

	Report			
	22-301_filtered	22-324_filtered	22-299_filtered	22-300_filtered
# contigs (>= 0 bp)	252	240	277	282
# contigs (>= 1000 bp)	129	138	129	140
# contigs (>= 5000 bp)	100	119	99	114
# contigs (>= 10000 bp)	90	102	80	100
# contigs (>= 25000 bp)	64	71	64	66
# contigs (>= 50000 bp)	45	43	38	40
Total length (>= 0 bp)	5249769	5368097	5253365	5252816
Total length (>= 1000 bp)	5216855	5336942	5213559	5216390
Total length (>= 5000 bp)	5152873	5286107	5136587	5155370
Total length (>= 10000 bp)	5079762	5166204	4996238	5057347
Total length (>= 25000 bp)	4671326	4640843	4703367	4489874
Total length (>= 50000 bp)	4002719	3593619	3741889	3522585
# contigs	142	153	147	154
Largest contig	159931	207457	224249	185361
Total length	5225752	5347785	5226380	5225709
Reference length	5625449	5625449	5625449	5625449
GC (%)	63.78	63.63	63.78	63.78
Reference GC (%)	63.34	63.34	63.34	63.34
N50	82172	62516	81953	69621
NG50	76587	62069	72895	67563
N90	24528	21357	24528	19030
NG90	10274	13335	8327	9560
auN	83046.4	74861.5	90578.8	77261.2
auNG	77145.8	71166.5	84153.2	71771.1
L50	23	28	21	26
LG50	26	30	24	28
L90	66	79	65	76
LG90	89	93	88	101
# misassemblies	107	111	106	107
# misassembled contigs	53	55	54	58
Misassembled contigs length	3731619	3237847	3730118	3675576
# local misassemblies	119	120	126	124
# scaffold gap ext. mis.	0	1	0	1
# scaffold gap loc. mis.	0	2	3	2
# unaligned mis. contigs	13	12	9	11
# unaligned contigs	13 + 92 part	9 + 98 part	14 + 92 part	11 + 102 part
Unaligned length	1223482	1202754	1230207	1222063
Genome fraction (%)	70.921	73.430	70.790	70.929
Duplication ratio	1.001	1.001	1.001	1.001
# N's per 100 kbp	4.40	5.76	6.79	5.59
# mismatches per 100 kbp	3377.41	3319.92	3374.07	3377.07
# indels per 100 kbp	134.77	129.65	134.29	134.22
Largest alignment	125165	114798	133434	125515
Total aligned length	3995016	4135907	3987677	3995057
NA50	22604	21729	22787	22057
NGA50	20916	20602	21205	20037
NA90	-	-	-	-
NGA90	-	-	-	-
auNA	28819.4	27482.7	30857.3	28132.1
auNGA	26771.8	26126.2	28668.3	26133.0
LA50	64	71	64	66
LGA50	74	77	73	75
LA90	-	-	-	-
LGA90	-	-	-	-

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

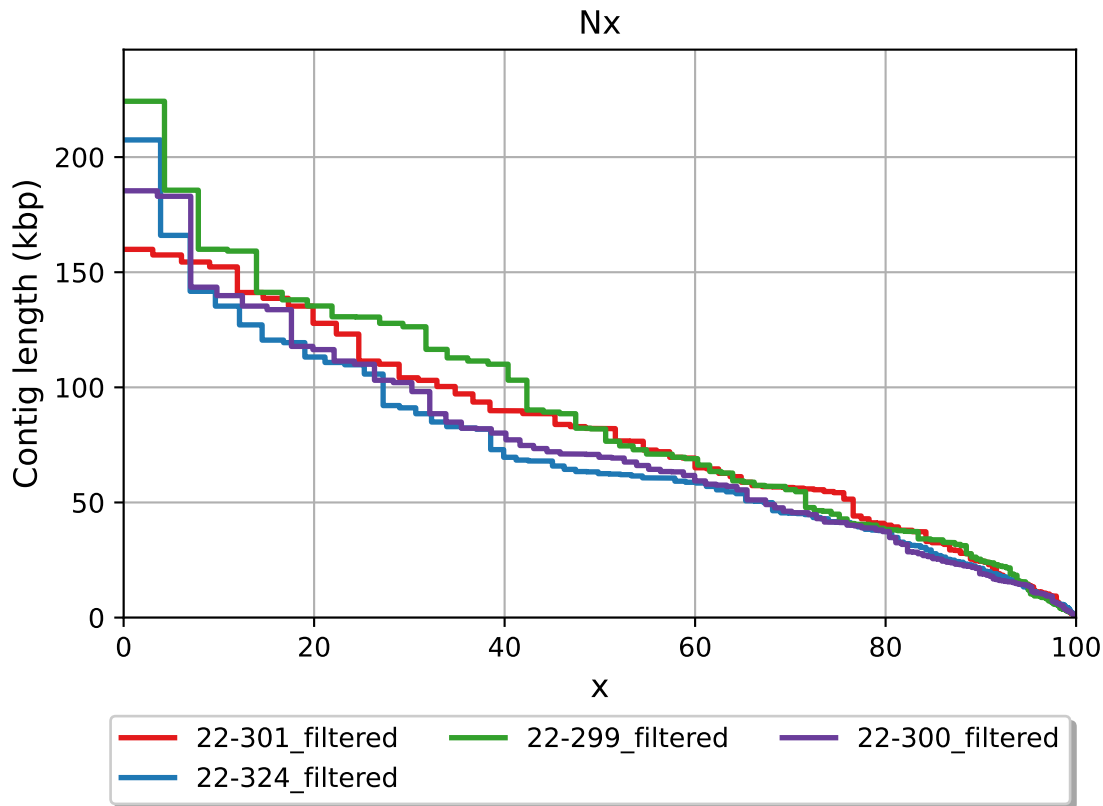
	22-301_filtered	22-324_filtered	22-299_filtered	22-300_filtered
# misassemblies	107	111	106	107
# contig misassemblies	107	111	105	106
# c. relocations	104	109	103	104
# c. translocations	3	2	2	2
# c. inversions	0	0	0	0
# scaffold misassemblies	0	0	1	1
# s. relocations	0	0	1	1
# s. translocations	0	0	0	0
# s. inversions	0	0	0	0
# misassembled contigs	53	55	54	58
Misassembled contigs length	3731619	3237847	3730118	3675576
# local misassemblies	119	120	126	124
# scaffold gap ext. mis.	0	1	0	1
# scaffold gap loc. mis.	0	2	3	2
# unaligned mis. contigs	13	12	9	11
# mismatches	134928	137309	134547	134916
# indels	5384	5362	5355	5362
# indels (<= 5 bp)	4722	4712	4703	4720
# indels (> 5 bp)	662	650	652	642
Indels length	25469	24681	25725	24814

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).

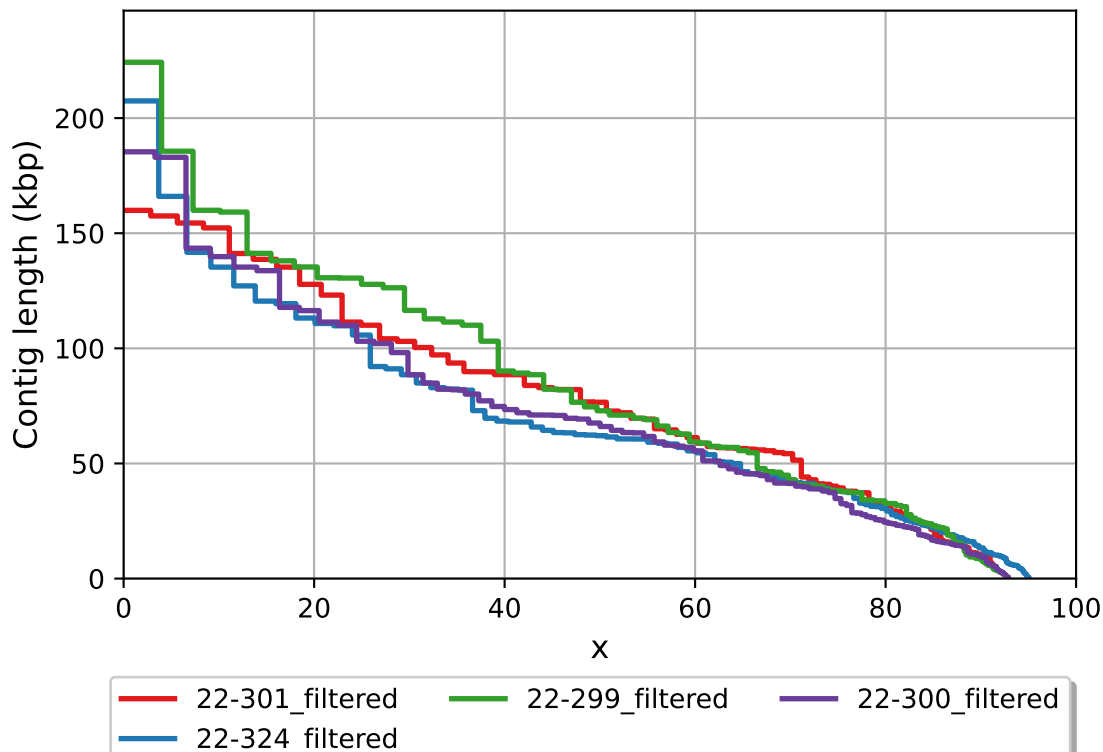
Unaligned report

	22-301_filtered	22-324_filtered	22-299_filtered	22-300_filtered
# fully unaligned contigs	13	9	14	11
Fully unaligned length	49475	21173	33450	35003
# partially unaligned contigs	92	98	92	102
Partially unaligned length	1174007	1181581	1196757	1187060
# N's	230	308	355	292

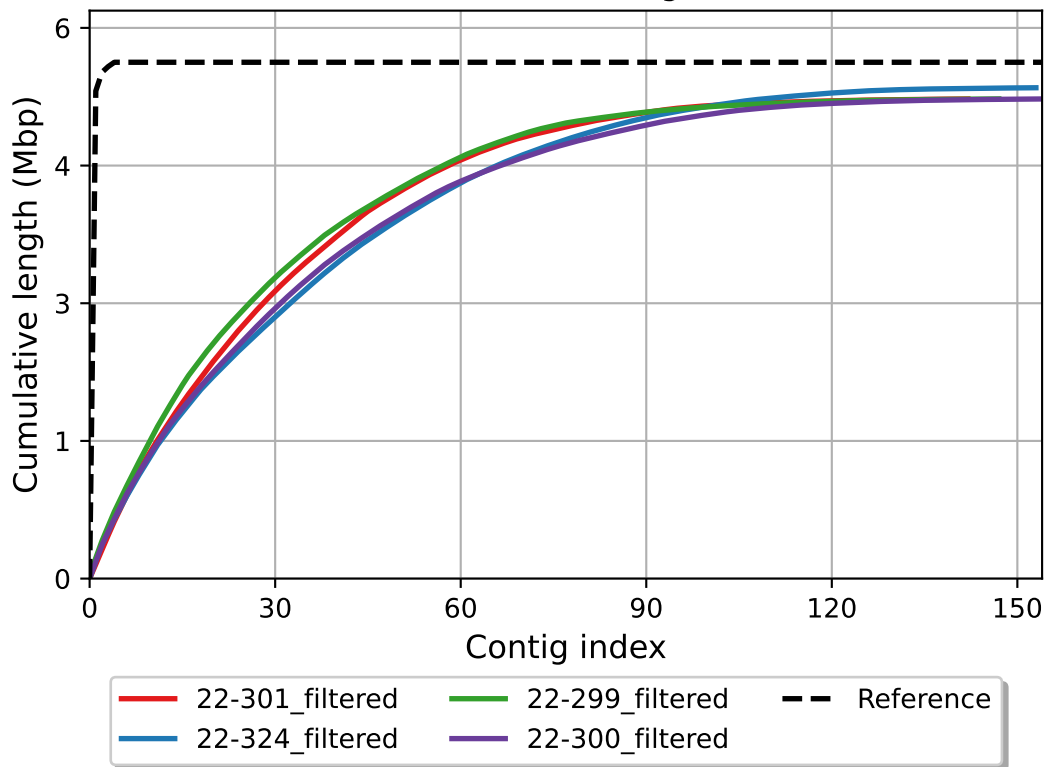
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



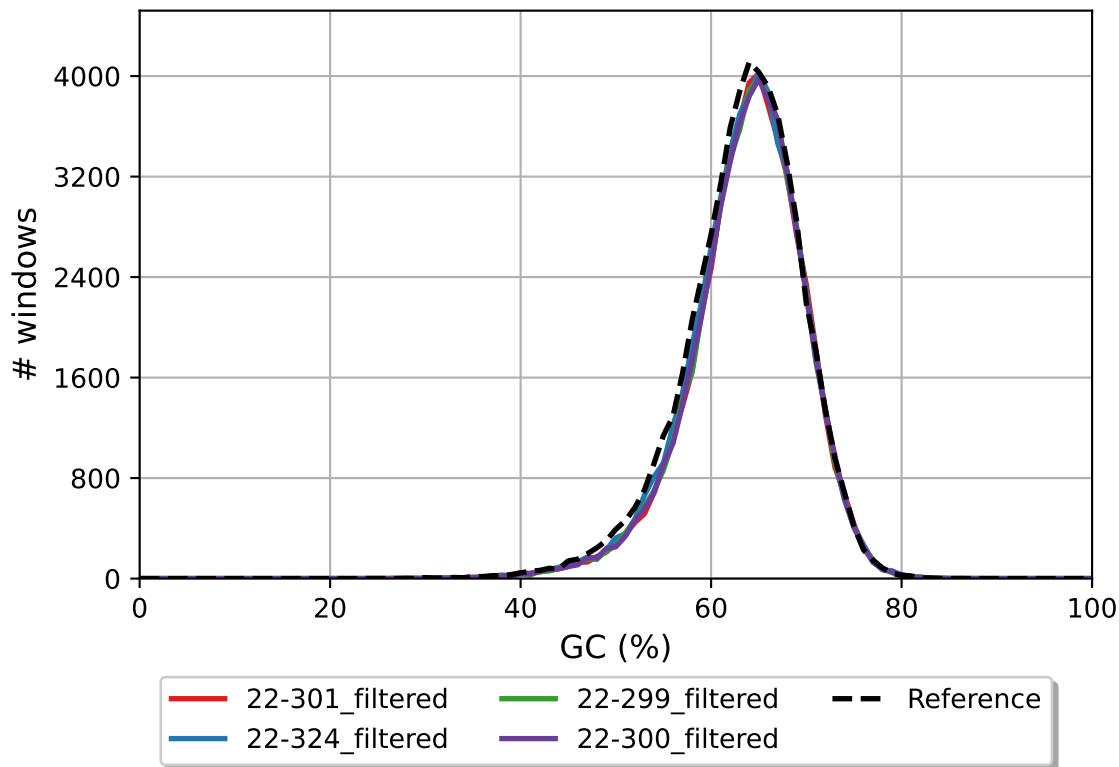
NGx



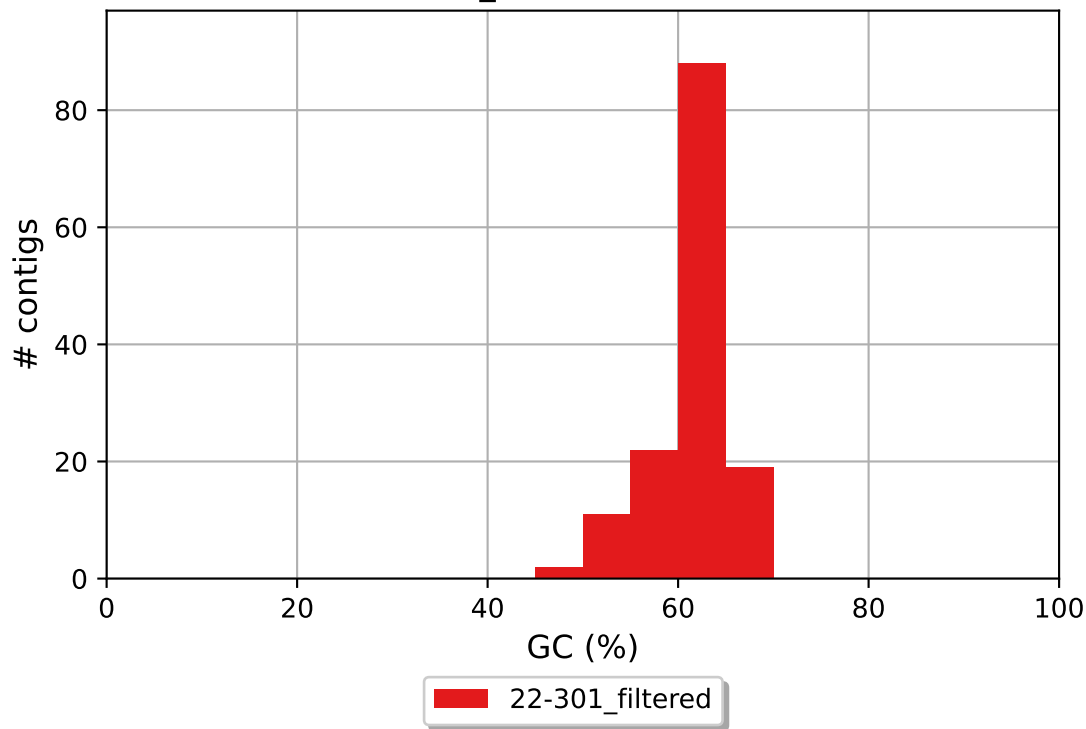
Cumulative length



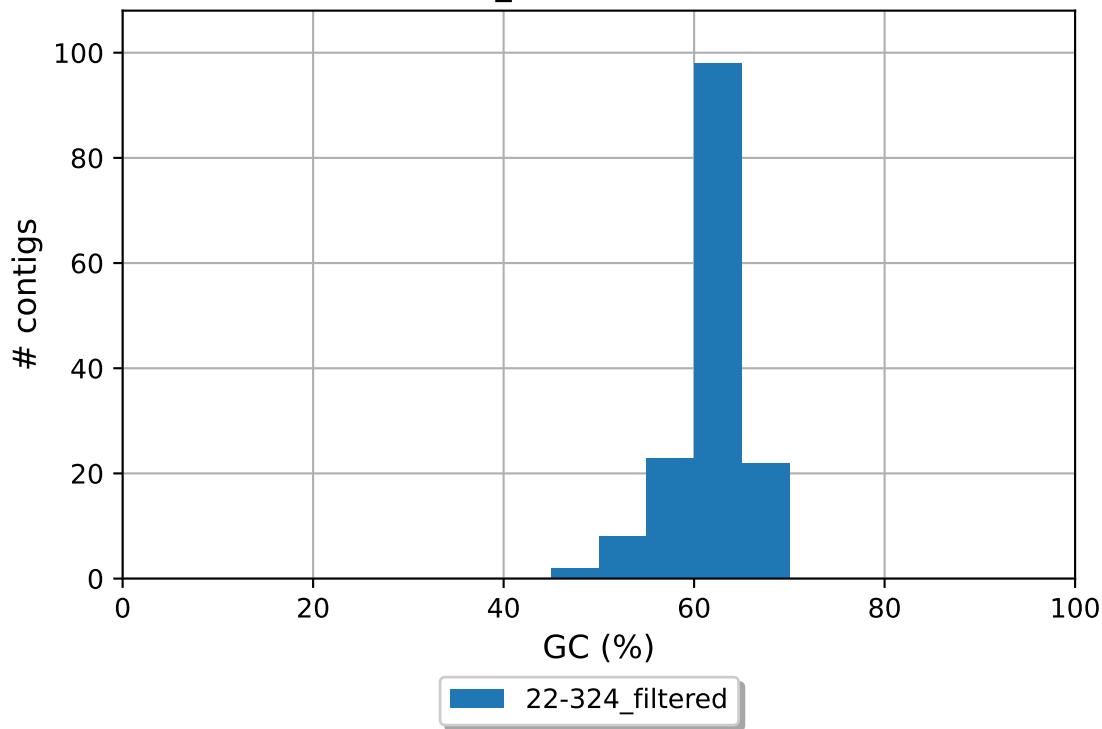
GC content



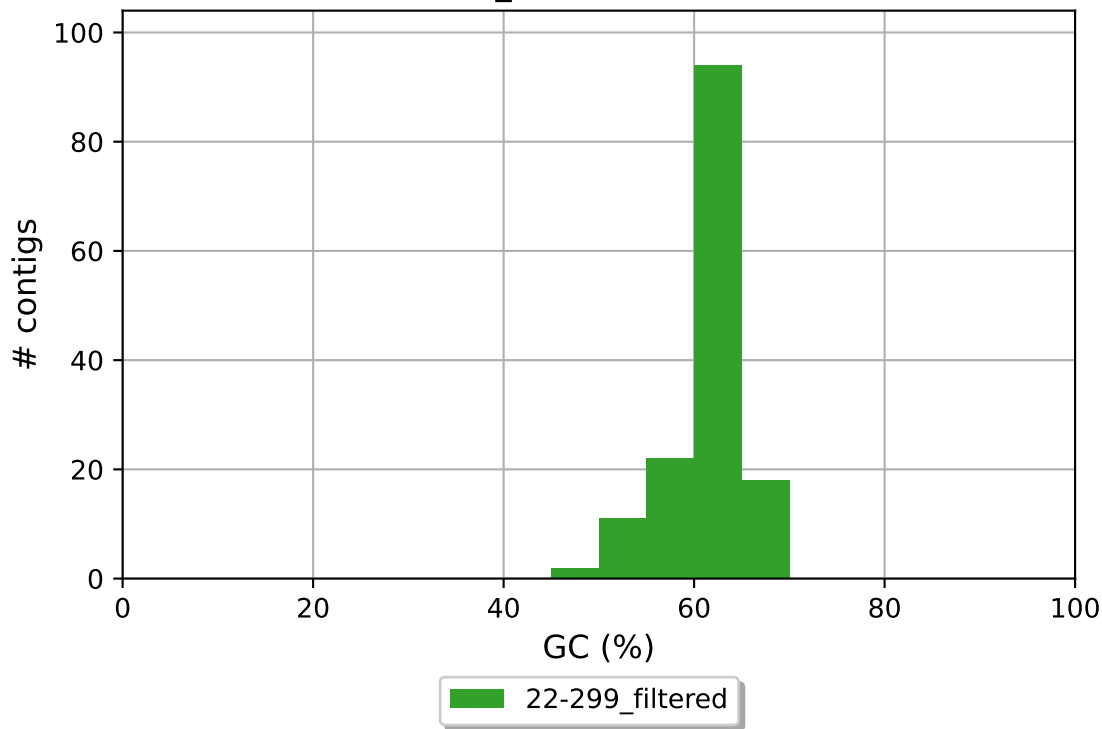
22-301_filtered GC content



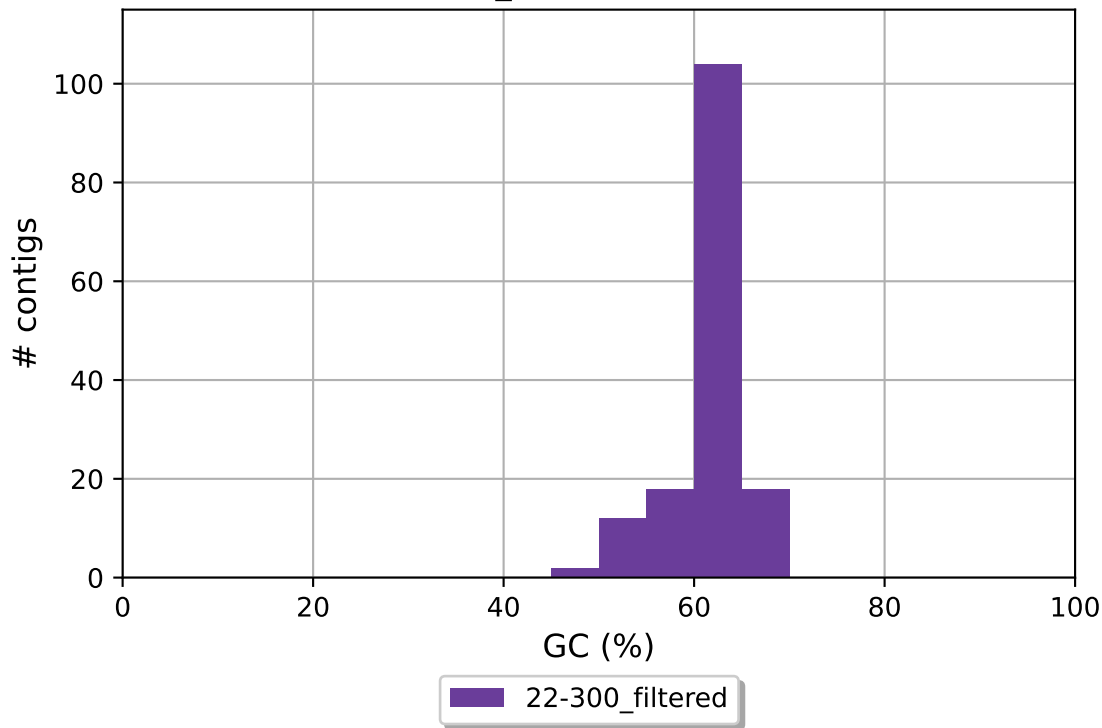
22-324_filtered GC content



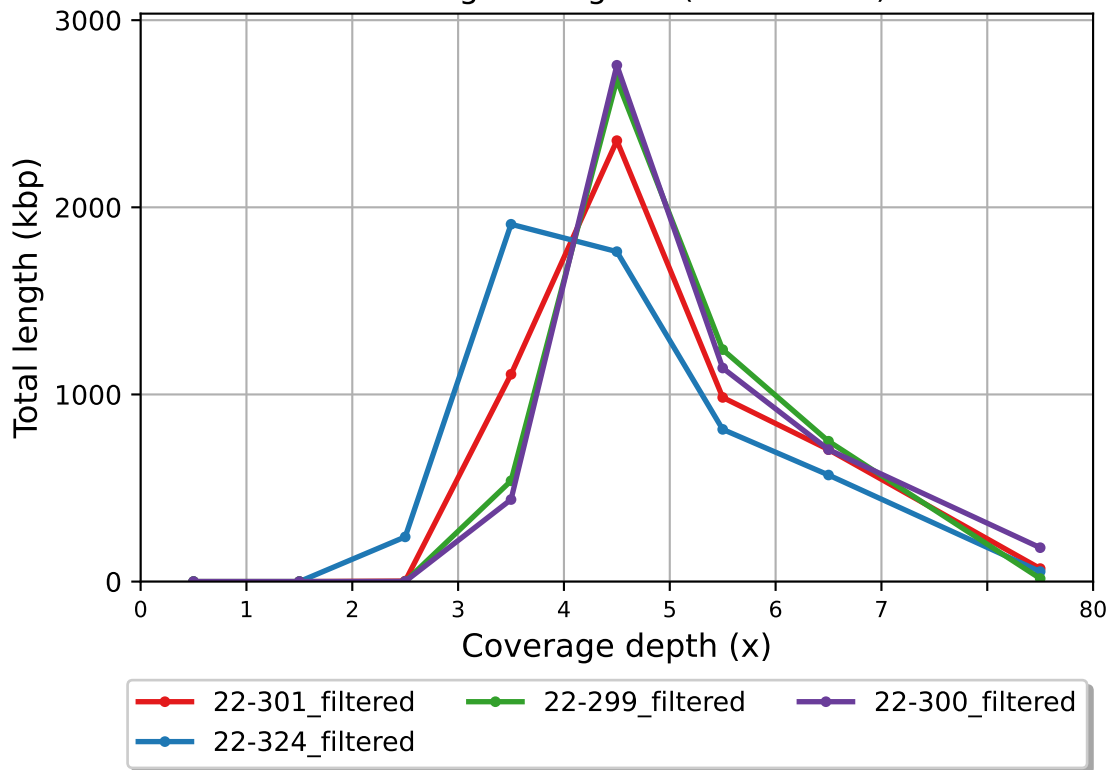
22-299_filtered GC content



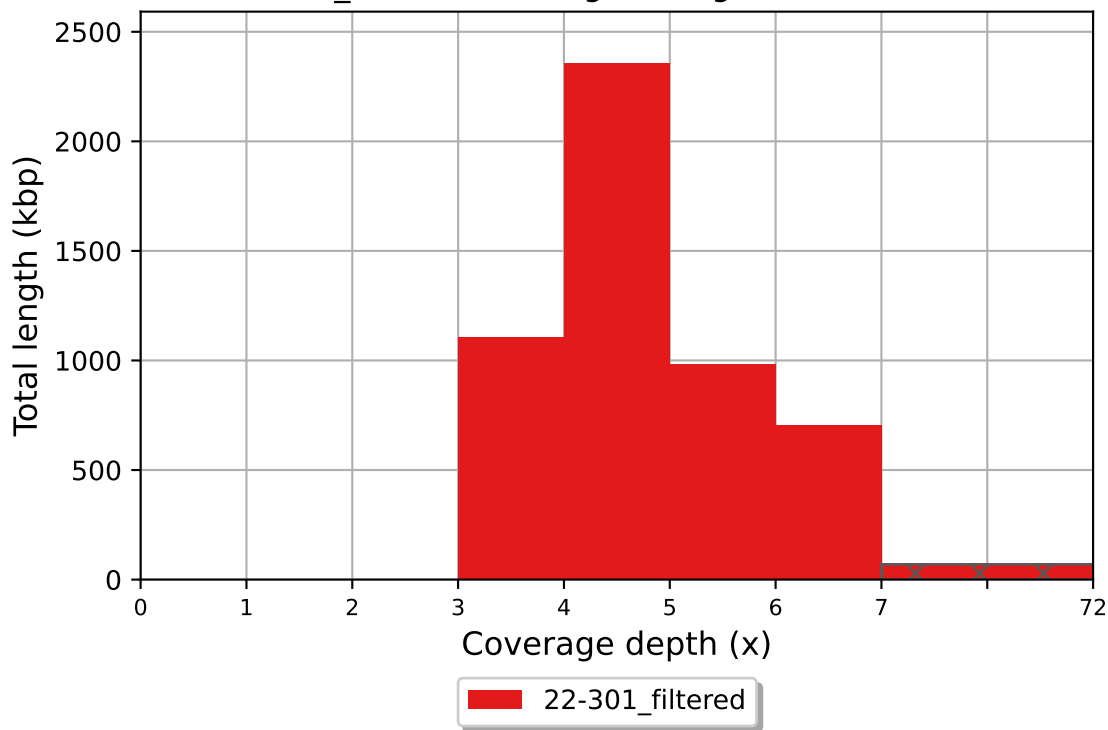
22-300_filtered GC content



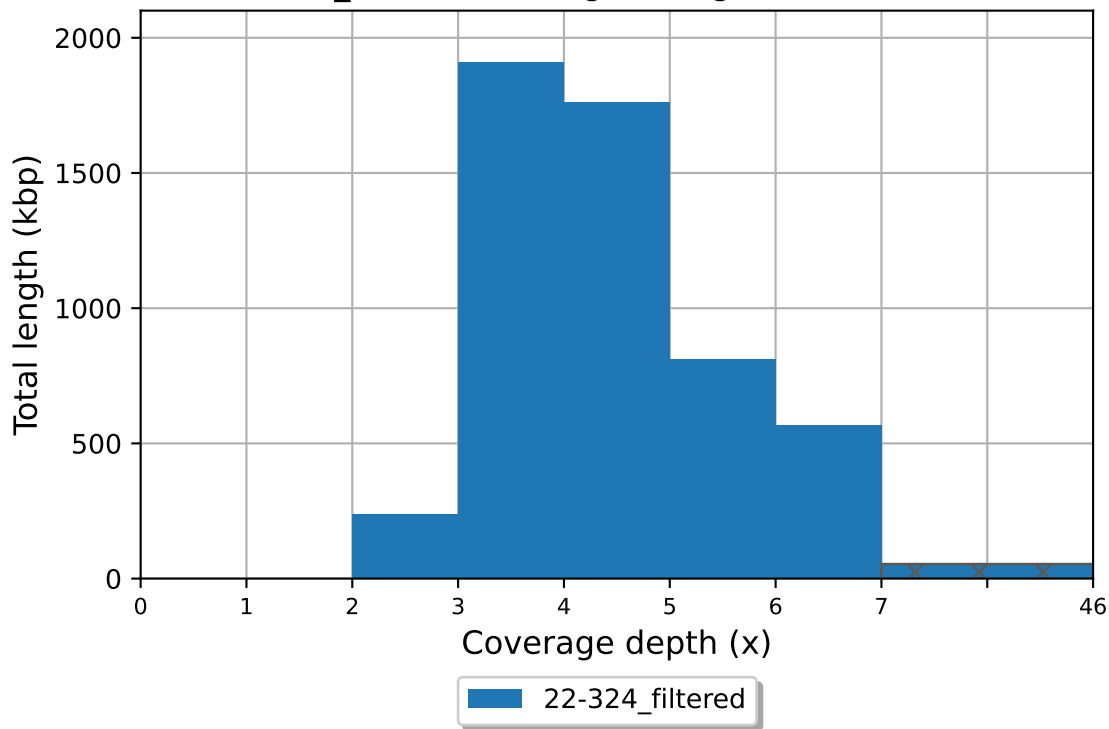
Coverage histogram (bin size: 1x)



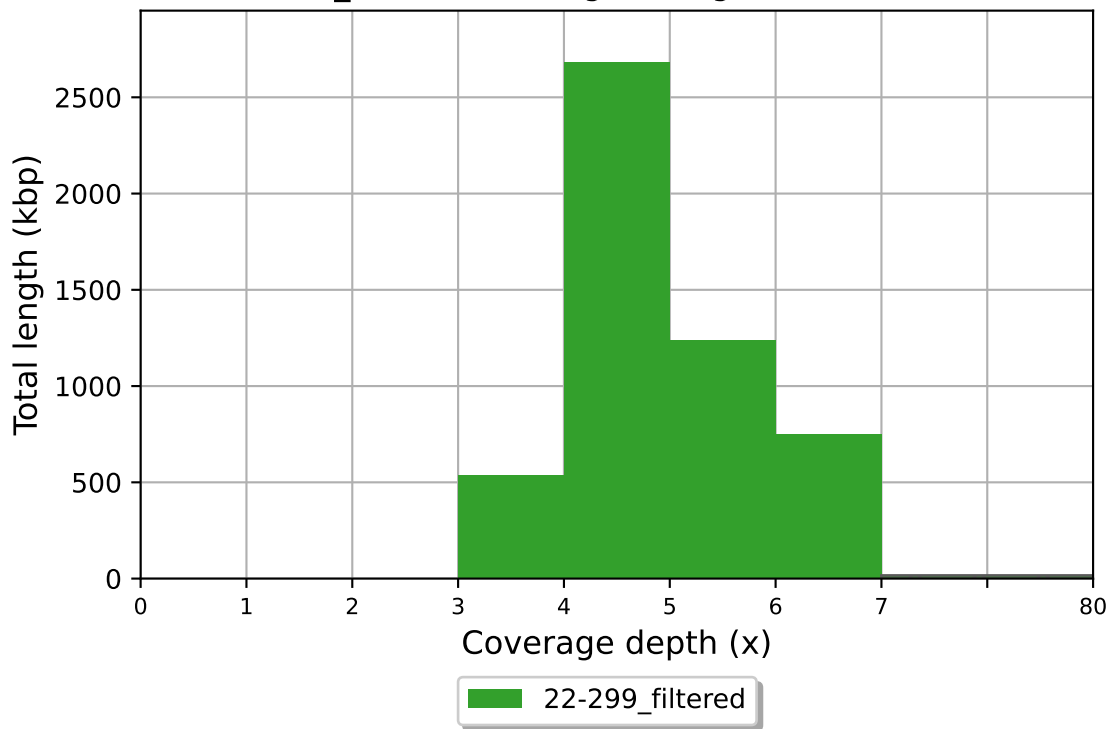
22-301_filtered coverage histogram (bin size: 1x)



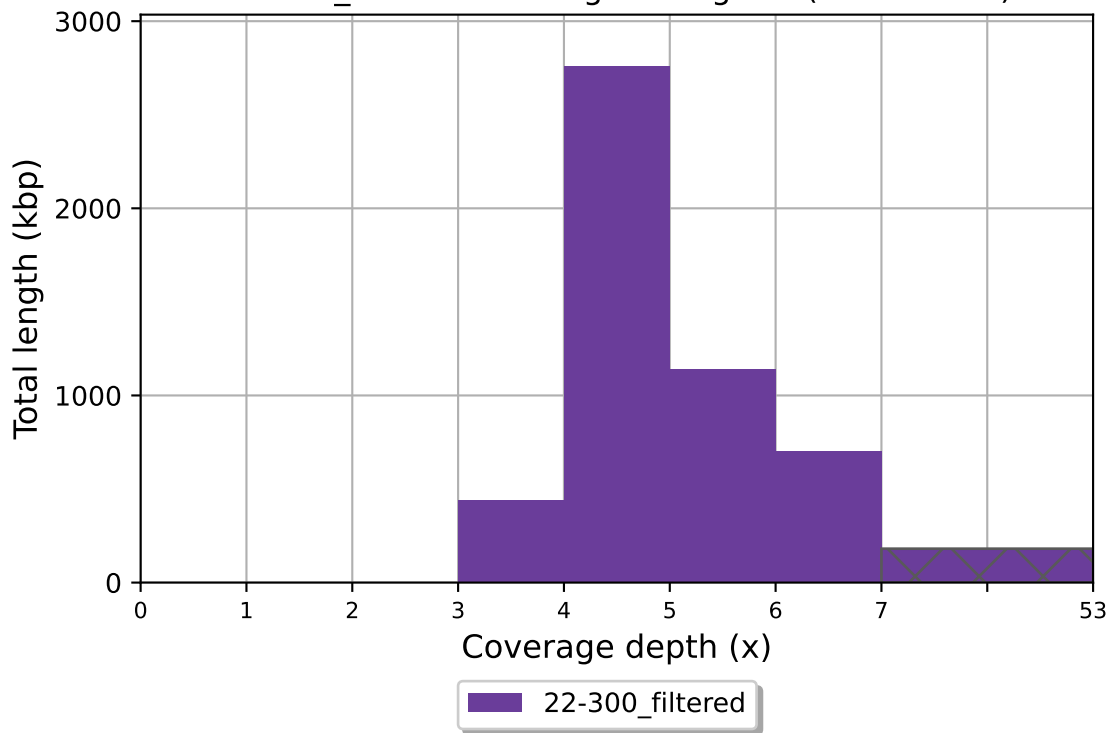
22-324_filtered coverage histogram (bin size: 1x)



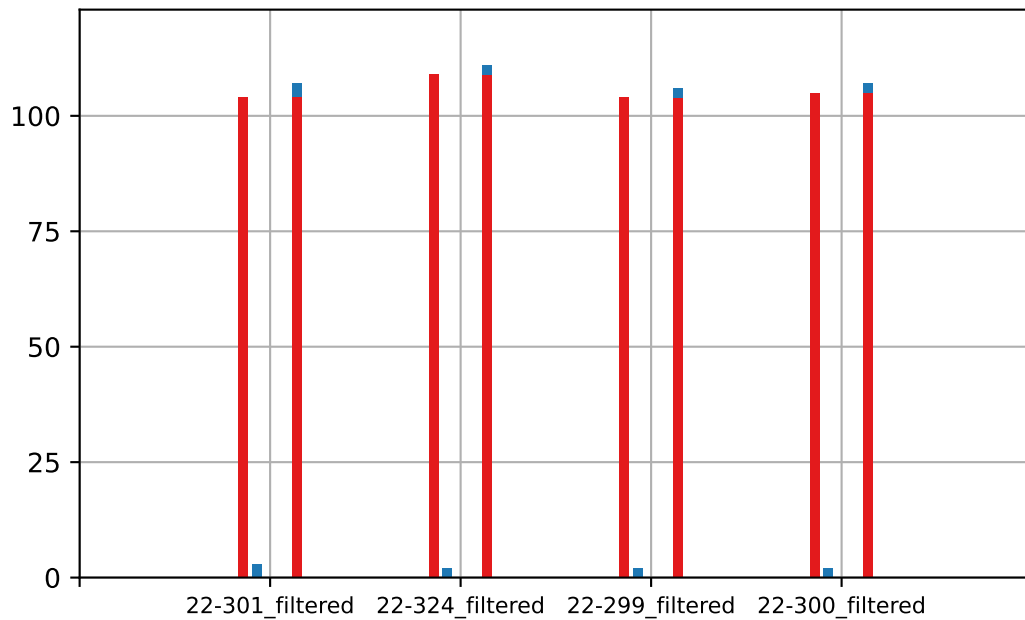
22-299_filtered coverage histogram (bin size: 1x)



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



Misassemblies

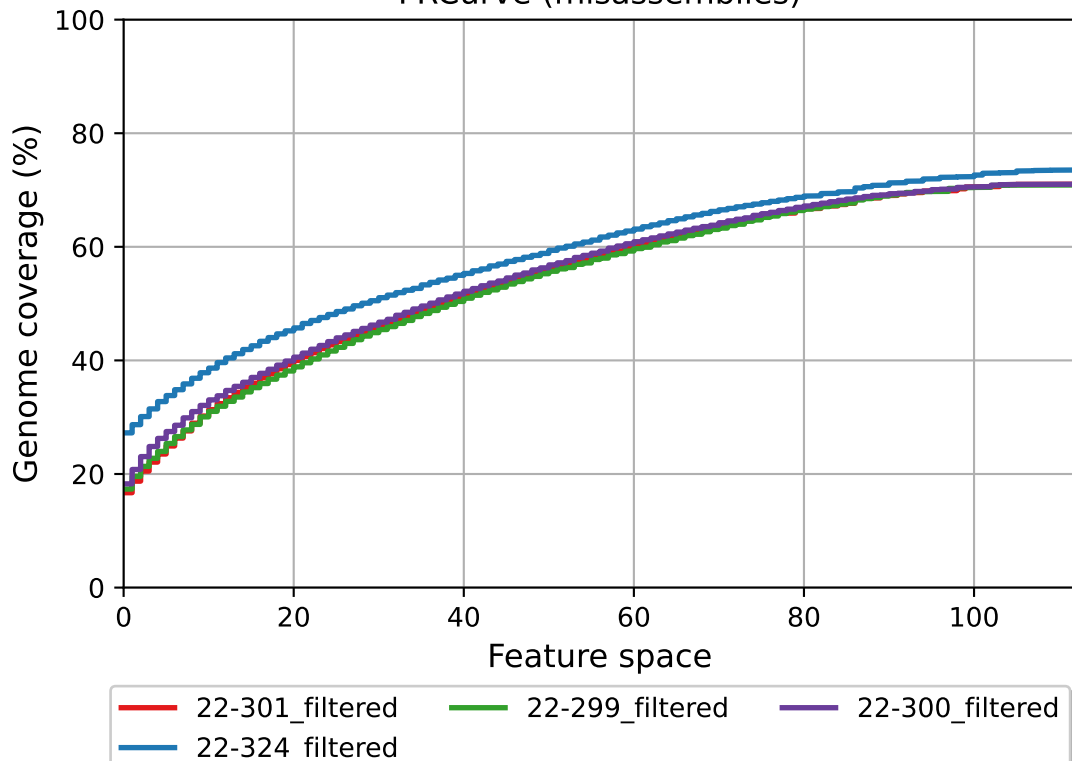


relocations

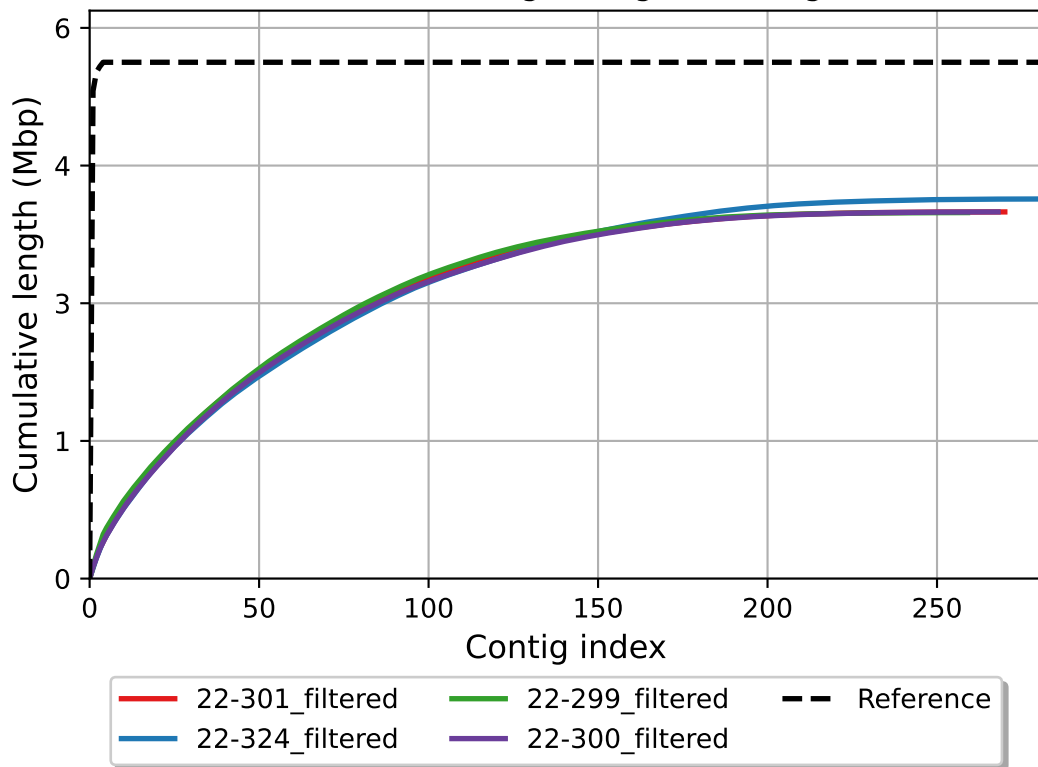


translocations

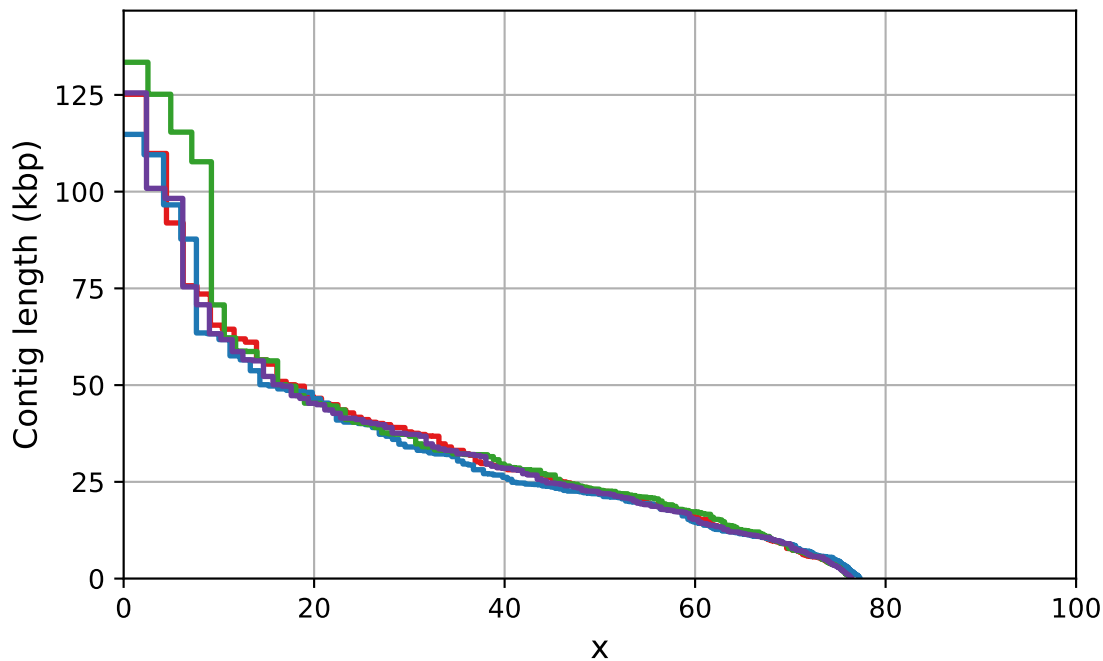
FRCurve (misassemblies)



Cumulative length (aligned contigs)

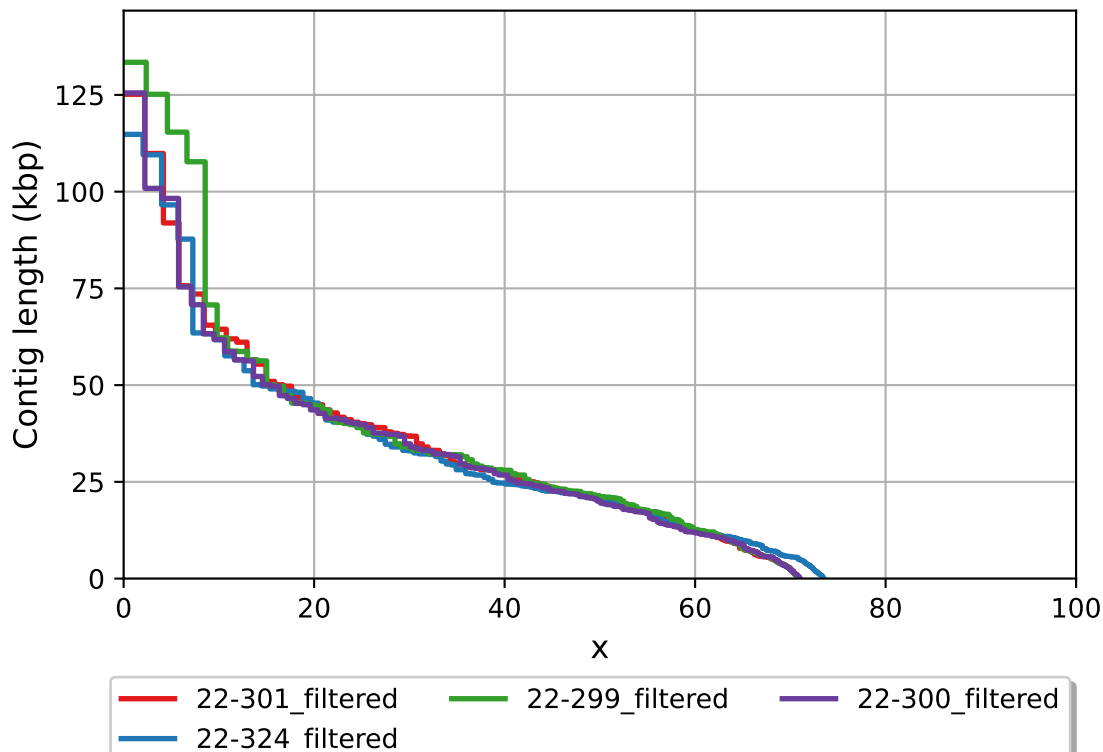


NAx

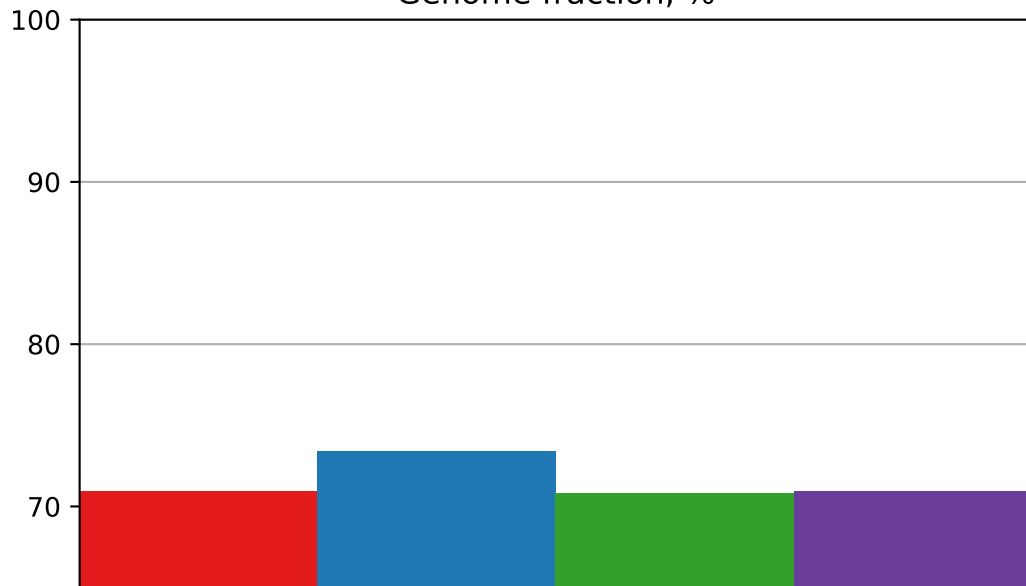


— 22-301_filtered — 22-299_filtered — 22-300_filtered
— 22-324_filtered

NGAx



Genome fraction, %



22-301_filtered

22-299_filtered

22-300_filtered

22-324_filtered