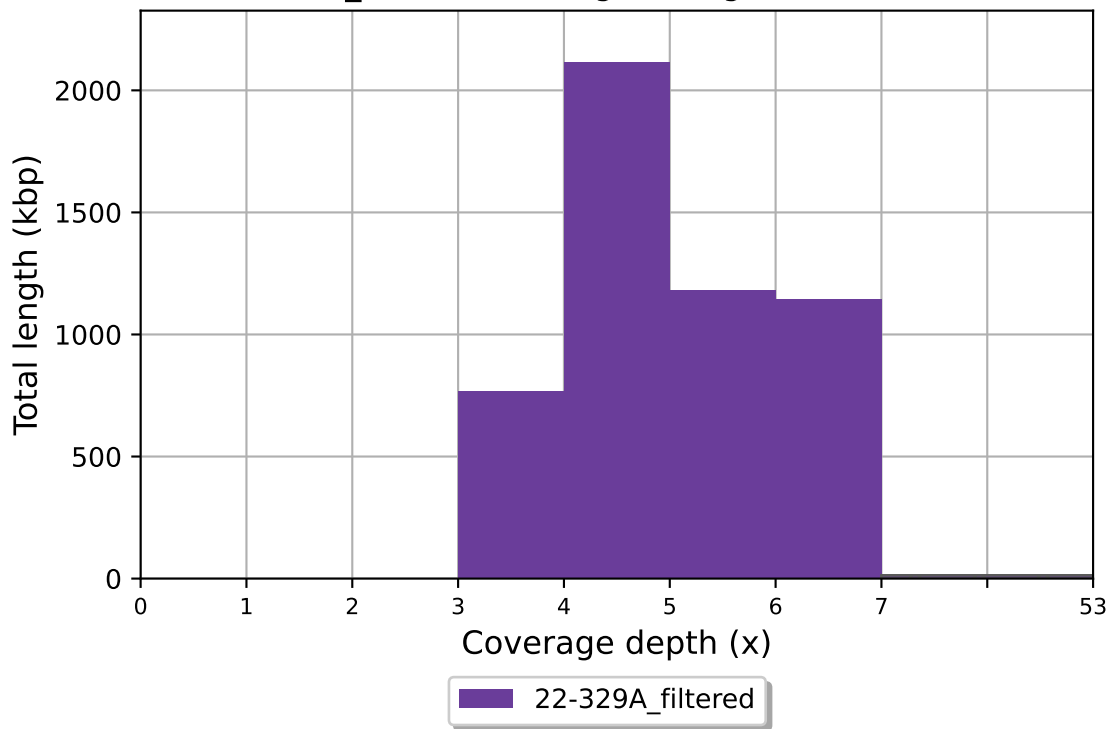
SRR17286018_filtered coverage histogram (bin size: 1x)



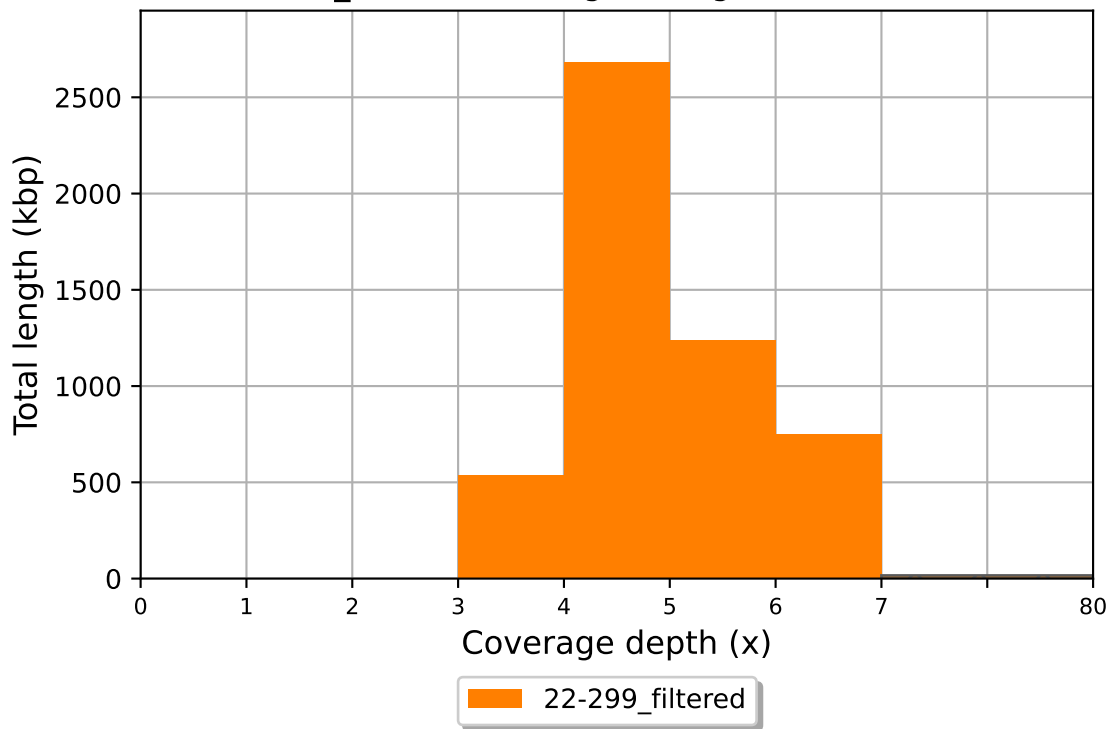
22-324_filtered coverage histogram (bin size: 1x)



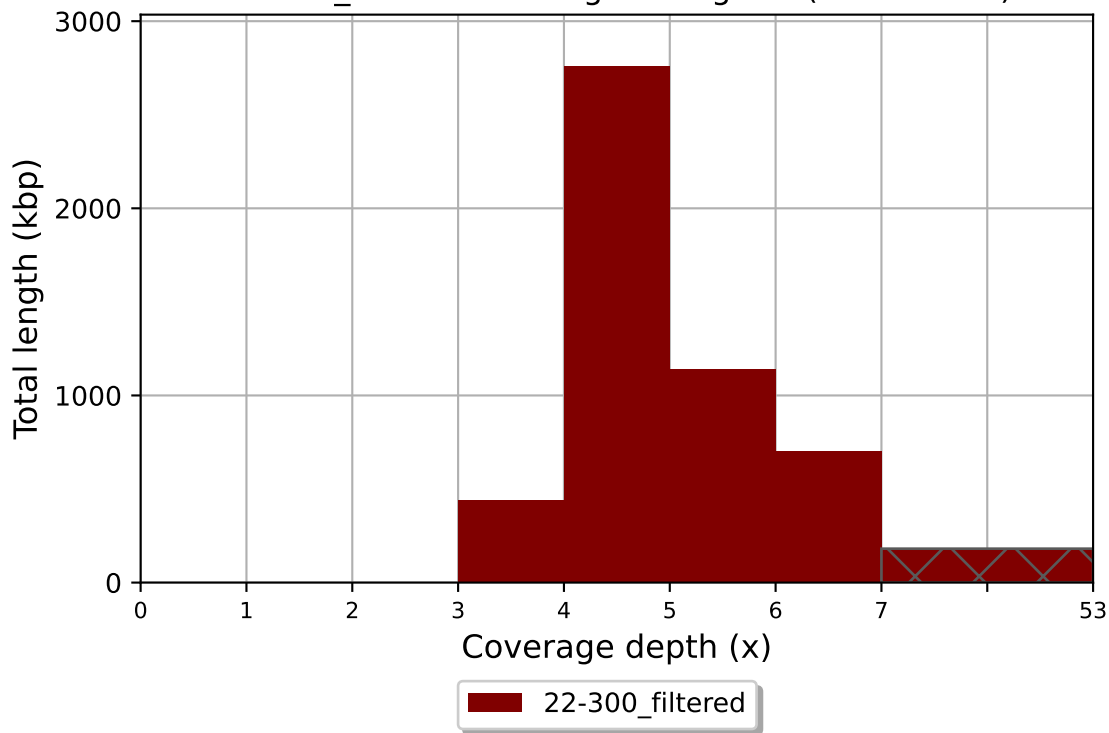
22-329A_filtered coverage histogram (bin size: 1x)



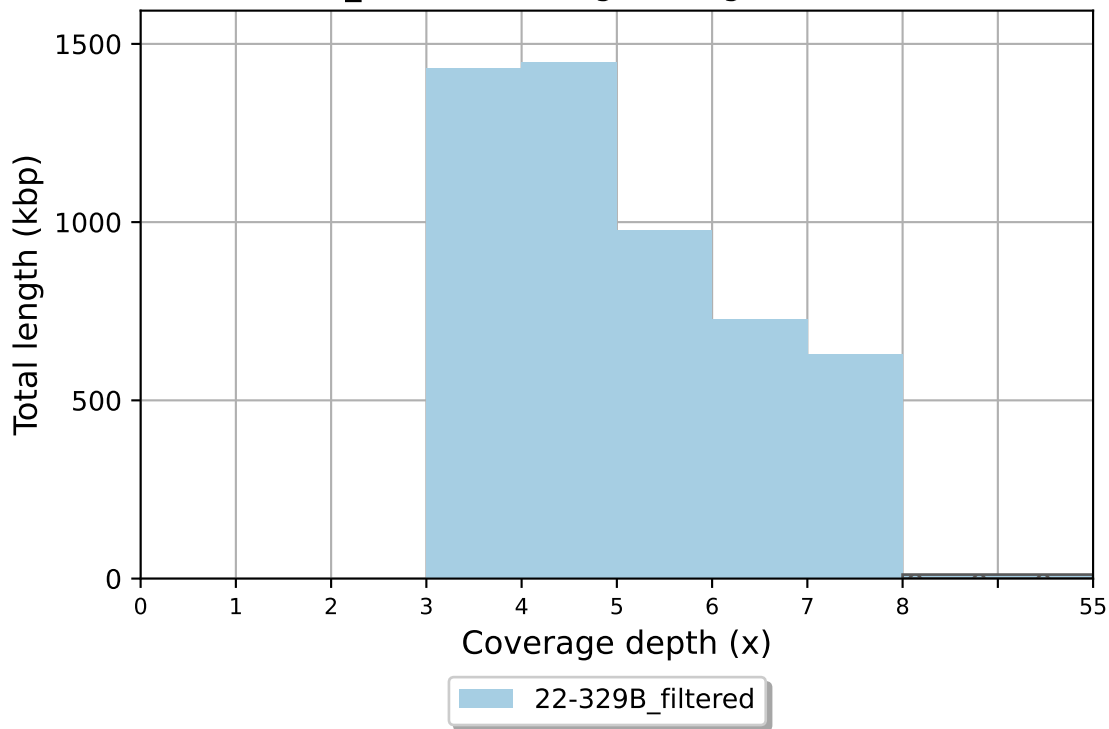
22-299_filtered coverage histogram (bin size: 1x)



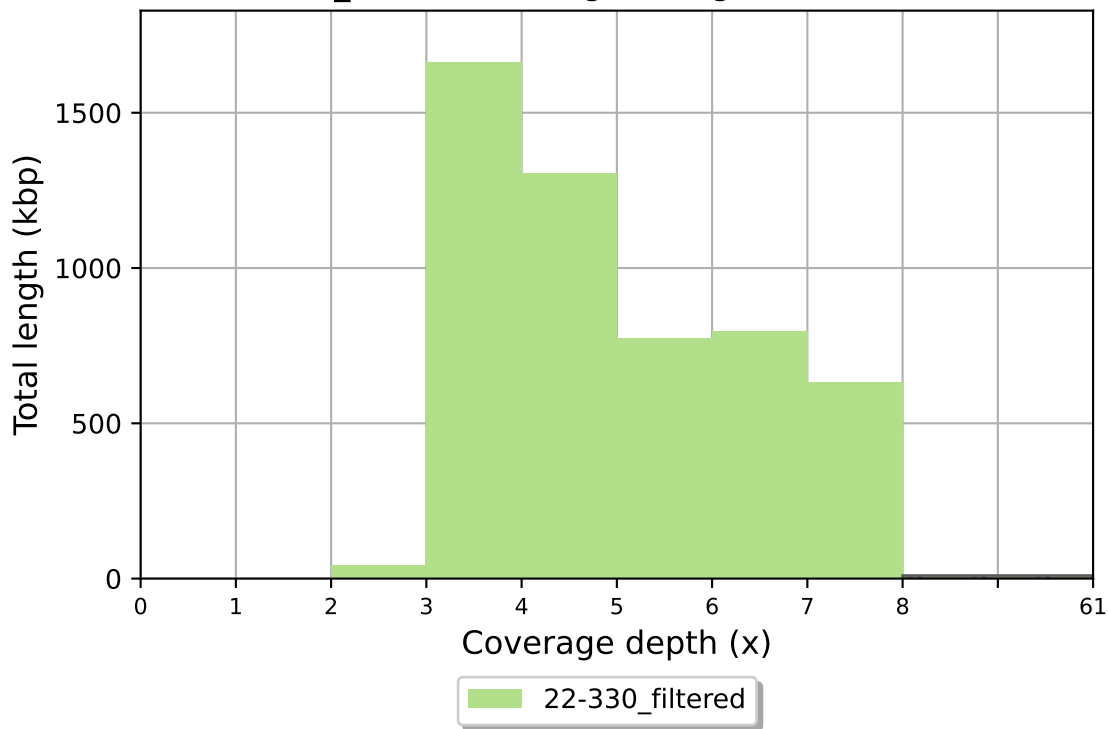
22-300_filtered coverage histogram (bin size: 1x)



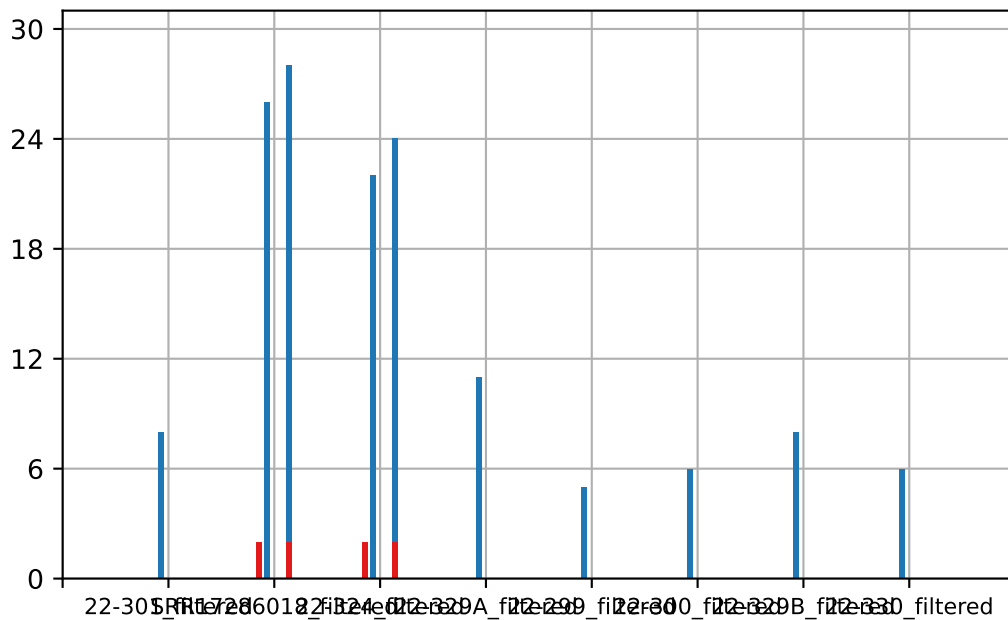
22-329B_filtered coverage histogram (bin size: 1x)



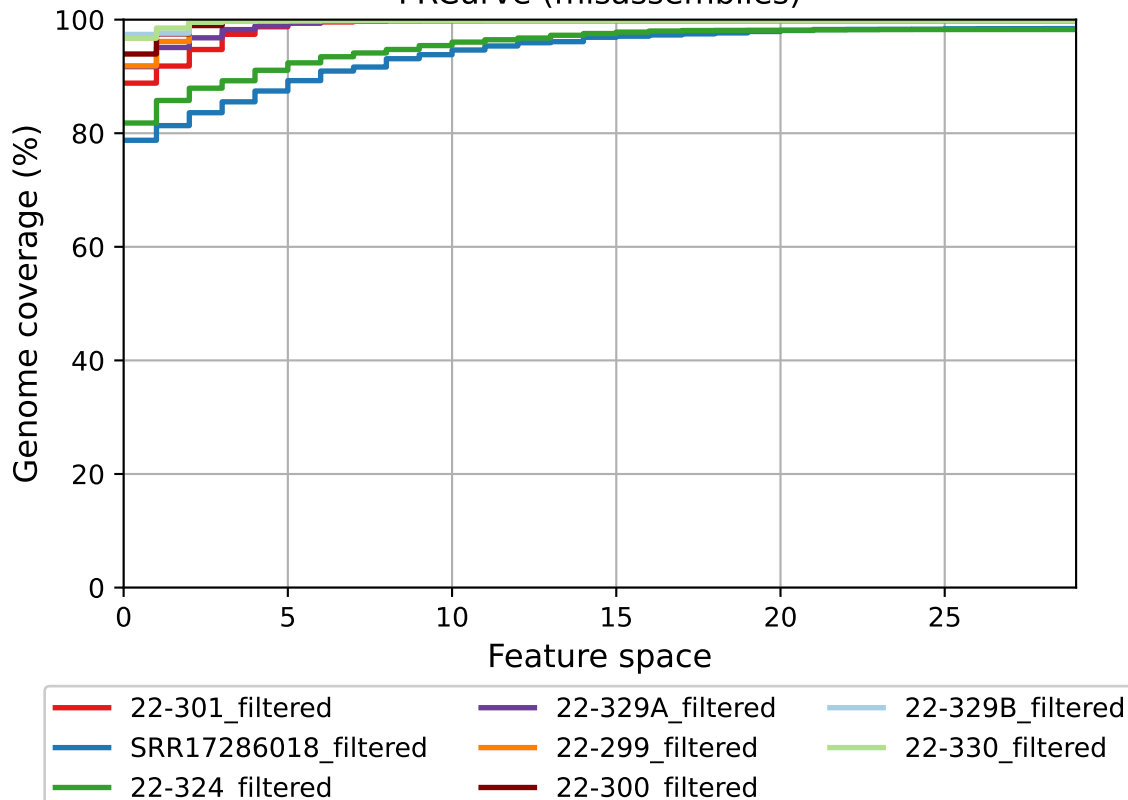
22-330_filtered coverage histogram (bin size: 1x)



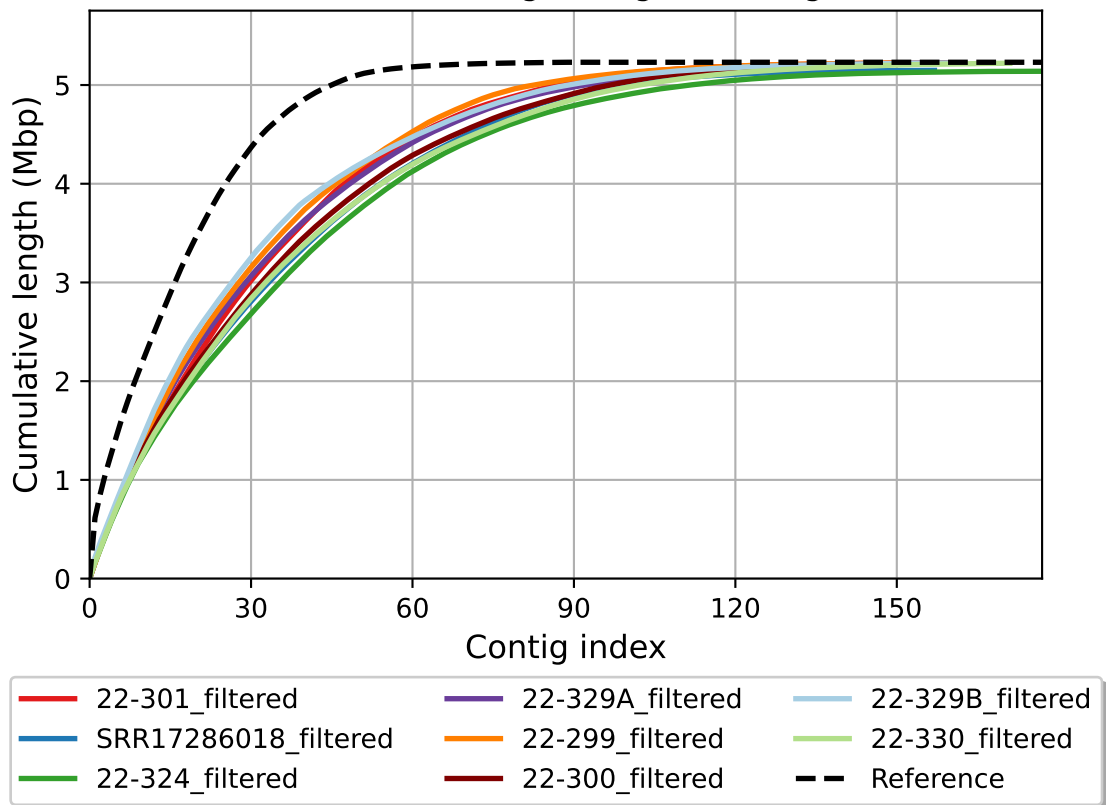
Misassemblies



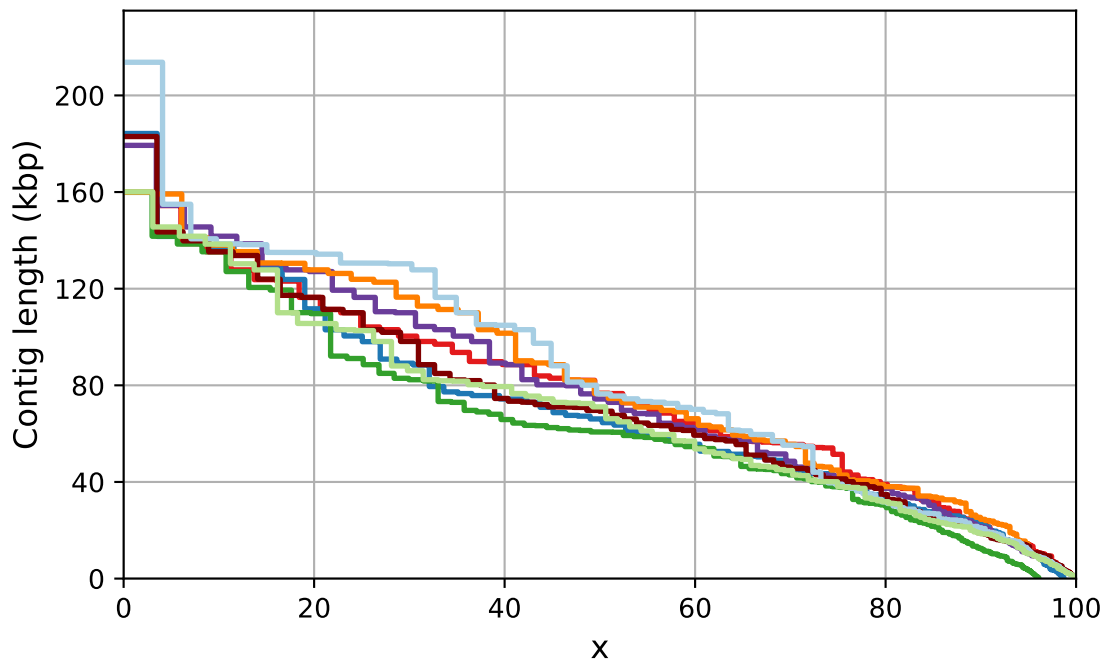
FRCurve (misassemblies)



Cumulative length (aligned contigs)

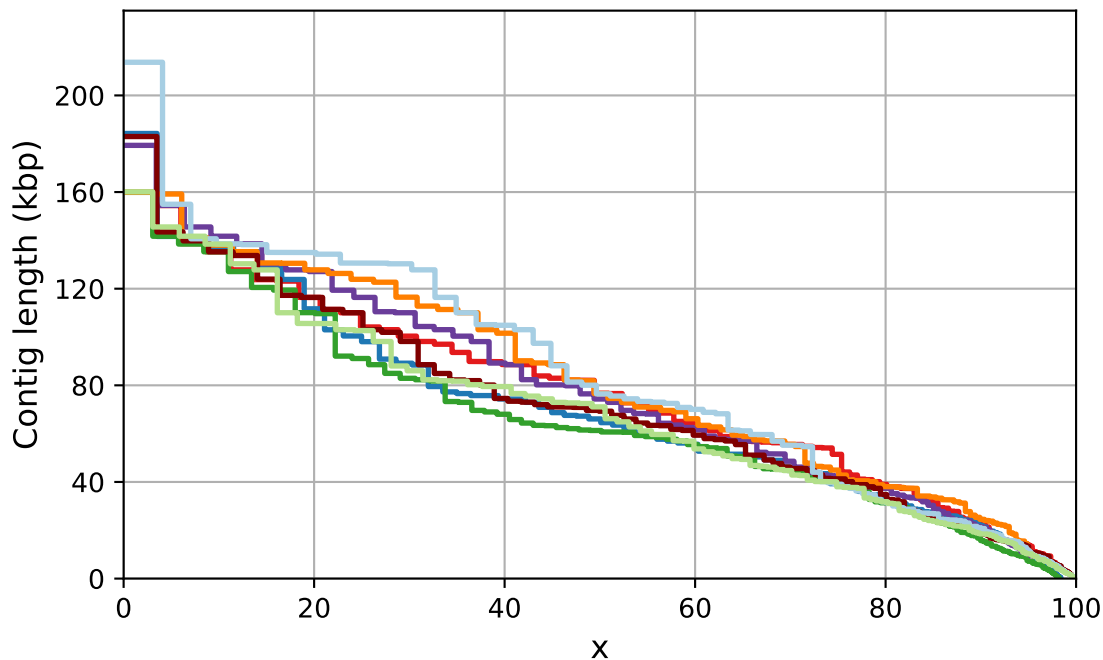


NAx



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|----------------------|------------------|------------------|
| 22-301_filtered | 22-329A_filtered | 22-329B_filtered |
| SRR17286018_filtered | 22-299_filtered | 22-330_filtered |
| 22-324_filtered | 22-300_filtered | |

NGAx



- | | | |
|----------------------|------------------|------------------|
| 22-301_filtered | 22-329A_filtered | 22-329B_filtered |
| SRR17286018_filtered | 22-299_filtered | 22-330_filtered |
| 22-324_filtered | 22-300_filtered | |

